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(71) Applicant (for all designated States except US): WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH [US/US]; Nine Cambridge Center, Cambridge, MA 02142 (US).

(72) Inventors; and
(75) Inventors/Applicants (for US only): LANDER, Eric, S. [US/US]; 151 Bishop Allen Drive, Cambridge, MA 02138 (US). WANG, David [CN/US]; Apartment 314, 276 Massachusetts Avenue, Arlington, MA 02173 (US). HUDSON, Thomas [CA/US]; 361 Metcalfe Avenue, Westmount, Quebec H3Z 2J2 (CA).

(74) Agents: GRANAHAN, Patricia et al.; Hamilton, Brook, Smith & Reynolds, Two Militia Drive, Lexington, MA 02173 (US).

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(57) Abstract

The invention provides nucleic acid segments of the human genome including polymorphic sites. Allele–specific primers and probes hybridizing to regions flanking these sites are also provided. The nucleic acids, primers and probes are used in applications such as forensics, paternity testing, medicine and genetic analysis.

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BIALLELIC MARKERS

RELATED APPLICATIONS

This application claims priority to U.S. provisional application Serial No. 60/030,455, filed November 6, 1996,

5 the entire teachings of which are incorporated herein by reference.

BACKGROUND OF THE INVENTION

The genomes of all organisms undergo spontaneous mutation in the course of their continuing evolution,

10 generating variant forms of progenitor sequences (Gusella, *Ann. Rev. Biochem.* 55, 831-854 (1986)). The variant form may confer an evolutionary advantage or disadvantage relative to a progenitor form or may be neutral. In some instances, a variant form confers a lethal disadvantage and

15 is not transmitted to subsequent generations of the organism. In other instances, a variant form confers an evolutionary advantage to the species and is eventually incorporated into the DNA of many or most members of the species and effectively becomes the progenitor form. In

20 many instances, both progenitor and variant form(s) survive and co-exist in a species population. The coexistence of multiple forms of a sequence gives rise to polymorphisms.

Several different types of polymorphism have been reported. A restriction fragment length polymorphism

25 (RFLP) Is a variation in DNA sequence that alters the length of a restriction fragment (Botstein *et al.*, *Am. J. Hum. Genet.* 32, 314-331 (1980)). The restriction fragment length polymorphism may create or delete a restriction site, thus changing the length of the restriction fragment.

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RFLPs have been widely used in human and animal genetic analyses (see WO 90/13668; WO90/11369; Donis-Keller, *Cell* 51, 319-337 (1987); Lander *et al.*, *Genetics* 121, 85-99 (1989)). When a heritable trait can be linked to a

5   particular RFLP, the presence of the RFLP in an individual can be used to predict the likelihood that the animal will also exhibit the trait.

Other polymorphisms take the form of short tandem repeats (STRs) that include tandem di-, tri- and tetra-

10 nucleotide repeated motifs. These tandem repeats are also referred to as variable number tandem repeat (VNTR) polymorphisms. VNTRs have been used in identity and paternity analysis (US 5,075,217; Armour *et al.*, *FEBS Lett.* 307, 113-115 (1992); Horn *et al.*, WO 91/14003; Jeffreys, EP

15 370,719), and in a large number of genetic mapping studies.

Other polymorphisms take the form of single nucleotide variations between individuals of the same species. Such polymorphisms are far more frequent than RFLPs, STRs and VNTRs. Some single nucleotide polymorphisms occur in

20 protein-coding sequences, in which case, one of the polymorphic forms may give rise to the expression of a defective or other variant protein and, potentially, a genetic disease. Examples of genes, in which polymorphisms within coding sequences give rise to genetic disease

25 include β-globin (sickle cell anemia) and CFTR (cystic fibrosis). Other single nucleotide polymorphisms occur in noncoding regions. Some of these polymorphisms may also result in defective protein expression (e.g., as a result of defective splicing). Other single nucleotide

30 polymorphisms have no phenotypic effects.

Single nucleotide polymorphisms can be used in the same manner as RFLPs and VNTRs, but offer several advantages. Single nucleotide polymorphisms occur with greater

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frequency and are spaced more uniformly throughout the
genome than other forms of polymorphism. The greater
frequency and uniformity of single nucleotide polymorphisms
means that there is a greater probability that such a
5   polymorphism will be found in close proximity to a genetic
locus of interest than would be the case for other
polymorphisms. The different forms of characterized single
nucleotide polymorphisms are often easier to distinguish
than other types of polymorphism (e.g., by use of assays
10   employing allele-specific hybridization probes or primers).
        Only a small percentage of the total repository of
polymorphisms in humans and other organisms has been
identified. The limited number of polymorphisms identified
to date is due to the large amount of work required for
15   their detection by conventional methods. For example, a
conventional approach to identifying polymorphisms might be
to sequence the same stretch of DNA in a population of
individuals by dideoxy sequencing. In this type of
approach, the amount of work increases in proportion to
20   both the length of sequence and the number of individuals
in a population and becomes impractical for large stretches
of DNA or large numbers of persons.

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SUMMARY OF THE INVENTION

The invention provides nucleic acid sequences comprising nucleic acid segments of from about 10 to about 200 bases as shown in the Table, column 7, including a

5 polymorphic site. Complements of these segments are also included. The segments can be DNA or RNA, and can be double- or single-stranded. Segments can be, for example, 10-20, 10-50 or 10-100 bases long. Preferred segments include a biallelic polymorphic site. The base occupying

10 the polymorphic site in the segments can be the reference (Table, column 3) or an alternative base (Table, column 4).

The invention further provides allele-specific oligonucleotides that hybridize to a segment of a fragment shown in the Table, column 7, or its complement. These

15 oligonucleotides can be probes or primers. Also provided are isolated nucleic acids comprising a sequence shown in the Table, column 7, or the complement thereto, in which the polymorphic site within the sequence is occupied by a base other than the reference base shown in the Table,

20 column 3.

The invention further provides a method of analyzing a nucleic acid from an individual. The method determines which base is present at any one of the polymorphic sites shown in the Table. Optionally, a set of bases occupying a

25 set of the polymorphic sites shown in the Table is determined. This type of analysis can be performed on a number of individuals, who are tested for the presence of a disease phenotype. The presence or absence of disease phenotype is then correlated with a base or set of bases

30 present at the polymorphic sites in the individuals tested.

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DETAILED DESCRIPTION OF THE INVENTION
DEFINITIONS
    An oligonucleotide can be DNA or RNA, and single- or
double-stranded. Oligonucleotides can be naturally
5 occurring or synthetic, but are typically prepared by
synthetic means. The oligonucleotides of the present
invention can comprise all of an oligonucleotide sequence
presented in column 7 of the Table or a segment of such an
oligonucleotide which includes a polymorphic site.
10 Oligonucleotides can be all of a nucleic acid segment as
represented in column 7 of the Table; a nucleic acid
sequence which comprises a nucleic acid segment represented
in column 7 of the Table and additional nucleic acids
(present at either or both ends of a nucleic acid segment
15 of column 7); or a portion (fragment) of a nucleic acid
segment represented in column 7 of the Table which includes
a polymorphic site. Preferred oligonucleotides of the
invention include segments of DNA, or their complements,
which include any one of the polymorphic sites shown in the
20 Table. The segments can be between 5 and 250 bases, and,
in specific embodiments, are between 5-10, 5-20, 10-20, 10-
50, 20-50 or 10-100 bases. The polymorphic site can occur
within any position of the segment. The segments can be
from any of the allelic forms of DNA shown in the Table.
25   Hybridization probes are oligonucleotides which bind in
a base-specific manner to a complementary strand of nucleic
acid. Such probes include peptide nucleic acids, as
described in Nielsen *et al.*, *Science* 254, 1497-1500 (1991).
    As used herein, the term primer refers to a single-
30 stranded oligonucleotide which acts as a point of
initiation of template-directed DNA synthesis under
appropriate conditions (*e.g.*, in the presence of four
different nucleoside triphosphates and an agent for

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polymerization, such as, DNA or RNA polymerase or reverse
transcriptase) in an appropriate buffer and at a suitable
temperature. The appropriate length of a primer depends on
the intended use of the primer, but typically ranges from
5   15 to 30 nucleotides. Short primer molecules generally
require cooler temperatures to form sufficiently stable
hybrid complexes with the template. A primer need not
reflect the exact sequence of the template, but must be
sufficiently complementary to hybridize with a template.
10 The term primer site refers to the area of the target DNA
to which a primer hybridizes. The term primer pair refers
to a set of primers including a 5' (upstream) primer that
hybridizes with the 5' end of the DNA sequence to be
amplified and a 3' (downstream) primer that hybridizes with
15 the complement of the 3' end of the sequence to be
amplified.

As used herein, linkage describes the tendency of
genes, alleles, loci or genetic markers to be inherited
together as a result of their location on the same
20 chromosome. It can be measured by percent recombination
between the two genes, alleles, loci or genetic markers.

As used herein, polymorphism refers to the occurrence
of two or more genetically determined alternative sequences
or alleles in a population. A polymorphic marker or site
25 is the locus at which divergence occurs. Preferred markers
have at least two alleles, each occurring at frequency of
greater than 1%, and more preferably greater than 10% or
20% of a selected population. A polymorphic locus may be
as small as one base pair. Polymorphic markers include
30 restriction fragment length polymorphisms, variable number
of tandem repeats (VNTR's), hypervariable regions,
minisatellites, dinucleotide repeats, trinucleotide
repeats, tetranucleotide repeats, simple sequence repeats,

and insertion elements such as Alu. The first identified allelic form is arbitrarily designated as the reference form and other allelic forms are designated as alternative or variant alleles. The allelic form occurring most

5   frequently in a selected population is sometimes referred to as the wildtype form. Diploid organisms may be homozygous or heterozygous for allelic forms. A diallelic or biallelic polymorphism has two forms. A triallelic polymorphism has three forms.

10   A single nucleotide polymorphism occurs at a polymorphic site occupied by a single nucleotide, which is the site of variation between allelic sequences. -The site is usually preceded by and followed by highly conserved sequences of the allele (e.g., sequences that vary in less

15 than 1/100 or 1/1000 members of the populations).

        A single nucleotide polymorphism usually arises due to substitution of one nucleotide for another at the polymorphic site. A transition is the replacement of one purine by another purine or one pyrimidine by another

20 pyrimidine. A transversion is the replacement of a purine by a pyrimidine or vice versa. Single nucleotide polymorphisms can also arise from a deletion of a nucleotide or an insertion of a nucleotide relative to a reference allele. Typically the polymorphic site is

25 occupied by a base other than the reference base. For example, where the reference allele contains the base "T" at the polymorphic site, the altered allele can contain a "C", "G" or "A" at the polymorphic site.

        Hybridizations are usually performed under stringent

30 conditions, for example, at a salt concentration of no more than 1 M and a temperature of at least 25°C. For example, conditions of 5X SSPE (750 mM NaCl, 50 mM NaPhosphate, 5 mM EDTA, pH 7.4) and a temperature of 25-30°C, or equivalent

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conditions, are suitable for allele-specific probe
hybridizations. Equivalent conditions can be determined by
varying one or more of the parameters given as an example,
as known in the art, while maintaining a similar degree of
5   identity or similarity between the target nucleotide
sequence and the primer or probe used.

     The term "isolated" is used herein to indicate that the
material in question exists in a physical milieu distinct
from that in which it occurs in nature. For example, an
10   isolated nucleic acid of the invention may be substantially
isolated with respect to the complex cellular milieu in
which it naturally occurs. In some instances, the isolated
material will form part of a composition (for example, a
crude extract containing other substances), buffer system
15   or reagent mix. In other circumstance, the material may be
purified to essential homogeneity, for example as
determined by PAGE or column chromatography such as HPLC.
Preferably, an isolated nucleic acid comprises at least
about 50, 80 or 90 percent (on a molar basis) of all
20   macromolecular species present.

I.   Novel Polymorphisms of the Invention

     The novel polymorphisms of the invention are listed in
the Table. The first column of the Table lists the names
assigned to the fragments in which the polymorphisms occur.
25   The fragments are all human genomic fragments. The
sequence of one allelic form of each of the fragments
(arbitrarily referred to as the prototypical or reference
form) has been previously published. These sequences are
listed at http://www-genome.wi.mit.edu/ (all STS's
30   (sequence tag sites)); http://shgc.stanford.edu (Stanford
STS's); and http://ww.tigr.org/ (TIGR STS's). The Web
sites also list primers for amplification of the fragments,

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and the genomic location of fragments. Some fragments are
expressed sequence tags, and some are random genomic
fragments. All information in the websites concerning the
fragments listed in the Table is incorporated by reference

5   in its entirety for all purposes.
        The second column lists the position in the fragment in
which a polymorphic site has been found. Positions are
numbered consecutively with the first base of the fragment
sequence as listed in one of the above databases being

10   assigned the number one. The third column lists the base
occupying the polymorphic site in the sequence in the data
base. This base is arbitrarily designated the reference or
prototypical form, but it is not necessarily the most
frequently occurring form. The fourth column in the Table

15   lists the alternative base(s) at the polymorphic site. The
fifth column of the Table lists a 5' (upstream or forward)
primer that hybridizes with the 5' end of the DNA sequence
to be amplified. The sixth column of the Table lists a 3'
(downstream or reverse) primer that hybridizes with the

20   complement of the 3' end of the sequence to be amplified.
The seventh column of the Table lists a number of bases of
sequence on either side of the polymorphic site in each
fragment. The indicated sequences can be either DNA or
RNA. In the latter, the T's shown in the Table are

25   replaced by U's. The base occupying the polymorphic site
is indicated in EUPAC-IUB ambiguity code.

    II.   Analysis of Polymorphisms
        A.   Preparation of Samples
        Polymorphisms are detected in a target nucleic acid

30   from an individual being analyzed. For assay of genomic
DNA, virtually any biological sample (other than pure red
blood cells) is suitable. For example, convenient tissue

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samples include whole blood, semen, saliva, tears, urine, fecal material, sweat, buccal, skin and hair. For assay of cDNA or mRNA, the tissue sample must be obtained from an organ in which the target nucleic acid is expressed. For
5   example, if the target nucleic acid is a cytochrome P450, the liver is a suitable source.

Many of the methods described below require amplification of DNA from target samples. This can be accomplished by e.g., PCR. *See generally PCR Technology:*
10   *Principles and Applications for DNA Amplification* (ed. H.A. Erlich, Freeman Press, NY, NY, 1992); *PCR Protocols: A Guide to Methods and Applications* (eds. Innis, et al., Academic Press, San Diego, CA, 1990); Mattila *et al.*, *Nucleic Acids Res.* 19, 4967 (1991); Eckert *et al.*, *PCR*
15   *Methods and Applications* 1, 17 (1991); *PCR* (eds. McPherson *et al.*, IRL Press, Oxford); and U.S. Patent 4,683,202.

Other suitable amplification methods include the ligase chain reaction (LCR) (see Wu and Wallace, *Genomics* 4, 560 (1989), Landegren *et al.*, *Science* 241, 1077 (1988),
20   transcription amplification (Kwoh *et al.*, *Proc. Natl. Acad. Sci. USA* 86, 1173 (1989)), and self-sustained sequence replication (Guatelli *et al.*, *Proc. Nat. Acad. Sci. USA*, 87, 1874 (1990)) and nucleic acid based sequence amplification (NASBA). The latter two amplification
25   methods involve isothermal reactions based on isothermal transcription, which produce both single stranded RNA (ssRNA) and double stranded DNA (dsDNA) as the amplification products in a ratio of about 30 or 100 to 1, respectively.

30   B.   Detection of Polymorphisms in Target DNA
There are two distinct types of analysis of target DNA for detecting polymorphisms. The first type of analysis,

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sometimes referred to as de novo characterization, is
carried out to identify polymorphic sites not previously
characterized (i.e., to identify new polymorphisms). This
analysis compares target sequences in different individuals
5   to identify points of variation, i.e., polymorphic sites.
By analyzing groups of individuals representing the
greatest ethnic diversity among humans and greatest breed
and species variety in plants and animals, patterns
characteristic of the most common alleles/haplotypes of the
10   locus can be identified, and the frequencies of such
alleles/haplotypes in the population can be determined.
Additional allelic frequencies can be determined for
subpopulations characterized by criteria such as geography,
race, or gender. The de novo identification of
15   polymorphisms of the invention is described in the Examples
section. The second type of analysis determines which
form(s) of a characterized (known) polymorphism are present
in individuals under test. There are a variety of suitable
procedures, which are discussed in turn.

20   1.   Allele-Specific Probes
         The design and use of allele-specific probes for
analyzing polymorphisms is described by e.g., Saiki et al.,
Nature 324, 163-166 (1986); Dattagupta, EP 235,726, Saiki,
WO 89/11548. Allele-specific probes can be designed that
25   hybridize to a segment of target DNA from one individual
but do not hybridize to the corresponding segment from
another individual due to the presence of different
polymorphic forms in the respective segments from the two
individuals. Hybridization conditions should be
30   sufficiently stringent that there is a significant
difference in hybridization intensity between alleles, and
preferably an essentially binary response, whereby a probe

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hybridizes to only one of the alleles. Some probes are
designed to hybridize to a segment of target DNA such that
the polymorphic site aligns with a central position (e.g.,
in a 15-mer at the 7 position; in a 16-mer, at either the 8
5   or 9 position) of the probe. This design of probe achieves
good discrimination in hybridization between different
allelic forms.

     Allele-specific probes are often used in pairs, one
member of a pair showing a perfect match to a reference
10   form of a target sequence and the other member showing a
perfect match to a variant form. Several pairs of probes
can then be immobilized on the same support for
simultaneous analysis of multiple polymorphisms within the
same target sequence.

15   2.   Tiling Arrays
     The polymorphisms can also be identified by
hybridization to nucleic acid arrays, some examples of
which are described in WO 95/11995. One form of such
arrays is described in the Examples section in connection
20   with de novo identification of polymorphisms. The same
array or a different array can be used for analysis of
characterized polymorphisms. WO 95/11995 also describes
subarrays that are optimized for detection of a variant
form of a precharacterized polymorphism. Such a subarray
25   contains probes designed to be complementary to a second
reference sequence, which is an allelic variant of the
first reference sequence. The second group of probes is
designed by the same principles as described in the
Examples, except that the probes exhibit complementarity to
30   the second reference sequence. The inclusion of a second
group (or further groups) can be particularly useful for
analyzing short subsequences of the primary reference

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sequence in which multiple mutations are expected to occur
within a short distance commensurate with the length of the
probes (e.g., two or more mutations within 9 to 21 bases).

        3. Allele-Specific Primers
5   An allele-specific primer hybridizes to a site on
target DNA overlapping a polymorphism and only primes
amplification of an allelic form to which the primer
exhibits perfect complementarity. See Gibbs, *Nucleic Acid
Res*. 17, 2427-2448 (1989). This primer is used in
10 conjunction with a second primer which hybridizes at a
distal site. Amplification proceeds from the two-primers,
resulting in a detectable product which indicates the
particular allelic form is present. A control is usually
performed with a second pair of primers, one of which shows
15 a single base mismatch at the polymorphic site and the
other of which exhibits perfect complementarity to a distal
site. The single-base mismatch prevents amplification and
no detectable product is formed. The method works best
when the mismatch is included in the 3'-most position of
20 the oligonucleotide aligned with the polymorphism because
this position is most destabilizing to elongation from the
primer (see, e.g., WO 93/22456).

        4. Direct-Sequencing
        The direct analysis of the sequence of polymorphisms of
25 the present invention can be accomplished using either the
dideoxy chain termination method or the Maxam Gilbert
method (see Sambrook *et al.*, *Molecular Cloning, A
Laboratory Manual* (2nd Ed., CSHP, New York 1989); Zyskind
et al., *Recombinant DNA Laboratory Manual*, (Acad. Press,
30 1988)).

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5. Denaturing Gradient Gel Electrophoresis

Amplification products generated using the polymerase chain reaction can be analyzed by the use of denaturing gradient gel electrophoresis. Different alleles can be identified based on the different sequence-dependent melting properties and electrophoretic migration of DNA in solution. Erlich, ed., *PCR Technology, Principles and Applications for DNA Amplification*, (W.H. Freeman and Co, New York, 1992), Chapter 7.

6. Single-Strand Conformation Polymorphism Analysis

Alleles of target sequences can be differentiated using single-strand conformation polymorphism analysis, which identifies base differences by alteration in electrophoretic migration of single stranded PCR products, as described in Orita *et al.*, *Proc. Nat. Acad. Sci.* 86, 2766-2770 (1989). Amplified PCR products can be generated as described above, and heated or otherwise denatured, to form single stranded amplification products. Single-stranded nucleic acids may refold or form secondary structures which are partially dependent on the base sequence. The different electrophoretic mobilities of single-stranded amplification products can be related to base-sequence differences between alleles of target sequences.

III. Methods of Use

After determining polymorphic form(s) present in an individual at one or more polymorphic sites, this information can be used in a number of methods.

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A.   Forensics

Determination of which polymorphic forms occupy a set
of polymorphic sites in an individual identifies a set of
polymorphic forms that distinguishes the individual. *See*
5 *generally* National Research Council, *The Evaluation of*
Forensic DNA Evidence (Eds. Pollard *et al.*, National
Academy Press, DC, 1996). The more sites that are
analyzed, the lower the probability that the set of
polymorphic forms in one individual is the same as that in
10 an unrelated individual. Preferably, if multiple sites are
analyzed, the sites are unlinked. Thus, polymorphisms of
the invention are often used in conjunction with
polymorphisms in distal genes. Preferred polymorphisms for
use in forensics are biallelic because the population
15 frequencies of two polymorphic forms can usually be
determined with greater accuracy than those of multiple
polymorphic forms at multi-allelic loci.

The capacity to identify a distinguishing or unique set
of forensic markers in an individual is useful for forensic
20 analysis. For example, one can determine whether a blood
sample from a suspect matches a blood or other tissue
sample from a crime scene by determining whether the set of
polymorphic forms occupying selected polymorphic sites is
the same in the suspect and the sample. If the set of
25 polymorphic markers does not match between a suspect and a
sample, it can be concluded (barring experimental error)
that the suspect was not the source of the sample. If the
set of markers does match, one can conclude that the DNA
from the suspect is consistent with that found at the crime
30 scene. If frequencies of the polymorphic forms at the loci
tested have been determined (e.g., by analysis of a
suitable population of individuals), one can perform a
statistical analysis to determine the probability that a

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match of suspect and crime scene sample would occur by
chance.

p(ID) is the probability that two random individuals
have the same polymorphic or allelic form at a given
5 polymorphic site. In biallelic loci, four genotypes are
possible: AA, AB, BA, and BB. If alleles A and B occur in
a haploid genome of the organism with frequencies x and y,
the probability of each genotype in a diploid organism is
(see WO 95/12607):

10 Homozygote: $p(AA) = x^2$
Homozygote: $p(BB) = y^2 = (1-x)^2$
Single Heterozygote: $p(AB) = p(BA) = xy = x(1-x)$
Both Heterozygotes: $p(AB+BA) = 2xy = 2x(1-x)$

The probability of identity at one locus (i.e, the
15 probability that two individuals, picked at random from a
population will have identical polymorphic forms at a given
locus) is given by the equation:

$p(ID) = (x^2)^2 + (2xy)^2 + (y^2)^2$.

These calculations can be extended for any number of
20 polymorphic forms at a given locus. For example, the
probability of identity p(ID) for a 3-allele system where
the alleles have the frequencies in the population of x, y
and z, respectively, is equal to the sum of the squares of
the genotype frequencies:

25 $p(ID) = x^4 + (2xy)^2 + (2yz)^2 + (2xz)^2 + z^4 + y^4$

In a locus of n alleles, the appropriate binomial
expansion is used to calculate p(ID) and p(exc).

The cumulative probability of identity (cum p(ID)) for
each of multiple unlinked loci is determined by multiplying
30 the probabilities provided by each locus.

cum $p(ID) = p(ID1)p(ID2)p(ID3) \ldots p(IDn)$

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The cumulative probability of non-identity for n loci (i.e. the probability that two random individuals will be different at 1 or more loci) is given by the equation:

cum p(nonID) = 1-cum p(ID).

If several polymorphic loci are tested, the cumulative probability of non-identity for random individuals becomes very high (e.g., one billion to one). Such probabilities can be taken into account together with other evidence in determining the guilt or innocence of the suspect.

B. Paternity Testing

The object of paternity testing is usually to determine whether a male is the father of a child. In most cases, the mother of the child is known and thus, the mother's contribution to the child's genotype can be traced. Paternity testing investigates whether the part of the child's genotype not attributable to the mother is consistent with that of the putative father. Paternity testing can be performed by analyzing sets of polymorphisms in the putative father and the child.

If the set of polymorphisms in the child attributable to the father does not match the set of polymorphisms of the putative father, it can be concluded, barring experimental error, that the putative father is not the real father. If the set of polymorphisms in the child attributable to the father does match the set of polymorphisms of the putative father, a statistical calculation can be performed to determine the probability of coincidental match.

The probability of parentage exclusion (representing the probability that a random male will have a polymorphic form at a given polymorphic site that makes him

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incompatible as the father) is given by the equation (see WO 95/12607):

p(exc) = xy(1-xy)

where x and y are the population frequencies of alleles A and B of a biallelic polymorphic site.

(At a triallelic site p(exc) = xy(1-xy) + yz(1- yz) + xz(1-xz)+ 3xyz(1-xyz))), where x, y and z and the respective population frequencies of alleles A, B and C).

The probability of non-exclusion is

p(non-exc) = 1-p(exc)

The cumulative probability of non-exclusion (representing the value obtained when n loci are used) is thus:

cum p(non-exc) = p(non-exc1)p(non-exc2)p(non-exc3)....
p(non-excn)

The cumulative probability of exclusion for n loci (representing the probability that a random male will be excluded)

cum p(exc) = 1 - cum p(non-exc).

If several polymorphic loci are included in the analysis, the cumulative probability of exclusion of a random male is very high. This probability can be taken into account in assessing the liability of a putative father whose polymorphic marker set matches the child's polymorphic marker set attributable to his/her father.

C. Correlation of Polymorphisms with Phenotypic Traits
The polymorphisms of the invention may contribute to the phenotype of an organism in different ways. Some polymorphisms occur within a protein coding sequence and contribute to phenotype by affecting protein structure. The effect may be neutral, beneficial or detrimental, or both beneficial and detrimental, depending on the

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circumstances. For example, a heterozygous sickle cell
mutation confers resistance to malaria, but a homozygous
sickle cell mutation is usually lethal. Other
polymorphisms occur in noncoding regions but may exert
5   phenotypic effects indirectly via influence on replication,
transcription, and translation. A single polymorphism may
affect more than one phenotypic trait. Likewise, a single
phenotypic trait may be affected by polymorphisms in
different genes. Further, some polymorphisms predispose an
10   individual to a distinct mutation that is causally related
to a certain phenotype.
        Phenotypic traits include diseases that have known but
hitherto unmapped genetic components (e.g.,
agammaglobulimenia, diabetes insipidus, Lesch-Nyhan
15   syndrome, muscular dystrophy, Wiskott-Aldrich syndrome,
Fabry's disease, familial hypercholesterolemia, polycystic
kidney disease, hereditary spherocytosis, von Willebrand's
disease, tuberous sclerosis, hereditary hemorrhagic
telangiectasia, familial colonic polyposis, Ehlers-Danlos
20   syndrome, osteogenesis imperfecta, and acute intermittent
porphyria). Phenotypic traits also include symptoms of, or
susceptibility to, multifactorial diseases of which a
component is or may be genetic, such as autoimmune
diseases, inflammation, cancer, diseases of the nervous
25   system, and infection by pathogenic microorganisms. Some
examples of autoimmune diseases include rheumatoid
arthritis, multiple sclerosis, diabetes (insulin-dependent
and non-independent), systemic lupus erythematosus and
Graves disease. Some examples of cancers include cancers
30   of the bladder, brain, breast, colon, esophagus, kidney,
leukemia, liver, lung, oral cavity, ovary, pancreas,
prostate, skin, stomach and uterus. Phenotypic traits also
include characteristics such as longevity, appearance

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(e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments.

Correlation is performed for a population of
5 individuals who have been tested for the presence or absence of a phenotypic trait of interest and for polymorphic markers sets. To perform such analysis, the presence or absence of a set of polymorphisms (i.e. a polymorphic set) is determined for a set of the
10 individuals, some of whom exhibit a particular trait, and some of which exhibit lack of the trait. The alleles of each polymorphism of the set are then reviewed to determine whether the presence or absence of a particular allele is associated with the trait of interest. Correlation can be
15 performed by standard statistical methods such as a κ-squared test and statistically significant correlations between polymorphic form(s) and phenotypic characteristics are noted. For example, it might be found that the presence of allele A1 at polymorphism A correlates with
20 heart disease. As a further example, it might be found that the combined presence of allele A1 at polymorphism A and allele B1 at polymorphism B correlates with increased milk production of a farm animal.

Such correlations can be exploited in several ways. In
25 the case of a strong correlation between a set of one or more polymorphic forms and a disease for which treatment is available, detection of the polymorphic form set in a human or animal patient may justify immediate administration of treatment, or at least the institution of regular
30 monitoring of the patient. Detection of a polymorphic form correlated with serious disease in a couple contemplating a family may also be valuable to the couple in their reproductive decisions. For example, the female partner

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might elect to undergo in vitro fertilization to avoid the
possibility of transmitting such a polymorphism from her
husband to her offspring. In the case of a weaker, but
still statistically significant correlation between a

5   polymorphic set and human disease, immediate therapeutic
intervention or monitoring may not be justified.
Nevertheless, the patient can be motivated to begin simple
life-style changes (e.g., diet, exercise) that can be
accomplished at little cost to the patient but confer

10   potential benefits in reducing the risk of conditions to
which the patient may have increased susceptibility by
virtue of variant alleles. Identification of a polymorphic
set in a patient correlated with enhanced receptiveness to
one of several treatment regimes for a disease indicates

15   that this treatment regime should be followed.

For animals and plants, correlations between
characteristics and phenotype are useful for breeding for
desired characteristics. For example, Beitz et al., US
5,292,639 discuss use of bovine mitochondrial polymorphisms

20   in a breeding program to improve milk production in cows.
To evaluate the effect of mtDNA D-loop sequence
polymorphism on milk production, each cow was assigned a
value of 1 if variant or 0 if wildtype with respect to a
prototypical mitochondrial DNA sequence at each of 17

25   locations considered. Each production trait was analyzed
individually with the following animal model:

$$Y_{ijkpn} = \mu + YS_i + P_j + X_k + \beta_1 + \ldots \beta_{17} + PE_n + a_n + e_p$$

where Y_{ijknp} is the milk, fat, fat percentage, SNF, SNF
percentage, energy concentration, or lactation energy

30   record; μ is an overall mean; YS_i is the effect common to
all cows calving in year-season; X_k is the effect common to
cows in either the high or average selection line; β_1 to β_{17}
are the binomial regressions of production record on mtDNA

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D-loop sequence polymorphisms; PE_n is permanent
environmental effect common to all records of cow n; a_n is
effect of animal n and is composed of the additive genetic
contribution of sire and dam breeding values and a

5   Mendelian sampling effect; and e_p is a random residual. It
was found that eleven of seventeen polymorphisms tested
influenced at least one production trait. Bovines having
the best polymorphic forms for milk production at these
eleven loci are used as parents for breeding the next

10 generation of the herd.

     D.   Genetic Mapping of Phenotypic Traits
     The previous section concerns identifying correlations
between phenotypic traits and polymorphisms that directly
or indirectly contribute to those traits. The present

15 section describes identification of a physical linkage
between a genetic locus associated with a trait of interest
and polymorphic markers that are not associated with the
trait, but are in physical proximity with the genetic locus
responsible for the trait and co-segregate with it. Such

20 analysis is useful for mapping a genetic locus associated
with a phenotypic trait to a chromosomal position, and
thereby cloning gene(s) responsible for the trait. *See*
Lander *et al.*, *Proc. Natl. Acad. Sci. (USA)* 83, 7353-7357
(1986); Lander *et al.*, *Proc. Natl. Acad. Sci. (USA)* 84,

25 2363-2367 (1987); Donis-Keller *et al.*, *Cell* 51, 319-337
(1987); Lander *et al.*, *Genetics* 121, 185-199 (1989)).
Genes localized by linkage can be cloned by a process known
as directional cloning. *See* Wainwright, *Med. J. Australia*
159, 170-174 (1993); Collins, *Nature Genetics* 1, 3-6

30 (1992).
     Linkage studies are typically performed on members of a
family. Available members of the family are characterized

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for the presence or absence of a phenotypic trait and for a
set of polymorphic markers. The distribution of
polymorphic markers in an informative meiosis is then
analyzed to determine which polymorphic markers co-
5   segregate with a phenotypic trait. *See, e.g.,* Kerem *et
al., Science* 245, 1073-1080 (1989); Monaco *et al., Nature*
316, 842 (1985); Yamoka *et al., Neurology* 40, 222-226
(1990); Rossiter *et al., FASEB Journal* 5, 21-27 (1991).
         Linkage is analyzed by calculation of LOD (log of the
10   odds) values. A lod value is the relative likelihood of
obtaining observed segregation data for a marker and a
genetic locus when the two are located at a recombination
fraction θ, versus the situation in which the two are not
linked, and thus segregating independently (Thompson &
15   Thompson, *Genetics in Medicine* (5th ed, W.B. Saunders
Company, Philadelphia, 1991); Strachan, "Mapping the human
genome" in *The Human Genome* (BIOS Scientific Publishers
Ltd, Oxford), Chapter 4). A series of likelihood ratios
are calculated at various recombination fractions (θ),
20   ranging from θ = 0.0 (coincident loci) to θ = 0.50
(unlinked). Thus, the likelihood at a given value of θ is:
probability of data if loci linked at θ to probability of
data if loci unlinked. The computed likelihoods are
usually expressed as the $\log_{10}$ of this ratio (i.e., a lod
25   score). For example, a lod score of 3 indicates 1000:1
odds against an apparent observed linkage being a
coincidence. The use of logarithms allows data collected
from different families to be combined by simple addition.
Computer programs are available for the calculation of lod
30   scores for differing values of θ (e.g., LIPED, MLINK
(Lathrop, *Proc. Nat. Acad. Sci. (USA)* 81, 3443-3446
(1984)). For any particular lod score, a recombination
fraction may be determined from mathematical tables. *See*

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Smith et al., *Mathematical tables for research workers in human genetics* (Churchill, London, 1961); Smith, *Ann. Hum. Genet.* 32, 127-150 (1968). The value of θ at which the lod score is the highest is considered to be the best estimate
5   of the recombination fraction.

Positive lod score values suggest that the two loci are linked, whereas negative values suggest that linkage is less likely (at that value of θ) than the possibility that the two loci are unlinked. By convention, a combined lod
10 score of +3 or greater (equivalent to greater than 1000:1 odds in favor of linkage) is considered definitive evidence that two loci are linked. Similarly, by convention, a negative lod score of -2 or less is taken as definitive evidence against linkage of the two loci being compared.
15 Negative linkage data are useful in excluding a chromosome or a segment thereof from consideration. The search focuses on the remaining non-excluded chromosomal locations.

IV.   Modified Polypeptides and Gene Sequences
20   The invention further provides variant forms of nucleic acids and corresponding proteins. The nucleic acids comprise one of the sequences described in the Table, column 8, in which the polymorphic position is occupied by one of the alternative bases for that position. Some
25 nucleic acids encode full-length variant forms of proteins. Similarly, variant proteins have the prototypical amino acid sequences encoded by nucleic acid sequences shown in the Table, column 8, (read so as to be in-frame with the full-length coding sequence of which it is a component)
30 except at an amino acid encoded by a codon including one of the polymorphic positions shown in the Table. That position is occupied by the amino acid coded by the

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corresponding codon in any of the alternative forms shown
in the Table.

   Variant genes can be expressed in an expression vector
in which a variant gene is operably linked to a native or
5   other promoter. Usually, the promoter is a eukaryotic
promoter for expression in a mammalian cell. The
transcription regulation sequences typically include a
heterologous promoter and optionally an enhancer which is
recognized by the host. The selection of an appropriate
10 promoter, for example trp, lac, phage promoters, glycolytic
enzyme promoters and tRNA promoters, depends on the host
selected. Commercially available expression vectors can be
used. Vectors can include host-recognized replication
systems, amplifiable genes, selectable markers, host
15 sequences useful for insertion into the host genome, and
the like.

   The means of introducing the expression construct into
a host cell varies depending upon the particular
construction and the target host. Suitable means include
20 fusion, conjugation, transfection, transduction,
electroporation or injection, as described in Sambrook,
supra. A wide variety of host cells can be employed for
expression of the variant gene, both prokaryotic and
eukaryotic. Suitable host cells include bacteria such as
25 E. coli, yeast, filamentous fungi, insect cells, mammalian
cells, typically immortalized, e.g., mouse, CHO, human and
monkey cell lines and derivatives thereof. Preferred host
cells are able to process the variant gene product to
produce an appropriate mature polypeptide. Processing
30 includes glycosylation, ubiquitination, disulfide bond
formation, general post-translational modification, and the
like.

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The protein may be isolated by conventional means of protein biochemistry and purification to obtain a substantially pure product, *i.e.*, 80, 95 or 99% free of cell component contaminants, as described in Jacoby,

5   *Methods in Enzymology* Volume 104, Academic Press, New York (1984); Scopes, *Protein Purification, Principles and Practice*, 2nd Edition, Springer-Verlag, New York (1987); and Deutscher (ed), *Guide to Protein Purification, Methods in Enzymology*, Vol. 182 (1990). If the protein is

10 secreted, it can be isolated from the supernatant in which the host cell is grown. If not secreted, the protein can be isolated from a lysate of the host cells.

The invention further provides transgenic nonhuman animals capable of expressing an exogenous variant gene

15 and/or having one or both alleles of an endogenous variant gene inactivated. Expression of an exogenous variant gene is usually achieved by operably linking the gene to a promoter and optionally an enhancer, and microinjecting the construct into a zygote. *See* Hogan *et al.*, "Manipulating

20 the Mouse Embryo, A Laboratory Manual," Cold Spring Harbor Laboratory. Inactivation of endogenous variant genes can be achieved by forming a transgene in which a cloned variant gene is inactivated by insertion of a positive selection marker. *See* Capecchi, *Science* 244, 1288-1292

25 (1989). The transgene is then introduced into an embryonic stem cell, where it undergoes homologous recombination with an endogenous variant gene. Mice and other rodents are preferred animals. Such animals provide useful drug screening systems.

30 In addition to substantially full-length polypeptides expressed by variant genes, the present invention includes biologically active fragments of the polypeptides, or analogs thereof, including organic molecules which simulate

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the interactions of the peptides. Biologically active
fragments include any portion of the full-length
polypeptide which confers a biological function on the
variant gene product, including ligand binding, and
5   antibody binding. Ligand binding includes binding by
nucleic acids, proteins or polypeptides, small biologically
active molecules, or large cellular structures.
     Polyclonal and/or monoclonal antibodies that
specifically bind to variant gene products but not to
10 corresponding prototypical gene products are also provided.
Antibodies can be made by injecting mice or other animals
with the variant gene product or synthetic peptide
fragments thereof. Monoclonal antibodies are screened as
are described, for example, in Harlow & Lane, *Antibodies, A*
15 *Laboratory Manual*, Cold Spring Harbor Press, New York
(1988); Goding, *Monoclonal antibodies, Principles and*
Practice (2d ed.) Academic Press, New York (1986).
Monoclonal antibodies are tested for specific
immunoreactivity with a variant gene product and lack of
20 immunoreactivity to the corresponding prototypical gene
product. These antibodies are useful in diagnostic assays
for detection of the variant form, or as an active
ingredient in a pharmaceutical composition.

V.   Kits
25   The invention further provides kits comprising at least
one allele-specific oligonucleotide as described above.
Often, the kits contain one or more pairs of allele-
specific oligonucleotides hybridizing to different forms of
a polymorphism. In some kits, the allele-specific
30 oligonucleotides are provided immobilized to a substrate.
For example, the same substrate can comprise allele-
specific oligonucleotide probes for detecting at least 10,

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100 or all of the polymorphisms shown in the Table.
Optional additional components of the kit include, for
example, restriction enzymes, reverse-transcriptase or
polymerase, the substrate nucleoside triphosphates, means
5   used to label (for example, an avidin-enzyme conjugate and
enzyme substrate and chromogen if the label is biotin), and
the appropriate buffers for reverse transcription, PCR, or
hybridization reactions. Usually, the kit also contains
instructions for carrying out the methods.
10   The following Examples are offered for the purpose of
illustrating the present invention and are not to be
construed to limit the scope of this invention. The
teachings of all references cited herein are hereby
incorporated herein by reference.

15   EXAMPLES
        The polymorphisms shown in the Table were identified by
resequencing of target sequences from three to ten
unrelated individuals of diverse ethnic and geographic
backgrounds by hybridization to probes immobilized to
20 microfabricated arrays or conventional sequencing. The
strategy and principles for design and use of such arrays
are generally described in WO 95/11995. The strategy
provides arrays of probes for analysis of target sequences
showing a high degree of sequence identity to the reference
25 sequences of the fragments shown in the Table, column 1.
The reference sequences were sequence-tagged sites (STSs)
developed in the course of the Human Genome Project (see,
e.g., Science 270, 1945-1954 (1995); Nature 380, 152-154
(1996)). Most STS's ranged from 100 bp to 300 bp in size.
30   A typical probe array used in this analysis has two
groups of four sets of probes that respectively tile both
strands of a reference sequence. A first probe set

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comprises a plurality of probes exhibiting perfect
complementarily with one of the reference sequences. Each
probe in the first probe set has an interrogation position
that corresponds to a nucleotide in the reference sequence.
5   That is, the interrogation position is aligned with the
corresponding nucleotide in the reference sequence, when
the probe and reference sequence are aligned to maximize
complementarily between the two. For each probe in the
first set, there are three corresponding probes from three
10 additional probe sets. Thus, there are four probes
corresponding to each nucleotide in the reference sequence.
The probes from the three additional probe sets are
identical to the corresponding probe from the first probe
set except at the interrogation position, which occurs in
15 the same position in each of the four corresponding probes
from the four probe sets, and is occupied by a different
nucleotide in the four probe sets. In the present
analysis, probes were 25 nucleotides long. Arrays tiled
for multiple different references sequences were included
20 on the same substrate.

      Multiple target sequences from an individual were
amplified from human genomic DNA using primers for the
fragments indicated in the listed Web sites. The amplified
target sequences were fluorescently labelled during or
25 after PCR. The labelled target sequences were hybridized
with a substrate bearing immobilized arrays of probes. The
amount of lable bound to probes was measured. Analysis of
the pattern of label revealed the nature and position of
differences between the target and reference sequence. For
30 example, comparison of the intensities of four
corresponding probes reveals the identity of a
corresponding nucleotide in the target sequences aligned
with the interrogation position of the probes. The

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corresponding nucleotide is the complement of the
nucleotide occupying the interrogation position of the
probe showing the highest intensity (see WO 95/11995). The
existence of a polymorphism is also manifested by
5   differences in normalized hybridization intensities of
probes flanking the polymorphism when the probes hybridized
to corresponding targets from different individuals. For
example, relative loss of hybridization intensity in a
"footprint" of probes flanking a polymorphism signals a
10   difference between the target and reference (i.e., a
polymorphism) (see EP 717,113). Additionally,
hybridization intensities for corresponding targets from
different individuals can be classified into groups or
clusters suggested by the data, not defined a priori, such
15   that isolates in a give cluster tend to be similar and
isolates in different clusters tend to be dissimilar.
Hybridizations to samples from different individuals were
performed separately. The Table summarizes the data
obtained for target sequences in comparison with a
20   reference sequence for the individuals tested.
       From the foregoing, it is apparent that the invention
includes a number of general uses that can be expressed
concisely as follows. The invention provides for the use
of any of the nucleic acid segments described above in the
25   diagnosis or monitoring of diseases, such as cancer,
inflammation, heart disease, diseases of the CNS, and
susceptibility to infection by microorganisms. The
invention further provides for the use of any of the
nucleic acid segments in the manufacture of a medicament
30   for the treatment or prophylaxis of such diseases. The
invention further provides for the use of any of the DNA
segments as a pharmaceutical.

All publications and patent applications cited above
are incorporated by reference in their entirety for all
purposes to the same extent as if each individual
publication or patent application were specifically and
5   individually indicated to be so incorporated by reference.

1	2	3	4	5	6	7
WI-7070	226	C	T	---		TGTGAAACTCCACTTGAAGCCAAAGAAAGAAAACTCACACTTAAAACACATGCCAGTTGGGAAGGTCT GAAAACTCAGTGCATAATAGGAACACTTGAGACTAATGAAAGAGAGAGTTGAGACCAATCTTTATTT GTACTGGCCAAATACTGAATAAACAGTTGAAGGAAAGACATTGGAAAAAGCTTTTGAGGATAATGT TACTAGACTTTATGCCATGGTGCTTT[C/T]AGTTTAATGCTGTGTCTCTGTCAG
WI-10744	61	G	C	---		AAGCCATTGACGTAACATCTCAGAGGTTATTTGCATGGAGGTTGACTCCTGGGACAAAAGGAC[G/C]AA AAACACTCTTCTGTGGGATATCTGTGCAGATAGATGACCCAAGATCAGATGCTACCCAGATGTGTTTT GATAATACATACAAGCCCCTAGGATTTAGATACAATCTTGAAAGAAAACTGAGACAGATAATTCTGAATT AAATGAGGTAAAGTTTCAGGCACTCA
WI-9975	126	C	T	---		GGGCAAATTACCAGCAAAAAAGTCAAATTACCAGCATCAAAGTCAGGTGCAAAGGAGGTAGAACAA TTACAGTAACTATGTCAAATCTTTGTTATATTAGTTATATCTGCCCAATGCCTAGAATA[C/T]AGTG GGTCCCTAATAGTTATTAGTTCCTTTTTCTTCCCTTTCTCAATCTCTGAATTTATTTTATACTTAA GGGATTAGTTACCACCAAAAATGTGTATGTCATTTGATTCATTTGATTCTTACTGAA
WI-8010	247	G	T	---		GCTAGGTTTGTTCTGTTGGCTGTGTCTCTCACTAGACTTGAGATGACTTGATTTACAGTAATCCCTATGT GATGTAACTAGTCTAGACCTTCCTCTCCGCAATTCCCAGTTCAGAAAGTATGCCACAC TCAACCCTTCTCTCCAGTTCATCTGTATTAATTCTTCCCATATTAATTCAAAGGGAGTGGACAGGT CCCTGGCTGAAAAGAAATAAAGAGAGATCCCCAAAGTGGTGGGG[G/T]CTT
WI-5222b	85	G	C	---		GCCCGGCCTATCTTTAATTTAACTGTATCTTTGGTGTTTCTCCATCCTAGGATTCTGCCTTATAAT CTTTGTTCCTGTCTGTA[G/C]ATTACCTGATTCTACTTTTGATACACAAGGCTGATGGCTCACAATGT AGTAGTGCCAATTCTTCAGGTCTCTTGAATTTTTCTCTGCTATTGAGGACATTCCACTTTCTACTTA TCTCGACTCTATAACAACTCCAACAGAA
WI-5222	52	G	C	---		GCCCGGCCTATCTTTAATTTAACTGTATCTTTGGTGTTTCTCCATCCTA[G/C]GATTCGCCTTAT AATCTTTGTCTGTGTGTGATTTACCTGATTACCTGATTCTTCTTGAATTTTTCTCTGCTATTGAGGACATTCCACTTTCTACTTA AGTAGTGGCCAATTCTTCAGGTCTCTTGAATTTTTCTCTGCTATTGAGGACATTCCACTTTCTACTTA TCTCGACTCTATAACAACTCCAACAGAA
WI-8007	242	C	A	---		TATGCACTTCCACAAAAGCGATATAATTTAAAAGTTTTTCATTAGAAATAAGTGTATAAAAATAA ATATGTTATTATAGGCATTTATTAATTACTAACTATAGTCCTTCTTGGAAGGAACACCCAAACCAATACTT ATAAAGTACACATGTAATTTATAGTAACACATATTTACTATATACATATGGAAAAATCATATTCTCACA GAAGAGCTGAACAGACATTCACCAGGATACGACTGTTGGAAC[C/A]AGCTGCTG
WI-9823	97	C	T	---		TCAGTTGCAAAAATTGCTGCCATAAACATGCTTCCGTTGCTTATCTCTGTCGTAAACATGTGTATGTGTTTTGTTAG TCTATATTCACACATATGAGTGAAATTTC[C/T]GGGGCATGGGAAATACATCTTTATGAGACATTGA ACTGCTCACCACTATCATCAGTAGTCATCCATTTAAACAGACCAACAATGTATAAGAATTCCCTTTGTTTTAC ATGCTTCCAATCTGATTTGTATGACTATTGTATGCACAGTTGGATCACC

WI-9651b	105	A T ---	TCTCTACATTCTATGGACAACCTCCATGCCTTTGCACATGCTGATCCCTCCTCCTCCTGGAATTCCTTCCT ACTTGTCCTCATGTACAATTTTCTGCTCGTCCTTCA[A/T]GGGGCAGCTTGCAAGCCTCCCTTTAGAC ACCTCTACAGGTACAGCCGACCATGCCCTACCTCCATGGCACTGCCAGGGACCCTTATAGGCCTCTG TCTTTAAACCTGTAATGGTATATTAATCCTTGGTGTTTGAATGTCTCTC
WI-9651	139	T C ---	TCTCTACATTCTATGGACAACCTCCATGCCTTTGCACATGCTGATCCCTCCTCCTCCTGGAATTCCTTCCT ACTTGTCCTCATGTACAATTTTCTGCTCGTCCTTCAAGGGGCAGCTTGCAAGCCTCCCTTTAGACACCT C[T/C]ACAGGTACAGCCGACCATGCCCTACCTCCATGGCACTGCCAGGGACCCTTATAGGCCTCTGT CTTTAAACCTGTAATGGTATATTAATCCTTGGTGTTTGAATGTCTCTC
WI-7676b	309	A C ---	GTGACCTTCCTGCAGCGTGGAGATGGCACATCCTTGCTCGTCTGGGGACTTGGCCCTGCTATTTATTTTTG TATTTATGTCTTAATCTCTTCCACTGATCGATCCTCCAAGGGTAGATGGGGAGGGTCGTGTGAAGGG GCCGGCTTCTTCTTGGTGCCTGCTGGGTTGCAGGGGCCAGGAAGCGTGTGGACTGCAGCCTTCTGGTGC TCCCCCGTCCTCCTGGAGGCAGCAGTATAGGAGAGAGAGCAAGGATT
WI-7676	139	C T ---	GTGACCTTCCTGCAGCGTGGAGATGGCACATCCTTGCTCGTGGGGACTTGGCCCTGCTATTTATTTTTG TATTTATGTCTTAATCTCTTCCACTGATCGATCCTCCAAGGGTAGATGGGGAGGGTCGTGTGAAGGG GC[C/T]GGCTTCTTCTTGGTGCCTGCTGGGTTGCAGGGGCCAGGAAGCGTGTGGACTGCAGCCTTCTGGTGC GTGCTCCCCCGTCCTCCTGGAGGCAGCAGTATAGGAGAGAGAGCAAGGATT
WI-10072	105	G A ---	CATTATCTGTCCTTGGGTCTGTTCATTCACTTCCTCTCTCCAATGAAGAGGATATTTAAGCATCATT CATCTGGCCCTTTTTGAGTTTGAATATTTTTGT[G/A]TGACTCCTATGCACATGATAAATTTGTTA TGCTTGTCTGTCTCTTATCTTTGTTATAGGAGTTTTGGCCCATGACCCCTTTATGGAGGAAAAGGGA TCACCCCCTTTTGCCTCTACAACCTTATAGATATTTAAATATCTTT
WI-9986	42	A T C ---	TTGGTGTGAACTCAGAATATAGGGAAAATATAAGACAATTTGAA[T/A,C]GTACCCCAGGAAACAAGAG CCCTGCACTTGACTCCAAAAGGAGTTCTATTATTCTGGCGTGTTTCCAGACTTTATTGTATCTTGAGAA GAGAACTGTTTCCCTCTAAATCAGTTTCATCATCTGTATCCAGGGTAGTACTCACAAGAACATGTCA ATATCAATAGCATGCATATGGGGTGTTGTTGGATTCTTAGAACTTATTGCAATT
WI-7041	174	C A ---	GTCTATTGCAGGAGAAACGTCCCTTGCCACTCCCCACTCTCATCAGGCCAAGTGGAGGACTGGCCAGA GGGCCTGCACATGCAAACTCCAGTCCCTGCCTTCCAGAGAGCTGAAAAGGGTCCCTCGGTCTTTTATTT CAGGGCTTTGCATGCCGGCTCTATTCCCCCTCGCCTCTGCCTCTC[C/A]CCACCTTCTTTGGAGCAAGGAGATGC AGCTGTATTGTGTAACAAGCTCATTGTAACAGTGTCTCGTTCATGTAATAA
WI-7224	134	T C ---	ATAAACCCTGTGTGTATGTATCACCCAACTCACTAATTATCAACTTATGTGCTATCAGATATCCTCTCT ACCCTCACGTTATTTGAAGAAAAATCCTAAACATCAAATACTTTCATCCATAAAAATGTCAGCATT[T /C]ATTAAAAAACAATAACTTTTAAAGAAACAATAAGGACAACATTTTCAAATTAATAAAAATAAAG GCATTTTAAGGATGGCCTGTGATTATCTTGGGAAGCAGAGTGATTCATGCTAG

ID	Pos			Sequence
WI-10826	132	A	C	TCTTATTTGCATTTCACAGTAGCCCCATGAAGTAGGTATAAACCAGCCTCTATTTAACATGAGAAGAT GGAGGCCTTTCCAAATGGACTAAGTAAGTGTGTCTCAGGTTTTCCTAATAAGCAAAGACCTGCA[A/C]]CCCTGGCTTCCTGACTCCAAAGCTTATCCCTTCATGCTGTTGCTGTCAGCCAGGACCCCATGCGCA GAAAGCCCAGCCTCTCCATCCCCCAC
TIGR-A004S25	145	G	A	AGATCTGCCATTAGTATTATTCCTTGAAGATACTTGGAGAGATTCATTTTCTTGAGTGGCACTGCAT GCTCATTCAGTGAAAACTTGTGGGGTATAGAAATGGAATGGAGAGTTTCAAACAGCTTGCTGAAAAC TGTACTTTGG[G/A]CTCCAGACTTCACTGTCCTTAGGCATTGAAACCATCACCTGGTTTGCATTCTTC ATGACTGAGGGTAACTTAAAATGACTGAGGTTAACTTAAAAC
WI-1021	24	A	T	AAACACACAGAATCATCAAAGCAC[A/T]ATCTGTGTTTGAGATAAATGATAGTCTGAGTCACCTATG TAAGAAGTAACTCTGAAATAGTAGGATAGTATTATCATTCCTGTAATAGATTCACCTCTCAGCAAT TGGTCTGTGTTTCATTCTATGGAAACTCTCCGTACTGTAATTTCATTCTATGGAAACTCCCCATACTGT AATTGGACAGTTTGGTTCCAC
WI-4687	121	G	T	TAGTATGTCACTGCCATGGTAAGGACTTTGATCACTAGGAAATAAGAACACTTGAATGGTCTTGTCC TTTCAATAAAAGAGTGACACATGTGTTTAGATAAAGGGCACT[G/T]GCAGGAGTGT TTAGGATGAAGAGAGAGATTAAGGAAGATCAGGAGAAGAAAGTAGCAATGGAATGAAAATAG GAGGCCCTGAGATCCACTGGATAATCTAAAAAACCAAGAGAAGAAAGAAACTTGAT
WI-4719b	107	T	G	TTCATTTCCCTTCCAAAATCCTTAGGAAATTTACATTATGGGCTAGTGCTTGGGTGTGAGCGGATT ATGTCTGACGCGCCATGGTGTTCATAAGTGACTTGAGAGTTACTGTGAGAGGCTACACAGAAATCT CTGTGAGGGGCATGTAATTGTATTCAACAATTCTGCTATGCTTCTCAGATTGCAGAAAAATCAC TGCTCAAAATTCCCCACTTGTCAAACTTTTTCACAGGA
WI-4719	70	G	A	TTCATTTCCCTTCCAAAATCCTTAGGAAATTTACATTATGGGCTAGTGCTTTGGGTGTGAGCGGATT AT[G/A]TCTGACGCCATGGTGTTCATAAGTGACTTGAGAGTTACTGTGAGAGGCTACACAGAAATCAC CTGTGAGGGGCCATGTAATTGTATTCATTCAACAATTCCTTAAGACATTTTCACAGGA TGCTCAAAATTCCCCACTTGTCAACTTATCATTCCTTAAGACATTTTCACAGGA
WI-9484b	216	G	C	TCAACACGCTTTATTGCCACTTCTGGCTCCCCGTCCCCAGCAAGATTCCTACCCTCTTACCCTGTAGG AATATGAGCTCCGATGCAGGGGAATGGGTGGGGGTGTTACCACTTCTCCTCTGCACACTGCCAAGT TAAAGAAAACCCTGCTTCTGGGAGAGGGACCAGCAGGGAGGAATTCAAGGGCATGTATGGCTC AGTCCCACTTCT[G/C]ACTGCAGAGTATAGGGACCAGGGTTCCAAACTTT
WI-9484	178	G	A	TCAACACGCTTTATTGCCACTTCTGGCTCCCCGTCCCCAGCAAGATTCCTACCCTCTTACCCTGTAGG AATACTGAGCTCCGATGCAGGGGAATGGGTGGGGGTGTTACCACTTCTCCTCTGCACACTGCCAAGT TAAAGAAAACCCTGCTTCTGGGAGAGGGAGGGCCAGACAGG[G/A]AGGAATTCAAGGGCATGTATG GCTCAGTCCCACTTCTGACTGCAGAGTATAGGGACCAGGGTTCCAAACTTT

ID	Position	Allele 1	Allele 2	Sequence
II-7330	207	C	T	AGGATGGAAGGAGACACGGGCAGGGAGAACTCTCTCTGCTAAATCGATAGGAGTCAGTTTTGTCT TAAATGCTGACTACAGCCACCACTGACATGGTTGGCTGGAATTTCTCTTTAATTGTGGCATATAGGTTT GTGACACAAGAAGTCATACTTTGGTGGCTAAGTTTTACTAAGGAAAATAACTGAAAAGATTAAAAG TGAGAG[C/T]TGAAAAGAGAAATGATAATGCTTCCAAACTGTAGCTGTCACAG
II-9443	211	G	A	TTAAAAACAGTTCAGGTTGGTGAAGCAGAAAAAGGGATGGTGATTACAATTTAAATGAATCAGTCACTT GCACAATTAATCCTCTGGCATCATACAAACTGGTTTAATGGCAAATGATGACATCATAGCATGA CCAACACTCATGGAAGGCAGTCTAGAGTCCATCACGCTCACCCTGAGGGGGAAGGCACTGCACCCA CTGACGAGGAC[G/A]ACAGAGACCTTGGACTACAGATGACCACCACATGCCCCACTT
VI-7166	59	C	T	TCTCTCAAAAGAGAAAACAAAACCCCTAAGAGACTGAGTTCTGCAAGCATCAGTTCTA[C/T]GGAT CATCAACAACAAGATTCCTTGTGCAAAATATTTGACTATTCTGTATCTTCATCCTTGACTAAATTCGTG ATTTTCAAGCAGCATCTTCTGGTTAAACTTGTTGTGTGAACAATTGTCGAAAAGAGTCTTCCAAT TAATGCTTTTTATATCTAGGCTACCTGTTGGTTAGATTCAAGGCCCCGAG
VI-7259b	189	T	C (C)	GCTTCTTCCCCAGGAAGCGGGGGTCTTGGCCTGGAACCTTCCAGAGAGGAGGCGGGAGCAATTTTAGCC CCACCCTGCTCCCATCGCCCCCCCTGCAACAGCTGCAGGCTGCTCCTCTCTCTGAGTTCCTCTGGGCT GCGCAGGCGGCTCCCCTGGGAATAGAGCAAGAGACGTGAGTCGTAACCTGGCCACAGT[G/C,T]TGGGGGGAGCAG AGCCAGCAGGTGGACAGGTGTTTGCAGGGGCCCAACTTCCCCTGGAGCTC
VI-7259	188	G	T	GCTTCTTCCCCAGGAAGCGGGGGTCTTGGCCTGGAACCTTCCAGAGAGGAGGCGGGAGCAATTTTAGCC CCACCCTGCTCCCATCGCCCCCCCTGCGACAGCTGCAGGCTCCTCTCTCTGAGTTCCTCTGGGCT GCGCAGGCCCCTGGGAATAGAGCAAGAGACGTGAGTCGTAACCTGGCCACAGTGAGTCGTAACCTGGCCACA GAGCCAGCAGGTGGACAGGTGTTTGCAGGGGCCCAACTTCCCCTGGAGC
VI-7322	275	A	G	GTACTTTAGGCTGTGTGGAGGGTGGGCATTTAGTGGTGAACCTTGCCACCAGGGTTTCTAACAGATGAC CCTGTGAATCATAATTTAAACCTGCATATATTTATAGCCAGTCACATTGCCCCTCTCACCCTATATG GCCATAAACTGCCTAAGCACTCAGCCTCACCCCTTTGACCAGAGAAAGAGCACTC TGGTTCTCTATCCCCTTGTCACATAGAGAGTTTGTCATGGGCCCTGGCTG
VI-7685	46	T	C	TCAGTTCTAGTCTCTCTGGGGCCACACAGAAACTCTTTTGGGCTC[T/C]TTTCTCCCCTCTGGATCA AAGTAGGCAGGACCATGGACCAGGTCTTGAGCGCCTCTCACCTGTACTCTTCCGAAAAATCCT CTTCCTCTGAGCGCTGGATCCTAGCCTTATCCTCTCTGATCTCCATGGCTTCCTCCTCCTCCCTCCTGCCGACTC CTGGGTTGAGCTGTTGCCTCAGTCCCCCAACAGATGCTTTTCTGTCTC
VI-563	87	G	A	TGTGACCAAATTGTTATTTAGAGAGGGTTAACAATGGCCTGACTATCACCTGATGGTGCGCCAGAATTTC CTGGGGGAGGGAGGCCTCCCCT[G/A]CCCTGACTCATGTTCATCTAACAATACTACTCC TGTGGTATGGGGATCCTAAGCCAAAAAGCTGAAATGAACATGTTCTAGCACTACAGAAAATCCATACT GCCCCTCAGTAAAGGCAAATTTAAATCTCTTTGGATAACCCAGGGCACAT

WI-931c	191	C A	GACCAGGGCACCAGAAAGCCACGGAAGCCACTAGCCCTGAACCTTGCACACCCCTGGAGTT TCTCTCCCCTCCCTATCCCCTCACCAACACCTTCCAGTGCTTATTCTGCTGTGTCAAAATGATCCTCT GTTGCTGCACTGTCATTACTGTATGGGGAAAGATGTGTCAGA
			TACAGAAAGGCATGGGGAAAGATGTGTCAGA
WI-931b	81	A G	GACCAGGGCACCAGAAAGCCACGGAAGCCACTAGCCCTGAACCTTGCACACCCCTGGAGTT TCTCTCCCCTCCCT[A/G]TCCCCTCACCAACACCTTCCAGTGCTTATTCTGCTGTGTCAAAATGATCCT TCTGTTGCTGCACTGTCATTACTGTTGTATGGATTTATAATTATTGTCCAAAAAAGCCCCGAGCCTGG
			TACAGAAAGGCATGGGGAAAGATGTGTCAGA
WI-931	31	A G	GACCAGGGCACCAGAAAGCCACGGAAGCCAC[A/G]GCCACTAGCCCTGAACCTTGCACACCCCTGGA GTTCTCTCCCCTCCCTATCCCCTCACCAACACCTTCCAGTGCTTATTCTGCTGTGTCAAAATGATCCT TCTGTTGCTGCACTGTCATTACTGTTGTATGGATTTATAATTATTGTCCAAAAAAGCCCCGAGCCTGG
			TACAGAAAGGCATGGGGAAAGATGTGTCAGA
WI-10870b	91	C T	GGATGACTTACCCAATAGCAGGGTGGGTACATTCATGGGTAACAACACCCTGGACTGGGATGGCAGA GACATCCACCTTAGCAAAGTGGGG[C/T]ACCTACTAGAGACAGTCAGTGGAGTACCCTGAGTACGACCCCC TTAGCAGCAGAATTACAAGAAATCTTGGGACCTGTACTCCTGATACAAAATAAGGACACATGGGGTCAGC CTGAGCCACTCTTAAACCATGAACCATCACCATTTAAATAACGTTGCCCCCC
WI-10870	103	G A	GGATGACTTACCCAATAGCAGGGTGGGTACATTCATGGGTAACAACACCCTGGACTGGGATGGCAGA GACATCCACCTTAGCAAAGTGGGGCACCTACTAGA[G/A]CAGTGGAGTACCCTGAGTACGACCCCC TTAGCAGCAGAATTACAAGAAATCTTGGGACCTGTACTCCTGATACAAAATAAGGACACATGGGGTCAGC CTGAGCCACTCTTAAACCATGAACCATCACCATTTAAATAACGTTGCCCCCC
WI-7719b	281	T C	AGTTTATTCTTCCAGATGACCAGCAGTAGACAAATGGATACTGAGCAGAGAGTCTTAGGTAAAAGTCTT GGGAAATATTTGGGCATTGGTCTGGCCAAGTCTACAATGTCCAATATCAAGGACAACCACCCTAGC TTCTTAGTGAAGACAATGTACAGTTATCC[A/G]TTAGATCAAGACTACACGGTCTATGAGCAATAATGTG ATTTCTGGACATTGCCCATGTATAAATCCTCACTGATGATTTCAAGCAA
WI-7719	163	A G	AGTTTATTCTTCCAGATGACCAGCAGTAGACAAATGGATACTGAGCAGAGAGTCTTAGGTAAAAGTCTT GGGAAATATTTGGGCATTGGTCTGGCCAAGTCTACAATGTCCAATATCAAGGACAACCACCCTAGC TTCTTAGTGAAGACAATGTACAGTTATCC[A/G]TTAGATCAAGACTACACGGTCTATGAGCAATAAT GTGATTTCTGGACATTGCCCATGTATAAATCCTCACTGATGATTTCAAGCTAAA
WI-10396	72	C A	GCCTTGGAGTATATCTAAACTGTGGCCTCCACTTTCATTTTCTTGAAACATTGCTATCAACTGGGAA GAGT[C/A]T[C/A]TGACTTATGCCCAGTTCCCCTCCAGTTTTATGACGGTTGTTTTCTTTTTGTTA TGCCATTTGAGGGATTGATGTTTCTTAAACTATGAAGTACTTGGCTGTGTCTCTCTCCATTGCTTCAGG
			TTAACAGCCACCATTTGTAAACACTTTGT

NI-10673	94	C	G	TCCCTTTATGCACCCAAGAGATATTTATTAAACACCAATTACGTAGCAGGCCATGGCTCATGGGACC CACCCCCGTGGCACTCATGGAGGGGG[C/G]TGCAGGTTGGAACTATGCAGTGTGCTCCGGCCACACA TCCTGCTGGGCGCCCCTACCCTGCCCCAATTCAATCCTGCCAATAAATCCTGTCTTATTTGTTCATCCTG GAGAATTGAAGGGAGGTCAAGTTGTTTGTCAATGATTTGTCAGAAACCT
NI-7842	57	T	C	CACAGCCATGCCCTTGAGGAGCCGGCCACCAGATGCTGAATCCCTATCCCATTCTGT[T/C]GTATGAG TCCCATTTGCCTTGCAATTAGCATTCTGTCTCCCCAAAAAGAATGTGCTATGAAGCTTTCTTTCCT ACACACTCTGAGTCTCTGAATGAAGCTGAAGGTCTTAGTACCAGAGCTAGTTTTCAGCTGCTCAGAAT TCATCTGAAGAGAGACTTAAGATGAAAGCAAATGATTCAGCTCCCTTATA
NI-7721	145	A	C	CTGCCCTCATCACGCCACTGGAGTCCACACTTGAATTTGGGCAGCTACCACGGGTCTGCCATGCTCTGG AGGAGCAAGGGGGGCCACATCCCACCCCAGCTGTTACCCAGCCCGGGCAGGTGCAGCCCTTCCTCCC TGTCTCTGC[A/C]TCTGACTCTCTTTGAGGTCCCTGTATGTCTCTGACTTCTGTGTGTCCCTCTG TGTCTGCTCTCATCCATTCCTCTTACTGGGGCCTCTAGCCCAA
NI-4767b	173	C	A	TTTCCAGTCTGTTTATCCTTCATTGTCAAAAAGATGCTCTTAGACTGAAATTCATAAAGAGTTCCT CAGGTCTGGGTAATCCTAGATCTTCCTATATCCTTGAGTGTGATGGAGTTGGAGAGGGGTATGTTT CTTGCCTTGAGAAATCCTAGAAAGCAACAGGGATGACA[C/A]AAATCACTAAGGAATTCCACTAAGA CTCCTCTCTAACCCAGAGATTTTTAACCT
NI-4767	50	A	G	TTTCCAGTCTGTTTATCCTTCATTGTCAAAAAGATGCTCTTAGACTGA[A/G]ATTCATAAAGAGTT CCTCAGGTCGTGGGTAATCCTAGATCTTCCTATATCCTTGAGTGTGATGATGGAGAGAGGGTATG TTTCTTGCCTTGAGAAATCCTAGAAAGCACAGGGATGACAAATCACTAAGGAATTCCACTAAGAC TCCTCTAACCCAGAGATTTTTAACCT
NI-7718f	222	C	T	ATTGCACTGAAGTTTTGAAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAAACTGATGCCAAGGAGGTGAGTTGAGTTCAACTACACATGTTCTGGGGGCCGGAGATAGATG ACTTTGCAGATGGAAGAGGTGAAAATGAAGAAGGAAGCTGTGTTGAAACAGAAAATAAGTCAAA AGGAACAAAAATTACAAAGAA[C/T]CATGCAGGAAGGAAAACTATGTATTAAT
NI-7718e	60	T	C	ATTGCACTGAAGTTTTGAAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGA[T/C]GCAA GGATTACAGAAACTGATGCCAAGGAGGTGAGTTGAGTTCAACTACACATGTTCTGGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAAATGAAGAAGGAAGCTGTGTTGAAACAGAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAAT
NI-7718d	31	G	A	ATTGCACTGAAGTTTTGAAATACCTTTGTA[G/A]TTACTCAAGCAGTTACTCCCTACACTGATGCAA GGATTACAGAAACTGATGCCAAGGAGGTGAGTTGAGTTCAACTACACATGTTCTGGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAAATGAAGAAGGAAGCTGTGTTGAAACAGAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAAT

			Sequence
II-7718c	91	C/G	ATTGCACTGAAGTTTTGAAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAAAACTGATGCCAAGGGG[C/G]TGAGTGAGTTCAACTACACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAAGAGGTGAAAATGAAAGAACCATGCAGGAAGGAAAACTATGTATTAAT AAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAAT
II-7718b	248	A/G (C)	ATTGCACTGAAGTTTTGAAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAAAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACACATGTTCTGGGGCCCGGAGATAGATG ACTTTGCAGATGGAAAGAGGTGAAAATGAAAGAAGGAGCTGTGTTGAAACAGAAAAATAAG AGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATT[A/G]AT
II-7718a	42	A/T	ATTGCACTGAAGTTTTGAAATACCTTTGTAGTTACTCAAGC[A/C;T]GTTACTCCCTACACTGATGC AAGGATTACAGAAAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACACATGTTCTGGGGCCCGGAGAT AGATGACTTTGCAGATGGAAAGAGGTGAAAATGAAAGAAGGAGCTGTGTTGAAACAGAAAAATAAG TCAAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTA
II-7227d	99	G/C	AGGGAATTGTGTTGCTCCTGGAGGAAGCCCAGGCATCATTAAACAAGCCAGTAGGTCACCTGGCTTC CGTGGACCAATTCATCTTTCAGACAAGCTTTA[G/C]AGAAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCCAGAAGGGACTGAGCTAAACA GTGTTATTATGGGAAAGGAAATGGCATTGCTTTCAACCAGCGACTAATG
VI-7227c	291	G/A	AGGGAATTGTGTTGCTCCTGGAGGAAGCCCAGGCATCATTAAACAAGCCAGTAGGTCACCTGGCTTC CGTGGACCAATTCATCTTTCAGACAA[G/T]CTTTAGAGAAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCCAGAAGGGACTGAGCTAAACA TTATTATGGGAAAGGAAATGGCATTGCTTTCAACCAGCGACTAATGCAAT
VI-7227b	93	G/T	AGGGAATTGTGTTGCTCCTGGAGG[A/G]AGCCCAGGCATCATTAAACAAGCCAGTAGGTCACCTGGC TTCCGTGGACCAATTCATCTTTCAGAGAAGCTTTAGAGAAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCCAGAAGGGACTGAGCTAAACA GTGTTATTATGGGAAAGGAAATGGCATTGCTTTCAACCAGCGACTAATG
VI-7227a	24	A/G	AGGGAATTGTGTTGCTCCTGGAGG[A/G]AGCCCAGGCATCATTAAACAAGCCAGTAGGTCACCTGGC TTCCGTGGACCAATTCATCTTTAGAGACAAGCTTCAGGAGAAGACTCAGGAAGAGACTCACATGC TTTGGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGCCCAGAAGGGACTGAGCTAAACA GTGTTATTATGGGAAAGGAAATGGCATTGCTTTCAACCAGCGACTAATG
VI-7310b	234	A/C	CCACAATGCCTCTCCCACGATGTCAAGGACTCCTGTCCTGGAGGTGGGAGACAAGGAACCTCCG AAGAGGAAGCAAGAAAGCCGTACTGTCTATGTTGTGATCCTTCATCGAACAAACTGATGCGAAAACT TGAATCTGTTACTGAAATGAGGAGAGAAGGACATGTCTATTGAACTGAGCCAAACACACTGTAAAT ATCCACAGACTCCCTCCCCTGCCCCCATCCCA[A/C]A[A/C]ATGATCTTGAGATTTC

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VI-7310a	64	T	A	---	CCACAATGCCTCTCCCACGATGTCAAGGACTCCTGTCTGTGTCCTGGAGGTGGGAGACAAGGAACC[T/A]CCGAAGAGGAAGCAAGAAAGCCGTACTGTCTATGTGTGATCCTTCATCGAACAAACTGATGCGAAAACTTGAATCTGTTACTGAAATGAGGAGGACATGTCTATTGCTATTGAACTGAGCCAAACACACTGTAAATATCCACAGACTCCCTCCCCTGCCCCCATCCAAATGATCTTGAGATTTC
VI-7878b	162	A	G	---	CCAGCAACACTACACCCTTGTCACCTGCCTGGGACTCCTATGATGGCCTGCTGGTTGATAATAATCAGATCATGCCCAAGACGGGCCCTCCTGATAATCGTCTTGGGCATGATTGCAATGCAAATGCGTCCCTGAGGAGAAAATCTGGGAGGAGCTG[A/G]GTGTGATGAAGGTGTATGTTGGGGAGGAGCACAGTGTCTGTGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAACTA
VI-7878a	51	C	G	---	CCAGCAACACTACACCCTTGTCACCTGCCTGGGACTCCTATGATGGCCTGCTG[C/G]TTGGTTGATAATAATCAGATCATGCCCAAGACGGGCCCTCCTGATAATCGTCTTGGGCATGATTGCAATGCAAATGCGTCCCTGAGGAGAAAATCTGGGAGGAGCTGAGTGTGATGAAGGTGTATGTTGGGGAGGAGCACAGTGTCTGTGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAACTA
VI-7381c	213	C	T	---	CTCCACATTCCCACAGGCCTTGAGCAGAATTTCTGAGACTGAAGGGAAATCCCCCTTTCTTTCTACCAGCCCTGCAAGTTCCTCATGGACGCTCGCGAGGAGCAGGCCAGGTTCCTGCCTATGGTGAGATCAGATGTGGCCAAGGGAAGGAGAGCTCTGGTTCCAGAGAATTGCACAAAGTTCCCTCTGTACAGACAAAACGGCCTC[C/T]GGCTTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
VI-7381b	54	C	G	---	CTCCACATTCCCACAGGCCTTGAGCAGAATTTCTGAGACTGAAGGGAAATCC[C/G]CTTTCTTTCTACCAGCCCTGCAAGTTCCTCATGGACGCTCGCGAGGAGCAGGCCAGGTTCCTGCCTATGGTGAGATCAGATGTGGCCAAGGGAAGGAGAGCTCTGGTTCCAGAGAATTGCACAAAGTTCCCTCTGTACAGAGACAAAACGGCCTCCGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
VI-7381a	53	C	G	---	CTCCACATTCCCACAGGCCTTGAGCAGAATTTCTGAGACTGAAGGGAAATCC[C/G]CCTTTCTTTCTACCAGCCCTGCAAGTTCCTCATGGACGCTCGCGAGGAGCAGGCCAGGTTCCTGCCTATGGTGAGATCAGATGTGGCCAAGGGAAGGAGAGCTCTGGTTCCAGAGAATTGCACAAAGTTCCCTCTGTACAGAGACAAAACGGCCTCCGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
VI-1017b	9.3	G	A	---	AAATTGCTCTATTCGGACCCTCATATTAAATAAGAGCAATGAAGAGCGAGGGAAAATTGAACTCTCAGGTACTGACTGTGGGACCAGACAAG[G/A]GATGTAGATTGTCACATTCAATCCTGAAAACAAACCTGCCAGGCAAGTCTTCTTCCCATTTACAAATAAGGAGACAAAAATTAGGAGATTAAATAACTCATCACTGTTTTCAAAATAAGGAGTGTGTGAGGTTTTGTCCC
VI-1017a	92	G	A	---	AAATTGCTCTATTCGGACCCTCATATTAAATAAGAGCAATGAAGAGCGAGGGAAAATTGAACTCTCAGGTACTGACTGTGGGACCAGACAA[G/A]GGATGTAGATTGTCACATTCAATCCTGAAAACAAACCTGCCAGGCAAGTCTTCCCATTTACAAATAAGGAGACAAAAATTAGGAGATTAAATAACTCATCACTGTTTTCAAAATAAGGAGTGTGTGAGGTTTTGTCCC

VI-1795b	130	T	C	---	GAAGCAACCAGAAAGTATCTTTATCCCCATCTAGATTATGTCTGGGTTCTTCCAGACTCCTACGATTA AATTGTATGCATGTGAACAACTGATGAGGTACTTAGATCTCAGTGCTTTGCAGAAGAAAAG[T/C]C GTCTACCATTTCACCAAATTTCGTAGTACAATTTAAGTATCTCTTGTTATCTCCCCTAGGAGTCTAA AGTGAGCTGGGGAAGGCAGGATTT
VI-1795a	47	T	C	---	GAAGCAACCAGAAAGTATCTTTATCCCCATCTAGATTATGTGTCTGGGT[T/C]CTTCCAGACTCCTACGA TTAAATTGTATGCATGTGAACAACTGATGAGGTACTTAGATCTCAGTGCTTTGCAGAAGAAAAGTC GTCTACCATTTCACCAAATTTCGTAGTACAATTTAAGTATCTCTTGTTATCTCCCCTAGGAGTCTAA AGTGAGCTGGGGAAGGCAGGATTT
VI-0616d	136	G	A	---	CACACAATTTGCAAACACTTCAAAGTGAACGCCCGACATCATCAGCCGTTAACGTCCAGGCCATGT CCCACATAGAGAACGCTTTACTTCCAGGTCTCCTATCACATTGCCA C[G/A]TAGCCCCTCCCTTCCCCTTCCCCCTACAGGCCCTTCAGGGGCCCCAGTCCCCCTCTGAGACTCCC ATGGATCATTCCTGTTTCTGTATCAGGCAGTGATTTAACTCCTTTTTGT
VI-0616c	136	G	A	---	CACACAATTTGCAAACACTTCAAAGTGAACGCCCGACATCATCAGCCGTTAACGTCCAGGCCATGT CCCACATAGAGAACGCTTTACTTCCAGGTCTCCTATCACATTGCCA C[G/A]TAGCCCCTCCCTTCCCCTTCCCCCTACAGGCCCTTCAGGGGCCCCAGTCCCCCTCTGAGACTCCC ATGGATCATTCCTGTTTCTGTATCAGGCAGTGATTTAACTCCTTTTTGT
VI-0616b	141	C	T	---	CACACAATTTGCAAACACTTCAAAGTGAACGCCCGACATCATCAGCCGTTAACGTCCAGGCCATGT CCCACATAGAGAACGCTTTACTTCCCCTTCCCCCTACAGGCCCTTCCTGGTCTCCTATCACATTGCCA CGTAGC[C/T]CTCCCTTCCCCTTCCCCCTACAGGCCCTTCAGGGGCCCCAGTCCCCCTCTGAGACTCCC ATGGATCATTCCTGTTTCTGTATCAGGCAGTGATTTAACTCCTTTTTGT
VI-0616a	116	G	C	---	CACACAATTTGCAAACACTTCAAAGTGAACGCCCGACATCATCAGCCGTTAACGTCCAGGCCATGT CCCACATAGAGAACGCTTTACTTCCCCTTCCCCCTACAGGCCCTTCCTGGTCTCCTATCACATTG CCACGTAGCCCCTCCCTTCCCCTTCCCCCTACAGGCCCTTG[G/C]TCTCCTATCACATTGCCCCCCTCTGAGACTCCC ATGGATCATTCCTGTTTCTGTATCAGGCAGTGATTTAACTCCTTTTTGT
VI-1126c	52	G	A	---	CTCTTATTTCTGGGCACTGCTTCTTGGGGGCAAACTTCCAGTATCACT[G/A]ATACTAATATAA AAACCCTGTAAGTCTGCTTGCATTTCAAGATTCAATATATATCCAGATTGTTTCCCAGCAAAGAA AATTTTATTTCTCAAGATATAAAAAAAATAAATATTAATTCAGTTCCTCAAAAGGAATATGAAATT TGTTAAAATGCAAATCCAGCTGTAACTTTTTGGACTTGTCTTTATTTCTT
VI-1126b	230	T	C	---	CTCTTATTTCTGGGCACTGCTTCTTGGGGGCAAACTTCCAGTATCACTGATGATACTAATATAAAA CCCTGTAAGTCTGCTTGCATTTCAAGATTCAATATATATCCAGATTGTTTCCCAGCAAAGAAATT TTATTTCTCAAGATATAAAAAAAATAAATATTAATTCAGTTCCTCAAAAGGAATATGAAATTTGTT AAAATGCAAATCCAGCTGTAACTTTTTT[T/C]GGACTTGTCTTTATTTCTT

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VI-1126a	97 T C	CTCTTATTCTCTGGGCACTGCTTCTTGGGGGCAAACTTCCAGTATCCACTGATGATCACTAATATAAAAACCCTGTAAGTCTGCTTGCATTTCAAGAT[T/C]CAATATATATCCAGATTGTTTCCCAGCAAAGAAAATTTTATTTCTCAAGATATAAAAAATAAATATTAATTCAGTTCCTCAAAAGGAATATGAAATTTGTTAAAATGCAAATCCAGCTGTAACTTTTTGGACTTGTCTTTATTTCTT
VI-1183c	124 C T	TAGTGCTAATTTTTGGAAAAGTTTGCTGATTTTTAAAAATCTTTTTAAACTTGAAAATTTAGAGTACATATAAATAAATAAAGACCAGATAGGTATTAATTCAGATGTATTTTGCCCTTGT[C/T]ACTAACATTTTTATGACATACAAATGACCAAAAATGATGTTTTATGAAGTGTAGGATAGAGTTTAAATATTGGTATGGTGGTGCTAGAGTTAGTAATGGAA
VI-1183b	192 T C	TAGTGCTAATTTTTGGAAAAGTTTGCTGATTTTTAAAAAATCTTTTTAAACTTGAAAATTTAGAGTACATATAAATAAATAAAGACCAGATAGGTATTAATTCAGATGTATTTTGCCCTTGTCACTAACAATGACATACAAATGACCAAAAATGATGTTTTATGAAGTGTAGGATAGAGTTTAAA[T/C]ATTGGTATGGTGGTGCTAGAGTTAGTAATGGAA
VI-1183a	118 C T	TAGTGCTAATTTTTGGAAAAGTTTGCTGATTTTTAAAAATCTTTTTAAACTTGAAAATTTAGAGTACATATAAATAAATAAAGACCAGATAGGTATTAATTCAGATGTATTTTGC[C/T]CTTGTCACTAACATTTATGACATACAAATGACCAAAAATGATGTTTTATGAAGTGTAGGATAGAGTTTAAATATTGGTATGGTGCTAGAGTTAGTAATGGAA
NI-10770b	174 G A	GCTTGGTTTGCTTAGTCTTATTGTCTCAGTCTTGAGTTCTCCCTTTCTGAGTTCTCCCTTTCAGCCCATACCTGCTCCTATCTGGAGCGGCTCTTCCTGTACTTTCTGTTCACCAACCTCTTTTATTCTTCAGGACACTCA[G/A]TTCACATGCCACATGTCTCGTGACACTGTCTCTTTCACATCTTTCTGTGTCCCTTTCCC
NI-10770a	49 G T	GCTTGGTTTGCTTAGTCTTATTGTCTCAGTCTTGAGTTCTC[G/T]GCCCTTTGTATTTCACCCATACCTCTATCTGGAGCGCTCTTCCTGTACTTTCTCCTGTTCACCAACCTCTTTTATCTTCAGGACACTCAGTTCACATGCCATGGTAGTCAACTAATGGATCTTGGCTTTCACATCTTTCTGTGTCCCTTTCCC
NI-9667b	82 C T	GATGACAACTTCTGCTGTGACCCTTAGTCCTTGCTCATGACACTTTCAATCTCTGCCTTGTATCATGGTTATCACTGGACA[C/T]AGCCACCTCCCCAGCAGGCTTAGAACTCCATGAGTAAGGGACCCTGTCTAATGTGCCGTTTCTCCTTATGGTATTACACACAGTCATAGGCATGGTAGTCAACTAATGGATCTTGGCTGTTTAAACCTTTTCTCTGTACCCAGTACCTAAGTCCAAACTTGCATTCT
NI-9667a	68 G C	GATGACAACTTCTGCTGTGACCCTTAGTCCTTGCTCATGACACTTTCAATCTCTGCCTTGTATCATG[G/C]TTATCACTGGACACAGCCACCTCCCCAGCAGGCTTAGAACTCCATGAGTAGTCAACTAATGGATCTTGGCTATGTGCCGTTTCTCCTTATGGTATTACACACAGTCATAGGCATGGTAGTCAACTAATGGATCTTGGCTGTTTAAACCTTTTCTCTGTACCCAGTACCTAAGTCCAAACTTGCATTCT

VI-0400d	189	A	G	ACATTTTATTAGCAAACAAATCAGCAAAATAATAAATAGAAAGTAATTGCATTCAGACATCTGCTGGTTAACTGTTATAAGATGGTTAGCACACGTAAGCACTTACTAACACAATATTTATTCTAATTTTTCTTTCCCTTACTTACTTGCAAATTATTCAAAGGCGTTAATGCATATATG
VI-10400c	166	A	C	ACATTTTATTAGCAAACAAATCAGCAAAATAATAAATAGAAAGTAATTGCATTCAGACATCTGCTGGTTAACTGTTATAAGATGGTTAGCACACGTAAGCACTTACTAACACAATATTTATTCTAATTTTTCTTTCCCTTACTTACTTGCAAATTATTCAAAGGCGTTAATGCATATATG
VI-10400b	165	A	G	ACATTTTATTAGCAAACAAATCAGCAAAATAATAAATAGAAAGTAATTGCATTCAGACATCTGCTGGTTAACTGTTATAAGATGGTTAGCACACGTAAGCACTTACTAACACAATATTTATTCTAATTTTTCTTTCCCTTACTTACTTGCAAATTATTCAAAGGCGTTAATGCATATATG
VI-10400a	46	T	C	ACATTTTATTAGCAAACAAATCAGCAAAATAATAAATAGAAAGTAAT[T/C]TGCATTCAGACATCTGCTGGTTAACTGTTATAAGATGGTTAGCACACGTAAGCACTTACTAACACAATATTTATTCTAATTTTCTTTCCCTTACTTACTTGCAAATTATTCAAAGGCGTTAATGCATTATG
VI-10809b	78	C	T	AAAGGGCTACAAACTAAGGCCAAAAACCATGAACGGTATAAGGAGGGGAGACCCACCTCTCACCA[C/T]TTAGAAAAAGGGCATTCAAGCACCATTCAATGAGGCTTCATATACTGGTTAGCAAACAAATGGAATGTATTAGCCCAAGGCATGTATGGACCAAAAGTGCCCAGTGATGAGGCCACAGTGAATATCCACCTAACGACCTTCTTGGATGATGTACACATGACATAGGCTTAA
VI-10809a	33	C	T	AAAGGGCTACAAACTAAGGCCAAAAACCATGAAC[C/T]GGTATAAGGAGGGTAAATGCAAGGGGAGACCCCACCCTCTCACCACTTAGAAAAAGGGCATTCAAGCACCATTCAATGAGGCTTCATATACTGGTTAGCAAACAAATGGAATGTATTAGCCCAAGGCATGTATGGACCAAAAGTGCCCAGTGATGAGGCCACAGTGAATATCCACCTAACGACCTTCTTGGATGATGTACACATGACATAGGCTTAA
NI-7038c	266	T	C	CGAGCTTGGGATAAAGCAAGGGGACCTTGGCGCTCTTGGCGCTTCCCTGCCCACATCCAGCTTGTTGTCCCAATGAAATACTGAGATGCTGGGGTCTCGGAGGGTCGGAAGGGTATCTGCATTTATGGTGAGTTCTGAGTCCAAGAAGACTGTCAGGAAGGGTCGGAGTCGTGTAAAACCAGCATACAGTTTGGCTTTTTCACATTGAT
NI-7038b	140	A	C	CGAGCTTGGGATAAAGCAAGGGGACCTTGGCGCTCTCAGCTTTCCCTGCCCACATCCAGCTTGTTGTCCCAATGAAATACTGAGATGCTGGGGTCTCGGAGGGTCGGAAGGGTCGTGTAAAACCAGCATACAGTTTGGCTTTTTCACATTAAGA[A/C]GACTGTCAGGAAGGGTCTGTAAAACCAGCATACAGTTTGGCTTTTTCACATTGATCATTTTTATATGAAATAAAAAGATCCTGCATTTATGGTGAGTTCTGA

ID	Pos	Var	Sequence
I-7038a	31	G/A	CGAGCTTGGGATAAAGCAAGGGGACCTTGGC[G/A]CTCTCAGCTTCCCTGCCACATCCAGCTTGTTG TCCCAATGAAATACTGAGATGCTGGGCTGTCTCCCTCCAGGAATGCTGGGCCCCAGCCTGGCCA GACAAGAAGACTGTCAGGAAGGGTCGGAGTTCGGAGTCTGTAAAACCAGCATACAGTTGGCTTTTTCACATT GATCATTTTATATGAAATAAAAAGATCCTGCATTATGGTGTAGTTCTGA
I-3429b	64	G/T	ATACGCTTTCTGTCTGTCCCACAGTGGAACCAGCACCCAGGTGGCCAGGGTCGGGCTCCACACA[G/T] CCCTCAGCCCCTTCAGCTTGCATGTGTCCATCGGTGACTCAGCACAGAGTTTCCAACCTCATGTGA CAAAAATACAGATTCCCAGTCTCCTCTCTGGATTGGATCTAGCAAGACCAGAGACGGTCCTAGAA TCCTGACTGTTAACAAGCACTCCAGGCAATTCTTAAGACCAAGCACGGAGC
I-3429a	62	C/T	ATACGCTTTCTGTCTGTCCCACAGTGGAACCAGCACCCAGGTGGCCAGGGTCGGGCTCCACACA[C/T]AG CCCTCAGCCCCTTCAGCTTGCATGTGTCCATCGGTGACTCAGCACAGAGTTTCCAACCTCATGTGA CAAAAATACAGATTCCCAGTCTCCTCTGGATTGGATCTAGCAAGACCAGAGACGGTCCTAGAA TCCTGACTGTTAACAAGCACTCCAGGCAATTCTTAAGACCAAGCACGGAGC
I-6786c	151	G/A	ATTTTAGGACAGTGAAAAAAAGGGATTTATAAATAAAATCTATGCCATCCAGGAGGTATGTGTCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCCTTTGGCGAAAGATAAAGAAGTGAGTGACGGTGACCT GTGAGCCCCCATTCTTCT[G/A]TGGGATAAGGTGTCCATTGTTCTTGGAGGGTGAAATGCCACATTC TTTTTGGCAGGGGACACTCCTTCTGGGTGCTCTATTGCTCAGTTTCATCATT
I-6786b	111	A/T	ATTTTAGGACAGTGAAAAAAAGGGATTTATAAATAAAATCTATGCCATCCAGGAGGTATGTGTCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCCTTTGGCGAAAGGAT[A/T]AAGAAGTGAGTGACGGTGA CCTGTGAGCCCCATTCTTCTGTGTGGGATAAGGTGTCCATTGTTCTTGGAGGGTGAAATGCCACATTC TTTTTGGCAGGGGACACTCCTTCTGGGTGCTCTATTGCTCAGTTTCATCATT
I-6786a	106	A/T	ATTTTAGGACAGTGAAAAAAAGGGATTTATAAATAAAATCTATGCCATCCAGGAGGTATGTGTCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCCTTTGGCGAA[A/T]GGATAAAGAAGTGAGTGACGGTGA CCTGTGAGCCCCATTCTTCTGTGTGGGATAAGGTGTCCATTGTTCTTGGAGGGTGAAATGCCACATTC TTTTTGGCAGGGGACACTCCTTCTGGGTGCTCTATTGCTCAGTTTCATCATT
I-6711b	226	G/T	GGCTATTTGTAAATGCTTGGTTATTTGACTCCAAAATTGAATAAGTATTGGGGAAGAATCCCTCACCT ACTTCCAAATCCCTACATATCAATTTACACAAAGCCCCTAAACCTTCAGTTCCAATCACTCTGAAT TTCATATACCTCCATTATTAAATTCAATACATCATTGCAGA[G/T]TGGCAACTAAGTGTAATCTCTAAA TGGTTGGTCGCTGCACACCCACAGTGCCAACTAAGTGTAATCTCTAAA
I-6711a	36	T/C	GGCTATTTGTAAATGCTTGGTTATTTGACTCCAAAA[T/C]TGGCAACTAAGTATTGGGGAAGAATCCCTC ACCTACTTCCAAATCCCTACATATCAATTTACACAAAGCCCCTAAACCTTCAGTTCCAATCACTCT GAATTTCATATACCTCCATTATTAAATTCAATACATCATTGCAGAGAAAAGACAACGGTGCCAACTG GGTTTGGTTGGTCGCTGCACACCCACAGTGCCAACTAAGTGTAATCTCTAAA

0613b	172	A C	ATTGTATGCCAAAATCATATAATACCCTGCATTCTAGAAACATACAGTGTAATAGAATTTTGAGCCATA TGGTGAAAAATTTAGAAGTATTATTCTCTATATGTATATACGTTTAACATCAATGAATGTGATTT TTTGTCAACTTTTGACAAGGCCAGGCAATTTTATTTG[A/C]GCCCTAGGAGGGTTACTATAATTTAGA AAGGCTCTTACCTTCCACTCTATAATTTAAGTCTCGGACTTAGGATGTAG
0613a	44	G A	ATTGTATGCCAAAATCATATACCCTGCATTCTAGAAACATACA[G/A]TGTAATAGAATTTTGAGCC ATATGTGAAAAATTTAGAAGTATTATTCTCTATATGTATATACTGTTAACATCAATGAATGTG ATTTTTGTCAACTTTTGACAAGGCCAGGCAATTTTATTTGAGCCCTAGGAGGGTTACTATAATTTAG AAAGGCTCTTACCTTCCACTCTATAATTTAAGTCTCGGACTTAGGATGTAG
-7587c	133	A T	GCTCTAGTGGGAAACCTCAGGTAGCTCCCGAAGATCTGTGCTTTCCAACAAGTGACTACCCTTGAAGC ACATCCCCTTCTGGATCTGAAAAGAGCCCTTGGCTCAGGGGCGTCTTTTCCAGCCCCTGAGGAAA[A/ T]GGAATGAACCACTCCCTGCCCATTCCCTATAAGAATATCCCAAGACCCAGGCAATTTGCCCCTCT TTCCCACATGCCCCATATGTCTGAGCCAAACTGCACTGGGGGCTGCCCTC
-7587b	81	G A	GCTCTAGTGGGAAACCTCAGGTAGCTCCCGAAGATCTGTGCTTTCCAACAAGTGACTACCCTTGAAGC ACATCCCCTTCTG[G/A]ATCTGAAAAGAGCCCTTGGCTCAGGGGCGTCTTTTCCAGCCCCTGAGGAAA AGGAATGAACCACTCCCTGCCCATTCCCTATAAGAATATCCCAAGACCCAGGCAATTTGCCCCTCTT TCCCACATGCCCCATATGTCTGAGCCAAACTGCACTGGGGGCTGCCCTC
-7587a	28	C T	GCTCTAGTGGGAAACCTCAGGTAGCTCC[C/T]GAAGATCTGTGCTTTCCAACAAGTGACTACCCTTGA AGCACATCCCCTTCTGGATCTGAAAAGAGCCCTTGGCTCGTCTTTTCAGCCCCTGAGGAAA AGGAATGAACCACTCCCTGCCCATTCCCTATAAGAATATCCCAAGACCCAGGCAATTTGCCCCTC TCCCACATGCCCCATATGTCTGAGCCAAACTGCACTGGGGGCTGCCCTC
0681b	103	T A	ATGACTCAGGTGACAAAGAAGAAGCATGTCCTAGACCCCATTGACTTACGCAAACTCAATCAGCCAACC ACAGAAAAGCTAAAGACACATCCTTTTAAAAAAGCC[T/A]AAAGACAGCCATTTAATCCTAATTCG TAGTTTATGATTTTCTCAAAATTCCCCACACAGAAAGAAACTTCAAGGTTAGGTTCTAAATGTTA CCATTGCTAACACTATTGTCTTTGGAGAAGGGAGGAGTGACGCTCTGTTAAAAG
0681a	41	A T	ATGACTCAGGTGACAAAGAAGAAGCATGTCCTAGACCCCATTG[A/T]CTTACGCAAACTCAATCAGCCA ACCACAGAAAAGCTAAAGACATCCTTTTAAAAAAGCCTAAAGACAGCCATTTAATCCTAATTCG TAGTTTATGATTTTCTCAAAATTCCCCACACAGAAAGAAACTTCAAGGTTAGGTTCTAAATGTTA CCATTGCTAACACTATTGTCTTTGGAGAAGGGAGGAGTGACGCTCTGTTAAAAG
-7222c	126	G T	GCCTCTCCTCAACTGTCCTGGACCCAGGCTAGGAAAGGGCTGCTTGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTCACCCTGTTCTCAAGTTGGGGGATGGG[G/T]AATAA AGGAGGGGGAATTCCCTGAACAAGAAGAACTGGGATAGTTATATTTCCACCTGCCCTTGAAGCTT TAAGACAGTGATTTTGTGTAAGGTTGTATTTCAAAGACTCGAATTCATTTT

				Sequence
/I-7222b	255	G	A	GCCTCTCCTCAACTGTCCTGGACCCAAGGCTAGGAAAGGGCTGCTTGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTCACCCTGTCTCCAAGTTGGGGGATGGGGGAATAAAGG AGGGGGAATTCCCTTGAACAAGAAGAACTGGGGATAGTTATATTTCCACCTGCCCTTGAAGCTTTAA GACAGTGATTTTGTGTAAGGTTGTATTTCAAAGACTCGAATTCATTTTCTCA
VI-7222a	126	G	T	GCCTCTCCTCAACTGTCCTGGACCCAAGGCTAGGAAAGGGCTGCTTGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTCACCCTGTTCTCAAGTTGGGGGATGGG[G/T]AATAA AGGAGGGGGAATTCCCTTGAACAAGAAGAACTGGGGATAGTTATATTTCCACCTGCCCTTGAAGCTT TAAGACAGTGATTTTGTGTAAGGTTGTATTTCAAAGACTCGAATTCATTT
VI-8054d	41	C	A	AAAGATGACACTTAGAACTGGATCACTTGGCCCTTCTCTT[C/A]TATCTCCTCCCAGTTCAAAATG CTTGCATCTTTAATAGCCAGCATTCTCTTAGATCTGCAGTTGGGCTCAACGCACTCAAGCCTTAGCA CAATCTCTTGTAGTTTAGCCTTTTCCGGAAAATCGGCTTAGTTTGCCCACCATAGCCACTCTGCT TCCTGTCATAACGCCGCTTTCCCTGGGCGTACAGAGAATCCTTGCCCTT
VI-8054c	237	G	T	AAAGATGACACTTAGAACTGGATCACTTGGCCCTTCTCTTCTTATCTCCTCCCAGTTCAAAATGCTT GCATCTTTAATAGCCAGCATTCTCTTAGATCTGCAGTTGGGCTCAACGCACTCAAGCCTTAGCACAA TCTTCTTGTAGTTTAGCCTTTTCCGGAAAATCGGCTTAGTTTGCCCACCATAGCCACTCTGCTTCC TGTCATAACGCCGCTTTCCCTGGGCGTACAGA[G/T]AATCCTTGCCCTT
VI-8054b	148	T	C	AAAGATGACACTTAGAACTGGATCACTTGGCCCTTCTCTTCTTCTCTCTCCTCCCAGTTCAAAATGCTT GCATCTTTAATAGCCAGCATTCTCTTAGATCTGCAGTTGGGCTCAACGCACTCAAGCCTTAGCACAA TCTTCTTTGTAG[T/C]TTAGCCTTTTCCGGAAAATCGGCTTAGTTTGCCCACCATAGCCACTCTGCT TCCTGTCATAACGCCGCTTTCCCTGGGCGTACAGAGAATCCTTGCCCTT
VI-8054a	131	C	G	AAAGATGACACTTAGAACTGGATCACTTGGCCCTTCTCTTCTCTTCTTATCTCCTCCCAGTTCAAAATGCTT GCATCTTTAATAGCCAGCATTCTCTTAGATCTGCAGTTGGGCTCAACGCACTCAAGCCTTAG[C/G]A CAATCTCTTGTAGTTTAGCCTTTTCCGGAAAATCGGCTTAGTTTGCCCACCATAGCCACTCTGCT TCCTGTCATAACGCCGCTTTCCCTGGGCGTACAGAGAATCCTTGCCCTT
VI-0854b	152	G	T	TTCCACAAAAACTTCCCTGGGCCGGGGTGACTAAGATGGGAGAGAACTGGATAGTTAATAA ATGTTTATATTTACTTAAAGCGAAGTTGAAACA[G/T]GGAGACGATAGTAACGTCTGGTAAGTT ACGGGTGTGCGAGGCAACAGGGAGAGGTACGGGAATAGTTCTACTTCCTTGTTTTTATTCTTGTG TTTTAGACACAGGGTCTGCTGTGTTG
VI-0854a	102	C	T	TTCCACAAAAACTTCCCTGGGCCGGGGTGACTAAGATGAGAAGTGGGAGAACTGGATAGTTAATAA ATGTTTATATTTACTTAAAGCGAAGTTGAAACA[C/T]GAAGACGATAGTAACGTCTGGTAAGTT TATACGGTGTGCGAGGCAACAGGGAGAGGTACGGGAATAGTTCTACTTCCTTGTTTTTATTCTTGTG TTTTAGACACAGGGTCTGCTGTGTTG

I-9826b	127	G/A	---	AATTTTATATGTGAAGGGTTAGCAAACTATGGCCCACAGGCCCATTCTAGCCATGCCTATTTTTGTGTGCCTGATGGCTGTTTGGTGTTTTGCACGCAGTTGAGCCATTGTGACAGAGGCTGTTAT[G/A]GCCTCAAAGCCAAAAAAAAAATTTACTCTCTGGCCTTGACGGGAAAGTTTGCTGATTCTAGATATTTAAAGGCAGAGAGATCAGAAGTGTTGAA
I-9826	125	A/T	---	AATTTTATATGTGAAGGGTTAGCAAACTATGGCCCACAGGCCCATTCTAGCCATGCCTATTTTTGTGTGCCTGATGGCTGTTTGGTGTTTTGCACGCAGTTGAGCCATTGTGACAGAGGCTGTTA[A/T]TGGCCTTCAAAGCCAAAAAAAAAATTTACTCTCTGGCCTTGACGGGAAAGTTTGCTGATTCTAGATATTTAAAGGCAGAGAAGATCAGAAGTGTTGAA
I-15986	60	T/G	TTTGTTTGTGT GTGGGTTTTT / TGACATTATAT AAACGTAAAA GAAAATGT	CGGACACGTGTATATACAAATACAGATCGTATGGGTTTGTTTGTTGTGTGTGGGTTTTTTTTTT[T/G]TTACATTTTCTTTACGTTTATATAAATGTCAGCATTTCAA
I-8655	29	A/G	AACTGCAAAT AGGAAACCAG AG / CCACCTGGGGC TCCC	TTCAAGTAACTGCAAATAGGAAACCAGAG[A/G]GGGGAGCCCCAGGTGGGACAAATCATGGCTACCCCTCCCCAACAGAACAGGGGGAGGAGGTGGCCCCTACACCCTTTAT
I-8170b	259	G/A	---	GCACTTCTCTCTGAGCAACAGGTACACTTTTTTTCTCTAACATTGATCTATAACACACCAGAACCGTGTTTTAATAGTGCTGATAAATGAACCTATTTAAGTACTCTACCAAGATGCTGTGTAAGGTTAGCATTTGGTGGAGAGATTTACAAGGTTAAGATCATGTTCCATCAAAGTGCAATCCTATCAATCAGAAATAAAGGTAAAAGTGACATCTACGGAAAAACATAACAAGA
I-8170a	204	T/A	---	GCACTTCTCTCTGAGCAACAGGTACACTTTTTTTCTCTAACATTGATCTATAACACACCAGAACCGTGTTTTAATAGTGCTGATAAATGAACCTATTTTAAGTACTCTACCAAGATGCTGTGGTAAGGTTAGCATTTGGTGGAGAGATTTACAAGGTTAAGATCATGTTCCATCAAAGTGCAATCCTATCAATCAGAAA[T/A]AAAGGTAAAAGTGACATCTACGGAAAAACATAACAC
I-8172	136	C/G	CCTTTATTAAA ATTGTTTTCTT GGACA / GAAGAGAAAT GTAATACCTGT AAAGGTAC	CAGGATTCCTTAAGTCATCATCTCCAATACTCCAGGTCACATGGTGAAGAGTCACCTGTTAAACACGAAATCTAACCATTAAACAAGCTTTAAAATCCTTCGGTAACTCCCTTATTAAAATTGTTTTCTTGACAT[C/G]AGTACCTTTACAGGTATTACATTTCTCTTCACGTTTACA
I-8183	56	G/A	TGAAATAAAA ACAATTTCTGT TGC / TGTGTTGAAAT CAAACCTGC	AGCAGGGTTTGAAATTGATCCCTTATTTTACATGAAAATAAAACAATTTCTGTTGC[G/A]GCAGGTTTGATTTCAACACAGTTGAATCTGTAAAAACCAAAGCTCGTTTCTGATGCAGGACAAATATCCACAATATTTAAAACTGCAAGCACCATGC
I-14149	83	C/T	---	GCTTTATTGGGATTGCAAGGCTTACAAGGTTAAAGACAAAACCCAAGCATGGGATTTTGCCGGAAATATTAGCGTTAAAGGAG[C/T]TTGAGTTGAGTCAAACACGGG
I-8712	44	G/A	CACAGGGAAG AGGTAGTGGA G / CAGGAAGCCTG ACCATCTC	TCAACAATGACACTGTGTAACAGCACAGGGAAGAGGTAGTGGAG[G/A]GAGATGGTCAGGCTTCCTGTTCCTTAACCAGCAGCAACCCCAGCAACCTAGAAGCGGCCTCACCTAGCCTCTTAAT

ID	Pos	1	2	5′ probe	3′ probe	Sequence
NI-8827	22	C	T	TCCCCTGGGAG ACTATGG	GCGATTAGGAT TTTAGTGTTCA C	GGTGTCCCCTGGGAGACTATGG[C/T]AGTGAACACTAAAATCTAATGCCATGCATTGGAATTATT CCGACTATTACTTCTTTAGTTCCTTCTTATCCACCCAGTCTCT
NI-8833	51	A	T	TCTTCCATGCC ATTCTCTG	CCTCACACATT ATAGGGGCA	CTCCGGCCTCTTAAAGCTCTCTGTGAGACTGTCTCTTCCATGCCATTCTCTG[A/T]TGCCCCTATAATGT GTGAGGGTATTACAATAGTCCCTATTCAAACTGCCTTGTCATAAAAGGTCAGCTATGT
NI-8377	63	A	G	...		ATTTTTTAGCCATGTTGGTAAAAGTTCATTTCAGTACATGGGTAACACCCAGGCCCTTTCCC[A/G]T TATATCCAGGTATGCTACAAGTTCTTTAACTCTTTATCAGAAGTTATTATTACTGTTCCTTAGAGAG GCTACCAGGCTAAAATTCACTTAGTTTGGTTGTCTAATGTCCTAATTTATCCTGAAGCTCGTG
NI-8850	21	A	G	GGGACTTAAC CTTTGGCCT GGCAGG		GAGGGACTTAACCTTTGGCCT[A/G]CCTGGCTGTTGGCTCTGCCGCTTGCTGTTTGGTTTCTT TCTCTTCTACTGGTCTTTCCTTTGTCTTTGCCAGCCACCTATGCTGCTGT
NI-8853	79	C	T	CCCGGCCATTG AGGATA	AGTCTTCCTGA GCCTTCCAT	ACTTTTCTTGAGCTGAGCAACCTCATCCATCCTTTAGCTTCTCTGGTTGATAACGCTGGTTAATCCCCGGG CATTGAGGATA[C/T]ATGGAAGGCTCAGGAAGACTTCATTCTCAA
NI-8865b	52	A	G	...		AGGGTGACTGGAATCACAGGCACAGACTGAGGAAGAACAGTCATGGTCGAACAAACAACATGCT TCGGACTTACCAAAGGGAGGAGGTCGAGCTTTCCATATAAA
NI-8865a	42	T	C	CACAGACTGA GGAAGACAGT CCA	GGTAAGTCCGA AGCATGTTG	AGGGTGACTGGAATCACAGGCACAGACTGAGGAAGAACAGTCA[T/C]GGTCGAACAAACAACATGCT TCGGACTTACCAAAGGGAGGAGGTCGAGCTTTCCATATAAA
NI-8895	32	A	C	...		GTGCCACAAACCTGGACACCAACCAACAGAAT[A/C]CTCCCCGTCCTTCTTGAAATTCCATTAGAGCA CAATGGGGTAATTATACCAGGGATGCTCCAATCGCTCTTTC
NI-8456	93	G	C	...		CCTTTAAAGTCACAGTCAACTCGACTGTGGACTGATATATTGTGAAATATAATAAAACTCTTTCC AAGGCTCCCATGCTTGGATGTCACA[G/C]TTATGTCAGTAAGTAATATAAACATTCTAAGTGCTCACTC TCAACTTCTGTGTTATCTTGCCATGGTCCAGTCAACAGTTCACACGGCAGACCACAAGTTGTGTAGCAC TGGCATAGACGAGGGCTTCTCAAACTCCCGTCTGCCGTCTCAGTCACCCAC
WI-8496b	157	A	G	...		TTTCATCATCAAAAGTTTCTTTCCCATAGAAGAATGGTAATGTTGTATCAGTGCATATTCTATGGAAA ATTCATATCTCAAGTAACTAGCCTAGAAATCAGAGAACCTAGAAATCAGAGAAT[A/G]TTAGTAGTATATAGAAATAATACGCAGCTAGTACAAG AAGACACAATGCTGCCAATGCAGTCAAAGACACAATGCTGCCAATGCAATTAGTAGTATATAGAAATAATACGCAGCTGTTAGAAAAAGTCT GTGGCCAAGTGGGAATAAAACAGTAGCAGTGCAC
NI-8496	41	G	A	GTGCAGGAAG GCCAGC	AACGGCAGGA GGGGA	TTTCATCATCAAAAGTTTCTTTCCCATAGAAGAATGGTAAT[G/A]TTGTATCAGTGCATATTCTATGG AAAATTCATATCTCAAGTAACTAGCCTAGAAATCAGAGAACCTAGAAATCAGAGAAT... GTCAAAGACACAATGCTGCCAATGCAATTAGTAGTATATAGAAATAATACGCAGCTGTTAGAAAAAGTC TGTGGCCAAGTGGGGATAAAACAGTAGCAGTGCAC
NI-14153	28	A	G	...		CTGCAGGTCTATGTGCAGGAAGGCCAGC[A/G]TCCCCTCCTGCCGTTGTCACCCACATCCACAGAGCA GCCCTAGTGCCAGGTGCAGCCCACTGCCACCACGGGAACAGGACCCATGCTGC

ID	Pos	A1	A2	Seq 1	Seq 2	Seq 3
I-12108	40	C	T	TGGAAAAGGG TTAAACTCAA ATA	TTGACCTGGTA TAATGAAAGT ATTTC	TCATGTATTACTTCTGAAAAGGGTTAAACTCAAATATC[C/T]GAAATACTTCATTATACCAGGTCAAGAAAAATGCCACAGCCAGAAAAATTTATTTTAA
I-5989	29	G	A	CCACAAAGGT CACAGGCA	GGGTATAAACAG AACCGTATGTA CG	CAGGCAAACGTCCACAAAGGTCACAGGCA[G/A]CGTACACATACGGTTCGTGTTATACCCCATATATTACCCCTTCATGTCCTAAAGAAGAGACATTTCTCTTAGAGATTTCATTTAGTGTATCTTTAAAAAAAAATCTTGTGTAACTTGCCTCCATCTTTTTCTTGGGTGAGGACACC
I-12201	61	C	T	CCCACTGATCA CCTGCATG	CCGACCACATA CCTGC	ATAGTCTTTAGCCTTTTCCTGGAGTGTTTATGTCCCAAGCCCACTGATCACCTGCATG[C/T]GCCAGGTATGTGGTGGGGGTGTGATGGACGTGGGTTGCAGCCCGTCCCACTGCTCGATAAAGGC
I-12018	31	A	T	GGCAGCCCAGC TCTGACTT	GGAGAGATGAC AGAAACAGAG AG	TTTTTATCTGTCAGGCAGCCAGCTCTGACTT[A/T]CTCTCTGTTTCTGTGTCATCTCTCCCCACATACCACTTCTTCACCATGATGATTATACCAATAATACAGTTCCTTATATGAGGGGCTCTGGAAAATTAGACAGTGAAGCATGTTGCAG
I-14162	57	A	G	TGGCCTTCGCTG CCTC	AGGGATCAAA GAGAAAAGGC	TTTTTCGTTTGTTTAATGATCCGAATGCTTGAGAAGAAACCCTGGCCTCGCTGCCTC[A/G]GCCTTTCTCTTTGATCCCTGAGTTGCTGAGATTAAAGATGAGGTCCCAAATGAGAGCTACCAAGATGTAGTCGAGCGG
I-15407	92	A	G	CATGCCCTTTA AGGATTAAGT TT	TCTTTTCTCTT TGGTAGTGTGG	AGCATGTAAGGAGCAGTTTTATTGATTGGTATATTCAGGTTCTAACCAGCTGAAAAATTCAAATACATGCCCTTTAAGGATTAAGTTTAA[A/G]CCACACTACCAAAAGAGAAAAGATTTATATGATCACATATAAGCAATGGAATCAGCA
I-12319	109	T	C	GTTGAGTGTATTT GTTCTGCTCAT AATT	GGGAAGGTCTG GTACATATTGG	TCTGATGTCATTTATTGGCACAAAAATTATTCTGATACAACATGGTGTCTAGACATGGCTACACTTATACTTTGTGCATTTAGTTGAGTATTTGTTCTGCTCATAATT[T/C]CCAATATGTACCAGACCTTCCC
I-12326	25	G	A	GACAGACTTC AAAAGCAATT ACA	AGGTTTGAAA TATGTATTAAG TACTTTGT	CTGACAGACTTCAAAAGCAATTCAC[G/A]CTTCCAGAATACAAAGTACTTAATACATATTTCAAACCTGTTTGCATTTCAAACAAAGTTAGCGTTTTGTAAATCAAATTTGATAACCGACTAAAAAT
I-12361	63	C	T	---	---	TTAAATTCCACACTGAAGATCTGGAGTATGGGGGGGATATAGGAATTTCAGCATCATATGTATTAT[C/T]TGAACTAAATTACAAAAGTGGAACAGTTGGAAGTTACTTATAGGTAGACCTGAGGGTCGTTACC
I-11305	87	C	T	CAGACACAGC ATCACACCA	GACCCTCCGT GGGC	ATACTGGTTTAATCCATGTCAAATGTAGTTTACAAAGGGAAAGGACAAGTACCTTTGTATAGAATAT ACAGACACAGCATCACACCA[C/T]AGGGCCCACGGGAGGTCGGGGAGGACGACACTTTTCCCTGGGAAAGG
VI-11321	67	A	G	GGGAGGAAAA TCCAATAAAT TTT	CATTGGGGAAT AGCTAAACCTT	ATTTTATATGAAGGGTTTCTGGTGAAATCTTTTAAGCAGGGAGGAAAATCCAATAAATTTTTTTAA[A/G]AAGGTTAGCTATTCCCCAATGCTATTTAATACAATTGAGGTTAGGACGTTAAGTCTTATCAGA
VI-11324	40	C	G	GGATAAATCA TGTGCCCCA	ATCAAGCTTTG GGGCTCT	AGCATACTGCATCTCCTTTATGGATAAAATCATGTGCCCCA[C/G]AGAGCCCCAAAGCTTGATGACATTCTGTAAGTTACACAAAATGTATCTGAAGAAGTTATCTGTCTTGTCC

352a	69	TCG	AGCACAGCACATAGTGGAAAG / GACCTCTGTAGGACACTTAGC	TGACACATGGTTTCTGTTTCCAGAAGGAGAGAGAAGTCATCTACATAAGCACAGCACATAGTGGAA AGT[T/C]GCTAAGTGTCCTACGAGAGAGGTCAGATCATATCCATAGAAAAACAGCTCTTTTACTTGCA / CACTTA
-11371	84	CTG	CAGCTTGGAG ATTCTGATTCA GCAC	TTAGCCCATGCTGTCATCACCTGTGAAACTATACCTGCCCAGGCTCAGCTT GGAGATTCTGATTCAG[C/T]GTGCTCAGGCGGCGGGGGCTGGACATCCATGTTTGGGAAGAGTTGCGCGGGGT GATTTCGATGCGTATAT
I-11385	75	TCG	ACAGAAGACT TTCATATTCT TTTTT	GATTCTATTCT AGTCATGGTCA TATTTT CTTAAAGCATTATAGTTTGGCCTGATGGTGGACACAGAAGACTTCATATTCTTGTTTTTAAAAGTC TCTTCAGT[T/C]GAGAAAAAAGCTACAGATTTAAAAAATATGACCATGACTAGAATCAGC
I-11388	88	CAT	TGTTTGAAATT ACACGTAACT AAGTTC	TGCCTTGTATC CAAGTTAAAAT T TCATGTGGCCAGTTAGCTCAGTTGGTTAGAGTGTGTGAGCTCATAAAAAATTAAAGAATGAATGTTTG AAATTACACGTAACTAAGTTC[C/A]TATAATTTAACTGGATACAAGGCATTGTTATGCTAAT
:-11392	55	TG	GGTTATGTGTT CTTGAACTTTA ATAAATAC	GTACATTCACG TGTTTTTGTAAA AAG TTCTATCATTCCATTAAAATGGGCAGGTTATGTGTTCTTGAACTTTAATAAATAC[T/G]CTTTTTACA AAACACGTGAATGTACTTTCTTGTCAGAAGGGGAACACTGAGTCTCCGCTCATTAACTGT CATACTCCTTCCCCAGA
-11396	52	ATT	TTTTGTTTTG AAATGGTGTTT TC	AGCTTATTTC ATATTCACCCA AAAGAATAAGATGGCATTTGTTCAGTTAATTTTGTTTTGAAATGGTGTTTTGAAAT[A/T]GATGGGTGAATA TGAAAATAAGCTTACCTCATCCCACTCTAAAAGGTAGTTGGTGATTTTGAACCGTTGTCAAT
-11441	100	CAT	TCCCCACCAAC TGCCAGGGCCT TATTTG	CTGTCAGTCTTTCCCAACTAAACCGTGAGTTCCAGTATGTCCAGTATGTCTGGCAGCACGTCGTGTCTTGTTCTTGGTG TATTCCCATTACTGAATCCCCAACCAGC[C/A]CAAATAAGGCCCTGGCACAAAGTAAGCTCTCC ATTTTTGTAGAATGAAT
I-11466	26	CTT	TGAGAAGCCA TAAAAATGAC CTACAACTT	GTTTATTGTTA TAAAAATGAC CTACAACTT ACTTTGAGAAGGCCATTTATTTTGCAG[C/T]TCTTCAGTCCAAAAAAAGTCAACATTTCAGAATTTTT TATATAAGTTGTAGGTCATTTTATAACAATAAACTTCTATTATCTCTCACATACATT CATGTATCCTG
I-13364	35	AG	...	TTTTCTTTGTGCTCTTTTTTTTTTTAGTAGAAGC[A/G]GGAACAGTTGTCAATACTACCTTCTGTTGG TCCCCTGTTAGACAACACTGCTTTATTAGGCCGGGCCGCGGGGCTCCCCACCCTGGTGCTCCCACTCAG
I-11276	41	AG	GGCAGGCCAGG AGCAGAC	TGTACTGAGGA GCCGGTG AGGCAACACTGCTTTATTAGGCCGGGCCGCGGGGCTCCCCACCCTGGTGCTCCCACTCAGTCAGTACACATT CCCCACCCTGCCTCGGGTGCTCCCCACTCAGGGGCCATGGGGGCAGCGTAGGTCTGGAA
I-12210	76	AGA	ACTGGGAAAA CAACTATTGC	TGCTAGTTTGC ATATGTTTTCC ATTGGAAACAACTTAATAATTTGCATCTCTACATATAGAAAGCTGCTTTGAATAACTGGGAAAAACAA CTATTGCATT[A/G]GGGAAAACATATGCAAACTAGCATCATTGTCTCTAGA
186b	88	AG	...	AATGGTCTGGTTTTATTGAAGAGCTCGGTTTCATTTGATGGAAGACACATACGGTACAAAATTACA GGTGGTTTAGTTGCTTCATTACATG[A/G]TACAAAATCATTACAAGTCTTTACAAGTCATTAGAGTCTTTTGGAT TTT

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36a	52	C	T	GGTCATTTGAT GGAAAGAGACAC A	AACTAAACCA CCTGTAATTTT GTACC	AATGGTCTGGTTTATTGAGAAGAGCTGTTGGTCATTGATGGAAAGACACATA[C/T]GGTACAAAATT ACAGGTGGTTAGTTCATTACATGATACAAATCATTAGAGTCTTTACAAGTCATTAGAGTCTTTGGAT TTT
2234	66	A	G	GAGAACACTT GTGGGGCTT	GGACCTATCAG TCCATGTTTGA	ATTTTTTGGCTATAGGTCAGTGGTTCATGGTTCTTCTAAACTTGAGCTTGCAAGAGAACACTTGTGGGGCTT[A/G]TTCAAACATGAGACTGATAGGTCCACCCCAGATTTCTAACTGGGTAGGTCTGGGGTG
2345	37	C	A	GTGGCAGGAA AAAGAGGAA	TTGCAGGAGGG TTCAGG	GGAACAGACCTGATCCACGTGGCAGGAAAAGAGGAA[C/A]CCTGAACCCCTCTGCAAGTATTCTTTCCTGACCAGCTGGGCTTGCGCACTTTGTGAGATTTGCAAA
13416	71	C	A	AAATTTTTGG AAGTTTTTTCAG AAA	AGTGTTTATAG TTCAATGAATA ATTTCAA	GAAAAGGCTGTAATTTTATTTCAAATTTTGGAAGTTTTTCAGAAAAAATAAAATGACAAGAACA CATA[C/A]AAATATTGAAATTATTCATTGAACTATAAACACTTAGCAGAGGAGGGACTTTTGAT
2310	46	G	A	AAAAGC	TTATTCCCAAG TATAATTTTA	TGTTTAAATAT GTTTGGGTCCT AAA	TTTGAAAAGATGCTGAATTTATTCCCAAGTATAATTTTAAAAAGCT[G/A]TTAGGACCCAAACATA TTTAAACATCTCTTACACATACAGAATTTCAGTTTACAAATATTCCAGAAGGCATTTCTTTAAGCAG T
2086	72	C	T	CCCGGGAAAC TTGGATTT	GGAGTCTTCGG GTCTTGG	GAACCGAGCTTATTGGAGGACAAAGAGTGTGGACACTGTTACAACAAAACGTTTCCGGGAAAACTTG GATTT[C/T]CCAAGACCCGAAGACTCCTCCAGTTCTCCACTGTTAGGTCAAATTGGGGGCCAGA ACAGGAACATGCCTTAGCT
11549	102	T	G	GGCATAAAGT TCATAATATTC TTTTATG	GGAAAGTCTGT ACAAATCCCC	ATGTCTTCACAGGTGTATTTGTTAAGAGTTGTCTATCTCAAATTTCATATTTATTGGCATAAAGT TCATAATATTCTTTTATG[T/G]GGGGATTTGTACAGACTTTCCTC
11585	79	T	C	TGGGTTTGCAA AAACAAAA	CCATGCTTCAC TGATACTTCC	TTAGAAGGAAAGAAATAAAAACGGTAATGGAAATCAGTTCAGAGGTAGGAAGGAAGCTGGGTT TGCAAAAACAAAA[T/C]GGAAGTATCAGTGAAGCATGAGCCTAGAGTCCAAGAGCCAGGGGTAGAGT T
1604	68	G	C	---	---	TTAGTTGGTTCCTGAAACTTTATGCTGTGTTTATTTTAACCAATAGGATGTTCCAGTTACCAGCATTT[G/C]AGAACTAGGGACTTTTCCATGAAAATAATTAAGAGCTAAGGAATTCTGACGCGCTACCATTTTTTC TTGTTACTCTGCAGTT
4c	108	C	A	---	---	CAAAATCAAAAATTGAGGAGGCAAAGAACAGAAGTAAAAATCCAGAAGACTCAGCTGCTTGAGGCAT GTTCCCACCCCTGGACTTTGCCAACTTTCACTGTGAAACTGCAA[C/A]ATATTAAGTATTCGTCAGCTAC GGACTTCGT
4a	60	A	G	CCAGAAGACT CAGCTGCTTG	AGGGTGGGAAC ATGCC	CAAAATCAAAAATTGAGGAGGCAAAGAACAGAAGTAAAAATCCAGAAGACTCAGCTG[A/G]GGCAT GTTCCACTGAAGGTAGGGATAAGTGTACAGGATATATACTCAGCAACATATTAAGTATTCGTCAGCTAC GGACTTCGT
5b	83	T	C	---	---	TTGAATTTTACTAAGGTCTTCCTCCACTGGAACATGAAGGTAGGGATAAGTGTACAGGATATATACTCAG ATATTTAAAATAAA[T/C]TACTTAATAATAAAGAAATTAGCCATACCACATTGTTCCATTTGCTAC AAGAACAAATTGGCAATGA

ID	No.			Col A	Col B	Sequence
326a	39	G	A	G	TCCACTGGAACATGAAGGTAG	GTGGTATGGCTAATTTCTTATTATTAAGT	TTGATTTTACTAAGGTCTTCCACTGGAACATGAAGGTAG[G/A]GATAAGTGTACAGGATAATATACTCAGATATTTTAAAATAAATTACTTAATAATAGAAATTAGCCATACCACATTGTTCCATTTGCTACAAGAACAAATTGGCAATGA
11627	23	T	C	CCTTTCCTTCC CATTTGCAACC CATTGTCCTC CATCTCAAG		ACCCCTTCCTTCCATTGTCCTCT[T/C]CTTGAGATGGGTTGCAAATGGGAAGTAAAGCAAAAGGGAGATGAGAAATACTGATGCCTTTTGTCTGGCTTACTTCCATTCGCATGTCAAGTCCATCCATG
11636	61	A	G	GGACTTAAAA AGATCTGCTTA AGAAACTTGCT AAATATTTTAT TCCT GTAACACT		TCAGAAATGTTGCAAGCAAATACTATTTGTAAAGGTGGACTTAAAAAGATCTGCTTATCCT[A/G]TATCCACATAACTCTAGTGTTACATAAATATTTAGCAAGTTTCTGTGACAGGTGCTCAGTAAACAC TTTGACTCCTTTTTGGTA
11537	119	C	G / T	ATTGCTCATCT TACTCTGACCA GACCCAGCAA AAAGAAATGAT T		GTACCATTTCTTATGGTGGCAAATAAGCAAACTGTGAGTAAACGAGGGCAGCTGAATAAATTTACAGTATACAATATTAGAGAATATATGTTGCAATTGCTCATCTTACTCTGACCAT[C/G]ATAATCATTCTT
11654	37	G	C	GCCAAAAGAC TATTCAGCAA GGCTCTCCCAG GACAGTT CTG		AGTAGAACATCAGTGCCAAAAGACTATTCAGCAACTG[G/C]AAACTGTCCTGGGAGAGCCACTCCAGAGCTATTTCTAAGACTTTCTGTGGTGTTCATACTCTACTCAGAGTTCACACTCATATTTCATATTTTT ATTTTGGGTGTTGGGT
11656	28	G	A	ATTGATTTTAG AAGGAACTGC AA CAAGGCTTGT CCTCAAGTAAA		ACCTGATTGATTTTAGAAGGAACTGCAA[G/A]CTTTACTTGAGGACAAAGCCTTGCCTGCAGTTGTTTAAAATGTCCTGAAACAATCAGATTCCCAGCCTGGAT
11680	55	T	C	---		ACAGATACTTTCCACGCAACATTCTGAAATGAAAGCTTTGATTCTCCCCTTTT[T/C]TTGCATAAAGGCTGGGAAGGTTGGTTGGCCAGACCGTACATCTTTT
11696	47	T	C	TTATCACAGC AGGGGACAG GGCATTAGAGA AGCCAACCTT		GTCCAAGAACAAAGATACTTTGACATCTTATCACAGCAGGGGACAG[T/C]AAGGTTGGCTTCTCTAATGGCCACCATCTGTGTTTCAGAATCTTTCCACTCGCC
11702	69	C	T	GAATAATACT GAAATAACCA CAGCAG AAGCAAATTAT ACTGAAA		TTACATGTGGTCAATGGTGACATACTTCAATAATTAAAAAATCGAATATAACTGAAATAACCACAGCAG[C/T]TTTCAGTAGTAATTGCTTAAGTGTTCTAGAAAACACTGCTAATTTTTGTTCTGCGAGA
11706	60	C	T	TGGCTGGAATT ATCACCAAAG TTTCTCTTCTT AACAAATTCCA		TGCTGATTCATCGCTTCTACCATCTGGCTGGAATTTTCTCTTCTTGTACAATTATTTGC[C/T]GGCTG
11709	105	T	A	AGAAGCTTGC TCATTTCTCT TTCAGTTTGC AATTTTACGGG A		AATATCATCACTCATATCAGGCATGTTTATAAAAATGAGAGATTATGTCCTTTTGGCATACTTCATCTTCTTCAGGACAGAGAGAAGCTTGCTTCAGTTTGC[T/A]GTCCCGTAAAATTAGAGAGAAATGAAT GGCCAGATGGGATGGAAAA
11710	103	C	A	GCACCTAGCCTT GTGTGGAGGAG CAGTCTTCA GGAGGAG		TTATTACCATCAACCTGTCCCCAGCTTCCAGCACAACAGCCAGCCCACACTCTAGACACGCCTTCAC[C/A]TCCTCCCTCCTCCCACACACTCCTTC TCCAGTCCATTCGGCACCTAGCCTTCTCAC

ID	Pos	A1	A2	5′ flank	3′ flank	Sequence
15b	123	C	T	AGGCTGGCTGC AGCTT	TCCCCATCCTG TGGCT	AGAATGGAGCTGTTGGGGAGGGACATGCACACAATGTAAAACAGACAAAATGCATTACAACTGTGG TGTAATGTGGCCACTATGAATCCCTATGTATAAGAGGAAAGAGAGGCTGGCTGCAGCTT[C/T]AGCCAC AGGATGGGGACTGGGGAAGA
715a	49	A	C	GCACACAATG TAAAACAGAC AAA	CATTACACCAC AGTTGTAATGC A	AGAATGGAGCTGTTGGGGAGGGACATGCACACAATGTAAAACAGACAAA[A/C]TGCATTACAACTG TGGTGTAATGTGGCCACTATGAATCCCTATGTATAAGAGGAAAGAGAGGCTGGCTGCAGCTTCAGCCAC A AGGATGGGGACTGGGGAAGA
-11727	43	G	C	AACAATCCTT AAAACAACTA	CCTGTGGGTTG TGTTGCAG	CTGGATTTCCTATACCTAACAATCCTTAAAACAACTATCAACA[G/C]CTGCAACACAAACCACAGGC AAAATGAAAAACAGATGCCCCAGCAGCACCCACCATGGCACACAC
I-11728	16	C	G	---	...	TTTTATTTATCAAACT[C/G]CAATTCCATTCACAAAATGTAAGTTATCATCAGCTCCCCATCCCACTTT CTCCCATCTTCTATCTCTTTCCCACCCTACACTTCTTCTCCCTACAACCGGGTTCCAAA
I-11758	61	A	G	ATCTGTGTGTTT GTCGCCTG	TGATTGGCCCT GTGGTCTA	TTTTTCCTCTTTTATTAAGTCCGCTATACTAACTAGAAGGAGAATCTGTGGTTTCGCCTG[A/G]TAG ACCACAGGGCCAATCACCACAGCTCTTGTAGAGAACATGGAGAGTGCCAAGATCACCATCA
I-11295	37	A	G	GCCTCACAAA GTATTTCTAA AATATAA	AAAAGTGCTCA TCTGTGAACTC T	CCGGCCTCACAAAGTATTTCTAAAATATAATTTGCT[A/G]TAGAGTTCACAGATGAGCACTTTTCA CATTAGGTGATATGCAAACAAATCACTATTGGCTCAGCAGGAAAACAGACTTT
I-11773	93	T	C	---	...	AGCACATGATATTCTGCCTGGAGTTTCTGTGAGCTCAGCAAACAGCAGAGTCAGAGATTAAGAATT ATTTATTGCCTCCTTTTTTCCCCCT[T/C]GTGATTGTTAATTAGGGAGTCAAGGCCAAGTTATC
I-11282	42	C	G	GGCTCAGAGA GCAAGGGAA	AAAACTCAGA CTGTAAATTT GTGTG	CATGACGAACCTCTTATTTAATGGGCTCAGAGAGCAGGCAAGGGAA[C/G]CACACAAAATTTACAGTCTGA GTTTGCGCGCAGAGACCCCTCCACCTTTTCATGCGTGTGTACACACACTGTCCAAGCCTC AGA
I-11790	28	A	G	CCCAACTTACC AAACCTCTG	CGGTAGGCGAG GCTAAGC	TAATTCACCCAACTTACCAAACCTCTGT[A/G]GCTTAGCCTCGCCCTACGTACACATGCTCAGAGCAC TTACATTAACCTACAATGGCAAAATCATCTAACACAAAGC
I-11879	61	C	A	TCATCTAATCT GTGAGGTATT AGTATACA	GATAGTTGAAC CTCTTCACTTT ATAAAAA	TTTTAATTCCCAAAGCTTACAACCATCTTTCATCTAATCTGTGAGGTATTAGTATACAG[C/A]AGT GATTTCTCTCTTTCCTTTTATAAAGTGAAGAGGTTCAACTATCCAGACAGTCCCATCTA
469b	91	C	T	GTTTTAATGT GGTATTAGAA AAGTTTAAA	CAATTTTCAGA TTGTCTATAGC AAAC	TTACTAATTTCCATTCCTCCCCTTTTTAATGTTTTATAGTTTAATGGTATTAGAAAAGTTTAAATTACAT ATGTGGCTTATATATTCTATTTCTA[C/T]TTGACAGCACAGTTCTTCAAAGTTTGCTATAGACAATCTGA AAATTGGGTTCTGAACT
-11906	52	A	G	TGTTATAACAT CAAAGAAAGA A	TTAATTTCTGC AGTTCCCTCA	ACATTTGAGTAGGAATGACTTTGTGTTATAAACATCAAAGAAAGAAATCTGAAT[A/G]TGAGGGAACTG CAGAAATTAAACTTTCAGTCTAATTCTCAGAATGCCAGAGTAAGATGAACCTTTACAG

ID	Pos	Allele		Seq A	Seq B	Seq C
VI-11909	78	A	G	TTTGTGTTGGG TGGTCAAG	CCTCCTCTGAG ATTTTCTGAAT AG	GCAGTTCTCTGAAAGACAATGGATTGTGGAGCATACTGAAGACTATTCCTAAATGGCTATTTGTGTTG GGTGGTCAAG[A/G]CTATTCCAGAAAATCTCAGAGGAGGACAAATGATAGTGCACTGCGAGCCAGCTCG GACTGGCTTGCAAGAGTC
VI-11806	60	T	G	CATGAAGAGT GGGCAGTTCA	TCCTGTAAAGC CAATTTTATAT ACTAATAA	AAAAATACCATTTAGCATCAATTGCCCCAAGTTGGCAGGCATGAAGAGTGGGCAGTTCA[T/G]TT TTATTAGTATATAAAATTGGCTTTACAGGAAGCATTATGG
VI-11946	31	C	A	---	...	CCCTAGTGAATACAACCTTTGTCCTGGAGAC[C/A]CCAGCTAGTCTCAAGAAACTTCCTAGGCTGAG CTCTCTTGGGAATCTAAGATAAAGAACTGAGATCCTGGGAGGAGGGAA
NI-11965	65	T	G	TGAAGATCAG ATCTCTGGTTT GATTT	CAGCTGTGGTG AATGTTGAT	ACAAAATTCACAAGTACAACACTGCTTATTTCTTGCTTGAAGATCAGATCTCTGGTTTATTTAAT[T/ G]ATCAACATTCACCACAGCTGAAGGAAATTAAACTGAACCT
NI-11027	90	T	A	TGCCCTACTAC GCTTTAAAA A	TGAGGAAATGT GTTACAGTATT TTTATT	ACCTATTTTGAAACTGCGAGAAAGGGCAGGACAAAACAAATCACTTCATAGATTTTCTGGGAAATAT TGCCCTACTACGCTTTAAAAA[T/A]AATAAAAATACTGTAACACATTTCCTCATTTCTTACGA ATACTTTCTTTTTGATATTGCAAATTCTATGGCATACACAGAGGCACCTCCTCCTCAATGCCCTG
NI-11049	95	C	T	---	...	TTCTGCTGAAGATCACAAAACAATTTCAACCTCTGTGTTCAAAATAATTTAAGGATCTTGTTGTACCTT GTGTTTATTTCTGTTCAACTAAGGA[C/T]AGACTTCAGAAGGCATAGCTTCCCTTGTAACGTTTT AAACATCTTTTCATTTGTAGGAAGGAACATTCAAAAGCCCAA
NI-15488	69	C	T	AAAAGGACAG CCAGATATCA AC	TTTCCATCTTA TTTCATTTCTG TAAC	CAACATTTATCAAACATGTAGGGAAAGTTCTCACTCTGCACTATAAAAGGACAGCCAGATATCA AC[C/T]GTTACAGAAATGAAATAAGATGGAAAATTTTAACAAATTG
NI-13654	49	A	G	AACAGTTAAT GAAACACATC CGT	GGCTGGTGAAA TGATGTCAT	TGCTCAATTAATGTGATAATCTCCAACAGTTAATGAAACACATCCGTA[A/G]GTATGACATCATTT CACCAGCCAGCTACTTCATGTGGCAGAAAAGGTAACCTTTCCCCATTTACAGACAAAACCAGT
NI-11070b	135	C	T	---	...	ATGAGACCCTGCTTGAACGTTTAAACGTTTGGAATAATGGAAAAGGAGCTAGGACAATTCTTGCTT TCAAGTAAAATTGTGACTGAGCAGAAAATCAGCCAGCTATCTTGGGTGCAGAGAGGTACTCCAAGTA C[C/T]GTGGGGGTTCTGATGACTTCCACGGTCACTGGGGATCCAACAGAAGGGAA
WI-11070a	110	G	T	CAGAAAATCA GCCAGCTATCT T	TTGGAGTACCT CTCTGCACC	ATGAGACCCTGCTTGAACGTTTAAACGTTTGGAATAATGGAAAAGGAGCTAGGACAATTCTTGCTT TCAAGTAAAATTGTGACTGAGCAGAAAATCAGCCAGCTATCTT[G/T]GGTGCAGAGAGGTACTCC AAGTACCGTGGGGGTTCTGATGACTTCCACGGTCACTGGGGATCCAACAGAAGGGAA
NI-12020	121	T	C	---	...	AATCTTTATATTCCAGCTGTTGAGACCGTATTTTGAGGGCTGATGTTACCTCTAGCGGCGGAAACC AGAGCCAGCTATTAAGCAGCCAGAAAGTACTACAGACCATT[T/C]CTCTTTTAGC AGGTTCTTTGTTCCTC

ID	No.	Allele		Flanking sequence	Sequence
WI-11076b	142	G	A	---	CATGGTTCTGCCAGCTTACAGGAAGCATGGTGCTGGCCATCGGCTTATCTTCTTGGGAGGCCTCAGGAAACTCTGAATTATGGCAGTAGGCAAAGGGGGAGGCAGGCAGGCATGTCACATACCCAGAGCAGCAGGAGAGAAAAGAGAG[G/A]AAGTGCCACACATTTTAAATGATGAGTTCTCTCAAGGAACTCACTCACTGTCATG
WI-11076a	106	T	C	AAGGGGGGAGC AGGCA / GTATGTGAC GGTTATTCAAA	CATGGTTCTGCCAGCTTACAGGAAGCATGGTGCTGGCCATCGGCTTATCTTCTTGGGAGGCCTCAGGAAACTCTGAATTATGGCAGTAGGCAAAGGGGGAGGCAGGCAGGCA[T/C]GTCACATACCCAGAGCAGCAGGAGAGAGAAAAGAGAGG
WI-14263	49	T	C	CGCAGAAAAA AATTAGTATGG GACA	ACCTTTAAAGTTTCTCCCCACCTACTCCCGCAGAAAAAGGCATATTCAA[T/C]GTCCCATACTAATTTTTGAATAACCTAACTCTCCCTTGTTCTACTAAGAGAGGTTCTTTTGGCTACAAGTAACA
WI-14267	28	T	C	---	AATTATTGCTGAAATTAGGAAGGGAGCAT[T/C]TGAAATGGGAAGGGGGAGGTTAGAGAAGACAGAGATTTAAAAGAAGCAAGTACCATTTCCAAGTATAAAACTCGTA
WI-13892	50	G	A	CTTTTCATTT TGATGATGTCA TGCTTTTTAAA TATACTAAAA ATCAAAG	GATTTGTTTATTCATTCTCGCTTTTCATTTTTTAAATAGAACA[G/A]CTTTGATTTTTAGTATATGACATCATCATCATGAATTTTTCTCTTACTTTGTATTTGATTAGGCTCCACCTCAGTTGTGACAAAGGTAGAATGAGTTCA
WI-15288	108	C	G	CATGAGAGGA AAAAGCTTCTT TTCCCTCTCTC TCCCTTGGA	ACCTCTTCTGATGACACTTGTACCTGTAAGGGGTCTAGAGAGAAAGAGTAGTAGACTCCTACTTTGCTACAATTCAGGATGCAGGCCATGAGAGGATTCCCTCCTCTC[C/G]TTCCAAGGGAAAGAAGCTTTTGGC
WI-3951b	88	G	C	---	AATAAATGGAAGAAGGAGTGAACAAAGTAATGAACAAAACAGACCCCAGATCGAAGAGGAAGAGATGGCTTCTTGTTAATTCTGGAGCA[G/C]ATTCAAGCAGCAAATATTTACTGAACACTTGCTATGTGCTGG
WI-3951a	39	C	T	GGAGTGAACA AGTAATGAA CAAAA / TTCCTCTGATC TGGGGTCT	AATAAATGGAAGAAGGAGTGAACAAAGTAATGAACAAAA[C/T]AGACCCCAGATCAGAGGAAGAGATGGCTTCTTGTTAATTCTGGAGCAGCAAATATTTACTGAACACTTGCTATGTGCTG
WI-13264	25	G	A	AAAAAGGCTC TTGCCCAT / GGAGGGGAG ACGGGAATA	GAGACCAAAAAAGGCTCTTGCCCAT[G/A]TATTCCCGTCTCTCCCTCCTGACTGACCCCAGTGTTCTTACAATGAAACATCCCTCAGCCCCATGGTCATCCCTTCTCTTGGGATCTGTGAATATAACCAACTGTCTTGTCAATGGC
WI-13960	39	A	C	AGCAAAAGGA AGTTAAATAC CTGATAGA / CATGAAAGGA CAAATTTGCAT C	TTATTTGTCATTAGCAAAGGAAGTTAAATACTGATAGA[A/C]GATGCAAATTTGTCCTTTCATGCATTTATAAACCAAGAGACTGTTAAACTTGTCATTTCCCTCACAAGGAGTTGAGCCCCTAGATGAC
WI-15843	62	C	T	ATCTTATAACC AAGAAGCCTT CAG / CTCTGGCTCAG ACTTGCTCT	AACTCTTTATTGTTTAGCTAGCCCCAGTGACTTTATCGCATCTTATAACCAAGAAGCCTTATGCATCTTATAAACCAAGAGCCTTCCACACTTGTCCTCAGGTCCCACCAGGAACCAGGTCTTGGCT

Marker	Pos			Sequence
VI-13983	52	G	A	TCTCTCCCCACT CCTTAAACCT · CAATACTCTCT · TTGTGTATCTGATTTCCGAAACACATAGAAATCTCTCTCCCACTCCTTAAACCT[G/A]CCACTGGCTAA
				AATCTCAGGG · TAGCCCAGTGG · GAGAGTATTGTACAGAATATGCACTCACTGACTTAACAGAATTAGAACATCCAGCACTCACTGAGA
VI-13850	51	A	G	TCACAGCTTTA TGTTCCCTGAC · CATGAATCTCAGGGTCACAGAGCTTTATTTATAGATTTTTAACACAGCCAT[A/G]TTACAAACATTGT
				TT · AATGTTTGTAA · CAGGGAACACATTACAAAGAATAAATAAGACTTGCAGGTGTAAAAGATTACACTTCA
NI-15295	27	G	C	ATGTATTCCTG TGAATAGTTGG · AGATGTCAGTTTGAATGTATTCCTGAT[G/C]TTTCCTTGCCAACTATTCATTATTGACCATCTTTC
				A · CAAAGGAAAA · CTCGTCAAGTGACCTGCCATCATCACAAGAAAAGGCCCGAAAAATATGAGTGAGACTCA
NI-14284	55	C	T	... · ATTTCAAACAAATCCAGAACAGGTTCTCACACTTTGAGCCTTT[A/G]GAGCGCTCCCCTGATGCATTGA
				GCGGGAAATAAAATGCTTATCCAGTGAGCCGTCTATATGAAGACAAACAGGTGGCCATACTTGGGTGGAGGGATA
NI-14288	85	G	C	CCGCTGCTATT GGTCTCCTTCC · ATGACCAGGAGAAGCCCCTGTTCTATATGAAGACAAACAGGTGGCCATACTTGGGTGGAGGGATA
				CCCAGAT ACCAAATCTT · CCGCTGCTATTCCCAGAT[G/C]AAGATTTGGTGGAAGGAGACCATGACAGATGACAAACGG
NI-13522	33	C	T	TGATGTAGTTA CATAATATTTG AAGTCAGTGGT CCCCACTAAT ACAAC TCTC · TTTATTTTGATGTAGTTACCCCACTAATACAAC[C/T]GAGAACCACTGACTTCAAATATTATGAGAG
				AAAATTACTCCAGGGAATTTTTGCAGAGAAGATAATA
II-13529	42	T	C	CACAAACATT TATTGAACAG TTACCA · TCTATACACTT CTCACTCTCTT GCTT · AAATATGATTCCATTCCACAAACATTTATTGAACAGTTACCA[T/C]AAGCAAGAGAGTGAGAAGTGT
				ATAGAGGTGATTTAAGAGGTGTCCCTGTCCTCGAGGGGTTTATAGTCTAACAGGGAACAACCTCTC A
I-13859	84	G	A	... · TTATTTGTCAGAATTCCAGAATCAGAGTCTCTACTGGGCAAGTAGAAAATAGAAAGTTTACTAC
				TTTGAAAAGGAAACTAT[G/A]ACAAACAAGTATATATTCAGGAAGGGACTCCTAGAACTTGAGCA ACA
I-13536	29	T	C	... · TGAAAAGGATACAGAAAAAACTCAGCGAAG[T/C]GAAAAGGTGGATAGCGTGGAGTAGAGGAGAAAT
				TAAGCACCACGCTTCCAGTTGTCCTCTCCCAGTGCCATTACACTGGAGTACACTTAATTTCTCAGCA
-13373	52	G	A	... · TTTTATTGTTTGGTAGAAAAÁCAGGCTCTTTAACACTGAATAAACATCTCAC[G/A]AACTGTCGCTC
				CTAGATTACAAAAAGTCAAAACCAATTTCCTTTGACGCGGCCCTTGAATCTGACATTCAAGTCAC CGTAATAGAAACCAGAGCT
477b	61	A	G	... · TTAATACCTCT TGTTGGATAA GAAGACAAGC · TTGGTTTTTAATACCTCTTGTTGGATAAAGGACATTGTTTTCATTAGCTTGTCTTCAAA[A/G]GAC
				AGAGAAATAAGATAAATTACCTTAAGAAAATTAAGGGAACATGTACCAAGGTGG TTTTAGACTCTCCTCAGTT
77a	32	A	G	AGGG · TAATGAAAAA CAATG · TTGGTTTTTAATACCTCTTGTTGGATAAAGGA[A/G]CATTGTTTTCATTAGCTTGTCTTGTTCTTCAAAGAC
				AGAGAAATAAGATAAATTACCTTAAAGAAAATTAAGGGAACATGTACCAAGGTGG TTTTAGACTCTCCTCAGTT

ID	No.	Allele			Sequence
I-14297	86	A/T	AATGTTGGGT ACTTTTCCAA G	TGTGCACATTC AGAAACATTTT	CTGACTTTATTTAGCATGCAATGCAATTTATTCTGGCAATAAATTAATATGTGCAGTTATAAAAAAT GTTGGGTACTTTTCCAAG[A/T]AAAATGTTTCTGAATGTGCACACTAGAATATATGCAGAATCCTTT AACAGTCGACT
I-12229	89	T/G	CATGTGCACA AAAAGAGTAA GAAA	ACATGTGAATT GTCCCAAAA	TCCATGTAAATATTCTCAACAGAGAACACTATCTTAAATGAAGGATTTACCATTAAGAAATCAACA TGTGCACAAAAAGAGTAAAAAAT[T/G]ACCAAAAAATTAAAGATTTTTGGGACAATTCACATGTTC AAAAT
I-13582	43	C/A	TGCAATCTAG AGACTGGGGA	TCTGCGCAGT AGATTCCA	AAGGCTGCCCCTACTGGACCAATGCAATCTAGAGACTGGGGA[C/A]TGGAATCTAACTGCGCAGAG AATCAAAGACCGATGGTGTGAAATCTGGGGCAGCTTCAAAATTCTGCCTCCTAAAAACATTTCAC CCAATTTTCATTATTGCC
I-13857	28	A/G	...	...	TCTGAGTTGATAAAATGCTTTTCTGAAC[A/G]TACATTTAGGTATCTGGCACAATTAACCAAATGT CTGCCCCATTTGTTGTAGCTTTCATACAGTACAGATTTCATTGATGTGCCCACATCTG
I-15809	77	T/G	TAAGGTAGCTA ATTCAATGTTT GTGTAAATGCC GTAA TGGTTTTCTGT		GTTTTAAGTTGCAGAGATGTGAATGGTTACAAATCTGAAGCTGAAGTTCAATCTTTGGTTTTCTGTT GTAAATGCC[T/G][T/G]TTTACAAACATTGAATTAGCTACCTTAAGTATTGAAGAGCTTCCATT
I-15892	123	A/T	...	...	TTAATCAGTCTGTGTCAAGAAGAAAACAGGACTTGATCAAGCTTCCAGCCTCCACCACTCTATCAGCA ACTCCACAGATCAACATGT
801b	81	T/G	CATACTCCACT CTAGCTGCAGT AGAAGAGTGG ATGGGATGC		TCTTTTATTCCAAGAATGGGAAGCGCATTTTCATTGGCTTGAAATGAGAAGCGCCATCCCATCCACTA GCTGCAGTAATAC[T/G]GCATCCCATCCACTCTCTTTTTTGACTGAAACTCTTCAAAGAACT GCTGAATGTCCTCTCTC
301a	24	G/A	TTTATTCCAAG TCATTCAAGCC AATGGGAAGC AATGAAAATG		TCTTTTATTCCAAGAATGGGAAGC[G/A]CATTTTCATTGGCTTGAAATGAGAAGCTTCATACTCCACT CTAGCTGCAGTAATACTGCATCCCATCCACTCTCTTTTTTGACTGAAAACTCTTCAAAGAACT GCTGAATGTCCTCTCTC
13763	59	T/C	GGCTGACACT CCCACACCTGC CCCT CGCAGTGAT		GCTCGTAATGAGAGACAGAAACGCTACAATCTGTTCAACATCTGTTGGGCTGGCAAATGTCCATGGGGGGCCTGGGGGTGTGGGCGCAGGGTGTGGGGGTGTTTGTGTCTTCAATAAAGAGCAGAAGAGAAACTCAAGAAT...
13578	48	T/A	TCAATAAAGA GCAGAAAGAA AACC CAGTGTGTAAG AACATCTTTT GTC		TTTTTTTTGGTGAGTGTTTGTCTTCAATAAAGAGCAGAAAGAAAACTCAAGAATT[T/A]AGACAAAAAGATGTT CTTACACACTGAGCTTACACAGTCACCCAAACATTGATATTTGCTTTTTCCCGAGGGCAAAAAGA GAGTCTTCCCAGAAACCTC
3789	62	G/A	TTGGATGGCTG AGGGAG CAGTGCGCTTC CTCTGTTC		TCCAAGGAAAAGAAAAGAAAACCAATCAGTGAGAAAACTCAAGTGAGAAAACTCAAGAATTGGATGGCTGAGGGAG[G/A]GGG GAACAGAGGAAGAGAGCCACTGGGACTGAATATGGACAGTGAATATGGACGTGGGGACTGGAGGTCCTCACTCTCTT GAGGTCCCT
3594	66	G/A	TTTTAACACA GATCACAAAA AGC	CCTTTGCGCCA GTACTTTTT	AATAACAAGTTAAGTTGCAGCTGCAATGTTGCAATGCAGGTTTTAACACAGATCACAAAAAGC[G/A][T/A]GCACAAAAAAGTACTGGCGCAAAGGACAAAATAATGCTAAGAATTAGGCCAAACAGCTGC

ID	No.	Allele	Flank	Sequence
NI-15625	40	C/T	...	GTTTCTCCCACCTACTCCCGCAGAAAAAGGCCATATTCAA[C/T]TGTCCCCATACTAATTTTTGAATAACCTAACTCTCCCTTGTTCTTGTTCTACTAAGAGAGGTTCTTTTTGGCTACAAGTAACA
NI-13367	84	C/G	A / CCACACTGAA GACTCACCAG	GTCTCACTTCTTGTCTGTCTAGGCTGTAAATTTCAGTTAACAAGTTTCTATGTGATTGTTGTGGCCACACTGAAGACTCACCAGAA[C/G]AGGGTGGGGGTGGGGAATACTTAATCAATATTTGTGGAATTTACCCGAT
NI-13600	26	G/T	TTAATGAGCC AAGCATCCAT / TGATGG	CATATTGAAAAACTCACTTTAATGAGCCAAGCATCCAT[G/T]CCATCATCTAGTAACAATTTCAATATGCACATTATATTTGTTACTAGATATACTGGAAACAAAGAATACGGATTGTGTAGGGAAGAGCATAGAGGAACTGATTCCCTTCTCTACCC
WI-13602	89	G/T	TCCATTCTGGA GACAACACA ATATTAAT / GCCCA	GCATACCTCATGATAGGAAAGAAGAATGAAGTCAATAGTCTTTAGCAAGCCAACTAGCTCAAGGAATAGACAGCCCTTTCCATTCTGGAGACAACACA[G/T]AAATCTATTAAATATTAAATATTGTCATGGTATGCACCTGCCCA
NI-13650	76	A/T	AAAGATTCAC AATATTTCACT TTTAAAAC GTTTTT	GCATTAACACATTTAAAAATTCTGAGGGATATTGATGAGAACTATGATGAAAGATTCACAATATTTCACTTTTAAAAAC[A/T]TAAAAAACTACTCTTCATATCCTGATGACTTAAAGTTACGG
VI-14319	83	C/T	CCAAATCATCT CACAAAGCTA ATATTGTTGCA TG / A	TGTTTGATTGAAGAAACATCTCTAAAAATACCATCTGAGTGCAAGATAAAAAAGGAAATAGCAATTCAAGGCACAAAGCTAAGC[C/T]ACATGCAACAACAATATAGATGATTGGGGTGGGACAGTACAGAATT
I-13528	80	A/G	CAATACATTT GCATTTTCCTA AGTTTCTCTG AAAA	ATTGGATACACATGCTTTTAAAAATGGTAGCTTTTAAACTGTAATCAATACATTTGCATTTTCCTAAAAAGAAGACATTT[A/G]TTCAGAGAAAAACTGTGGTATCATGCAGAAAAGCAGAAAAAAATT
1909c	93	A/T	...	ACTTAAACTGGCTTATCTTCAAACTCGAATATCTTTTC[A/T]GAGATGTCTAGCTGTATGTCTAGTACCCACTGACTCTCACTCTCTTCAAACTCGAATATCTTTTC[A/T]GAGATGTCTAGCTGTATGTCTAGTACCCACTGAACATCTCTCAA
1909b	80	G/A	TTCCTCACACT CTCTTCAAACT GCAGTGGGTAC TAGCTAGACAT CTC	ACTTAAACTGGCTTATCTTCACGGTAATCTATTCTGTATTTCCCAGTGAAGTTCATCTTCCTCACACTCTCTTCAAACT[G/A]AATATCTTTTCAGAGATGTCTAGCTGTATGTCTAGTACCCACTGAACATCTCTCAA
323b	86	C/A	...	TTTTTATTGAATTCCAAATGTAGCAAAATCATTAAAACAAATTATAAAGGGACAGAAAAATTAAGAATCAAACATCATTCTGGAC[C/A]ATGGGAACCTTGAAAAGGCATGGGAGACCAGTAACTA
323a	78	T/C	ACAGAAAAAT TAAGAATCA ACATCA / GCCTTTCAAG GTTCCCAT	TTTTTATTGAATTCCAAATGTAGCAAAATCATTAAAACAAATTATAAAGGGACAGAAAAATTAAGAATCAAACATCA[T/C]TCTGGACCATGGGAACCTTGAAAAGGCATGGGAGACCAGTAACTA
189b	104	G/A	AGATAATGAA ACATCTGCGA AAA / GATGAGGTGAT TCCCACACTT	AAAATTGACAAATCAACTAGCTTGCTTTTGTCGTTTGGAAGACTACCATTATTCAAATTTATTATGTAATACACTCATCCAGATAATGAAACATCTGCGAAAA[G/A]AAGTGTGGAATCACCTCATCTGTGC

ID	No.	Allele				Sequence
NI-15389a	33	G A	TC	AATCAACTAG CTTGCTTTTG	TTTGAATAATG GTAGTCTTCCA AA	AAAAATTGACAAATCAACTAGCTTGCTTTTGTC[G/A]TTGGAAGACTACCATTATTCAAATTATT ATGTAATAACACTCATCCAGATAATGAAACATCTGCAAAAGAAGTGTGGGAATCACCTCATCTGTGC
NI-15747	88	T C	AGTGTTT	TGCTTCATTTT AAACTAATTT CATAATTCACC AAAAGTTCATA TAATTT		TGTAATCTGCTTACAGTCCTTTGCAAAGACAGACATATGTTTTGCATAAAGATATAAATTGCTTCAT TTAAAACTAATTTAGTGTTT[T/C]TTTAAATTATATGAACTTTGGTGAATTATGAACTGTACCAAAC C
WI-13752b	117	C T	...	...		AAGAAAAGCACATACATTTCCAGAATTTTGGAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTTCCTTCGTTAAGTGCTGGATATACTTGGCTTGCAC(C/T)GGACACCTTTTACG GAGGGATTCCGGACAACT
WI-13752a	106	T C	AGTGTCC	CCTTCTCGTTA CCCTCCGTAAA AGGTGTCC		AAGAAAAGCACATACATTTCCAGAATTTTGGAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTTCCTTCGTTAAGTGCTGGATATAC[T/C]TGGCTTGCACCGGACACCTTTTACG GAGGGATTCCGGACAACT
NI-14339	102	T G	TTAC	CCCAATCAAA CAGTACATGA	TCCAGATTTCT GGAAACCG	AATCATTTAATGAATGTTCCAAACACACCCTTCACTGGCTAAATTTCACTGGGATGGAAG CAGATGAACCAACATCAAACAGTACATGATTAC[T/G]CGCGTTTCCAGAAATCTGGATAC
WI-13744	115	C T	GC	TGGTGCTGAAC GATAAGCACA GC	AATCAGGAAA AAAACTGAA	TGGATGGATGGATGAGGCCCACCTGTGTTCAACAAAACACGTAATGAACTTCATGCAGCTTAGAT TTCCTTTGCCCAGCTAGGAGCTTGTGTATGGTGCTGAACAAAACTGAA[C/T]GCTGTGCTTATCTTTC CTGATTCT
WI-14061	68	C T	...	...		CCTTTGACTATATGTTTTTCCAAAAATAGGACTATGTGTAGAAGAGAGAGCCCCGTACATACCTTAT [C/T]AACCATTTCATCCACCATTTGTAAAAATCTCATCTTCTGGGTCTGGATACTCAAAAACAGAT
WI-15719	69	A C	ATT	ACCCTTTCATC CATTCAGC	TGATACTTGGC AAGAGTTTAA ATT	TTACAGTTGGATTAACACTACCACACTGAATACTGAACTTAAAACTCTTGCCAAGTATCATGAACTTAT C[A/C]AATTTAAAACTCTTGCCAAGTATCATGAACTTACGAAGAGGAGATAAGAGATCTGATC
-13810	106	T C	AACTT	CTCTAAATCG ATACATCCAA AACTT	GAACTGATGCT TGCTGCTAACT	TAATCCATCATCTAAAATCACACATACTAGATCAAACAGAAGTACCACAGTATGCTTTATTTTGCA GGTATTAATTGGTTCTCTAAATGATACATCCAAAACT[T/C]AGTTAGCAGCAAGCATCAGTTCTTC
'36a	27	G T	CACA	ATTTTATTCAC ATTAAACTTG CACA	GTTCTTTGATA TGTGGCTTAGT TTT	GGATTTTATTCACATTAAACTTGCACA[G/T]TAGCAAAAAATCAAAACATAAAACTAAGCCACA TATCAAGAACAATATACACTATAAAGTGCTTCAATGCAGCAGGTATTTCCATAAATA
'85d	72	G A	...			TCAAAACTGCACACTATAAAAGTGCTTTAAAATGCAGCAGGTATTTCCATAAATA AAGTGC[G/A]TAGTGACACATAGCTGTCACAACACAGTG
85c	56	A C	...	...		TCAAAACTGCACACTATAAAAGTGCTTTAAAATGCAGCAGGAGATGTGAAGAC[A/C]CAAATG AACAAGTGCGTAGTGACACTATAAAGTGCTTTAAAATGCAGCAGGAGATGTGAAGAC[A/C]CAAATG

3785b	40	C	G	...	TCAAAACTGCACACTATAAAAGTGCTTAAAATGCAGCAG[C/G]GAGGAGATGTGAAGACACAAATG AACAAGTGCGTAGTGACACATAGCTGTCACACAGTG
3785a	27	T	C	AAAACTGCAC ACTATAAAAG TGCTT	TGTTGTGACAG CTATGTGTCAC T	TCAAAACTGCACACTATAAAAGTGCTT[T/C]AAAATGCAGCAGCAGCGAGCAGGAGATGTGAAGACACAAATG AACAAGTGCGTAGTGACACATAGCTGTCACACAGTG
VI-13793	88	C	G	GGATTTTACAT TCAGCCTAGAT ATAGG	GGGCAGGAGGA TTTGTTACT	AGAAACCAAGTATATCATAGGCAAATAAAATAGTTTTACCCCCATTGATACAACATAAGGGATTT TACATTCAGCCTAGATATAGG[C/G]AGTAACAAATCCTCCTGCCCATAAATCTATGACTTG
VI-13794	52	A	G	TTCCTCACCCT TTTCTTTCTC	AGAATGGGCTC TTAACCTTGTA	TAGTCTCCTACAATTCCTTCAATCCATTTCTTCTCCTCACCCTTTTCTTTCTC[A/G]TACAAGGTTAAGA GCCCATTCTTCAAACAAACAAAAAACAACATAGAGCAAT
VI-15729	35	A	G	CTTTGAACCAT GTGTAGACTGC	CTCAGCTTCTT TCTAAAGTGCC	TCATTTAAGTGCACTTTGAACCATGTGTAGACTGC[A/G]GGCACTTTAGAAGAAGCTGAGACTGAA AGTGTCTGTCTTGACTTCCCAAGGAAGGTAAGTCCCGTTGCAGCCCGGGCCTGCTCATTGTTA
VI-13424	66	G	A	TGAGGTTTTTC ACCCTATTCTT C	TTTTTCTCCCC AGGGTCTA	GTCCTTTGCACAAGTCTCCCAACTGGTTTGGAGTTTCCCTTCTGAGGTTTTTCACCCTATTCTTC[G/A] TAGACCCTGGGGAGAAAAACACATGTAAGGTGAAGTGTAAGGCAGGCCGTTCACAAGAT GCTGGCTAAGCGGCTTC
I-14065	29	T	C	TCTTATAAAA GGTCAGAGGC AATT	CAAGCTGAATC TGGGATCTC	AACTGTCTTATAAAAGGTCAGAGGCAATT[T/C]GAGATCCCAGATTCAGCTTGTCTCATAAAAGAT TCAACTTCAAGTAGCACAATTTCTTGTCTGCTTTAATCCTGAACATTCTTGAAGCACGAA
-13446	22	G	C	GCCATGTGTTCTT CTCACTCATCA G	AAGGGAATCA AAATCAGAAG	TGCCATGTGTTCTTCTCACTCATCA[G/C]CCTTCTGTTTGATTCCCTTCCTTCTGCTCTGTAATTTTTTCTC TTCCCTTTTAGGGCCTAGTGTCTGTTAGAAATTCTGGTTTTGAGAGTAGTGAGCCCTTTACTTTTTT CTGACTGCCTAATT
-13725	56	A	C	TGAGCACATA TGGGTGCC	CCTGCTGTCTC GGGC	TCACACAAGGCATTTGGAAATGTCACCTTACACATGGTGCTGAGCACATATGGGTGCC[A/C]GCCCGAG ACAGCAGGATAAGTTTCACAAAACTTGACCAGGCAGGTTAGAAGCAAGGCATGGTTCAGGATG
'02d	107	T	C	...		CAAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAAACTGTAACCCCTGTAAACAATACTAA[T/C]GGGTTCTTTGAACAAATAGTTT GA
02c	101	T	C	...		CAAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAAACTGTAACCCCTGTAAACAATACTAACAA[T/C]ACTAATGGGTTCTTTGAACAAATAGTTT GA
02b	90	C	T	...		CAAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAAACTGTAAC[C/T]CTGTAAACAATACTAATGGGTTCTTTGAACAAATAGTTT GA

ID	No.	Allele		Seq 1	Seq 2	Sequence
702a	48	G	C	AACAAAATAA AGGCTTTCAA AAAG	CCTCACCCCTT TACCCC	CAAATGTTTATGAAGAGACTCCGAACAAATAAAGGCTTCAAAAAG[G/C]GGGTAAAGGGGTG AGGAAAGCATGTGAGAGAAAACTGAAACAATACTAATGGGTTCTTTGAACAAATAGTTT TGA
831b	113	T	C	...	...	TTTTTTTATGGATGCACTGTTACATGTTTATTTAGGCGAAGGTGACTTGGAAAAGGAGATTCACAT ACTTCCACTGTATCCTCCGGGTAAGTTTTCCTTCTCTGTGTAGA[T/C]GTCTCCCATGTTACAGTCAAC TATAAAACATGGCTCA
831a	56	G	C	...	...	TTTTTTTATGGATGCACTGTTACATGTTTATTTAGGCGAAGGTGACTTGGAAAAG[G/C]GAGATTCA CATACTTCCACTGTATCCTCCGGGTAAGTTTTCCTTCTCTGTAGATGTCTCCATGTTACAGTCAAC TATAAAACATGGCTCA
-13806	62	G	A	...	...	TGATTGAGCTTAGAAAGGAAGTCATGTTGAAATCAGAGAGAGGCCAAACTAGGCCTCAGGT[G/A]C CCATTAAGCATGCTGTGAATGCAAAGGAAAAGCTTAAAAAATTTTTTAAGGGTGACTCCAGTAAA CAT
-14372	86	A	G	...	...	CACATTTTCAGCAAACAAATCGAGGTGCAAACAGGGTTTATTTCACATTAATATATTAACTGGATTT TTTGTCAAATAAATAGGGA[A/G]TTCTCTTTAAATAACCATCTCCTCACTTCATGGCCAGT
-14373	95	A	G	...		AGGCTGTTTTTGAGGCCTGAGGACCCCAAACATGACACGTAACCATGGTCATGTGAGTT ATGAGCTAGGAAACCCTGGACGAAACCA[A/G]CACATATACAATCATCTCCCACCTCCCAACGCCCTTT ACTTTCACAGCCTCTGCA
14078	61	C	T	AAAGAAGTAA ATTAGGAAGA GCAAGA	TGTGTGCATGT CTCTTACTGC	AGAAACCGAGAACTCAAAGAACCACATGGTGTATCAAAGAGTAAATTAGGAAGAGAGCAAGA[C/T]G CAGTAAGAGAGACATGCACAAAATGCAAACAAGGCATGGGAAGACTTTAGATGGTCACG
14083	47	C	T	AGACTTGAGA GCTTAAAACA ACACT	GCCTACTGGAC CTCTAAACTAC TGA	TTGCTACATAACACATTACTCCGACTTGAGAGCTTAAAACAACACTC[C/T]ATTTGTTTATTTCACAG CTCAGTAGTTTTAGAGGTCCAGTGAGGCTTGGCTGAGTGTTGCTTAAAGTCTTTACAAGGCCAA
4085	31	A	G	CATTTATTTC ATGTGTAAGA AGAAAAA	CAGTCATGTTC ACGTGCTAGTT	TGCATTTATTTCATGTGTAAGAGAAGAAAAC[A/G]TAACTAGCACGTGAACATGACTGGATAC ACGGGCTCAGCACGAGGCTAAAGTCAGAAGTGAGTGAAAAACAAAATAGCATGTTGATTAAGTGAAA TAACAGAACAGGAGGCCTT
2169	121	G	C	AATAAAACTT CCTATTTCTT TTGCTT	GGGTTCTGAGG TGAAAGAAAA A	GTCAAAGGTTGGCAAATTTATTTCACTTATTGTAAATTTATTCCACTTATCAAGAACTTACAAAATATTTTTGTTTCATTTCTAAA TTTTCACCTTATTGCTAAGTTATAAGTTATAAAAATAAAACTTCCTATTTCTTTTGCTT[G/C]TTTTTCTTTCA CCTCAGAACCCCTTA
705	50	A	G	GGAGGGGAGAT TTAGACTGA GATC	AGCTGTAGTCG TCAAATACTCT AGAA	TTGTTTTTATTTGGGGAGAATGAAGAGGAGGAGGAGATTTTAGACTGAATC[A/G]TTCTAGAGTATTT GACGACTACAGCTCTCTTTGTACTACGGAGACCCCTGCTTATAGCGAGAAATCCTCA TCTGCGGTTGCCAGACAG

ID	No.	Allele	Allele	5' flank	3' flank	Sequence
WI-14379	102	C	T	TCTATTAACA GGGTTATGTCA CACC	ATCATCTGTTT	TTTATGCTGTGTTGTTGTTCTACTGGTCGGTCGCTCACTAATATCCAATCCTAGTATGATTTTCTTT
WI-14102	22	C	A	...	TGAGGTTGACA	TACTTGTGTCTATTAACAGAGGGTTATGTCAACCTCAACCTCAAAACAGATGATACT TAAATAAAACAAAGCAGAAAA[C/A]CCCACCATTAACAGAGGACACTGCAGAGGCTTATGTACA ACACGTGTCCCGCGAGGCTGCGCCAGGACTGCCACTCACCCAAAATTCTTTGGAGCAGAG
WI-15937	24	A	G	CGCAGAGCTG CTGTATTTAAA A	GCAGAGATCCA GACGCTTGT	ACCGCAGAGCTGCTGTATTTAAA[A/G]ACAAGCGTCTGGGATCTCTGCAGGGGCTGGGACCAGCTGC AGTGGGGGCTCCGGCCACTGTCCTGCTCCCAGGACTCTTCCCACCACCCC
WI-15944	24	A	C	AAACTGAAAC GTATTTCCTCC A	GGCCTTTAAGT TTCTACGGTG GGTT	TGAAACTGAAACGTATTTCCTCCA[A/C]ACACCGTAGAAACTTAAGGCCGCAAAAGACTCACACCC ACCACCTAGCGCGCGAAAAAGGAAGTTTCAGGTGATACAAGATGTCCTGCCATCACACCTGAAGGAT GGTT
WI-14124	92	A	G	...	...	ATGTTTTATGATCAATTCCAAACATACAGTACAGGGAAGGTGAAATGAGTAAGAAAAAAATCAT ATTTAAGTCCCCGTTAACACTAAGCC[A/G]TATTATTCAAAATGTTTCAAAATACTCAGCCAGAT CACCAAAGCTCAGTCACTAC
WI-14125	88	C	T	GGTTTGACCTG CATAGATTTTT	GGAATGGCATG GCCAC	GACAAAGAGGCAGTTCTGTAGTTCCAGCAGGGCCAGAGCAGTTATCAGAACGGGTTGGTTTGACCT GCATAGATTTTTGACGACTA[C/T]GTGGCCATGCCATTCCTGTAAGTGAAATTAATGAACA
VI-14136	120	G	A	GCTTTCTCACC ATGTCTTCACA	CTTGTTCTGTC TCTTTGGGC	GTTTATTTTCTCACAGTTCTGGAGGTTAGAAGTCTGAGATGAGGATATCACCAGCATGGTTAGGTTCT GGTGAGGACTCTCTGGCTTACAGCTGCTGGCTGCTTCTCACCATGTCTTCTCCACCATG[G/A]GCCCAAAGAGAC AGAACAAGCTCTCTGGT
VI-14138	23	C	T	TGTTGGCACCA GAAAAGCT	CAGTATGTACA GTGACATAACA TAGAACA	TTGTTGTTGGCACCAGAAAAGCTC[C/T]ATGTTCTATGTTATGTCACTGTACATACTGTAAACAAGACT GCATTAATATTGTTTCTTATGATTTGTTTCAATG
Il-13551	74	G	A	TCCTTCAGTAG TAGTATATTCA GACAATC	GCTCATTCTT TTAGTGCTAAG TAATATT	GGCAGGTTATTCATAATTTCAAAACTTGGAAGCAACCAAGATGTCCTTCAGTAGTATATTCA GACAATC[G/A]AATATTACTTAGCACTAAAAGAAATGAGCTATCAAGTCATGAAAAGACATGCAGG AACCTTAAATGGATATTACT
1-953b	59	C	T	TTTTAAGAGTG TCCTTCACATC	...	TTTTTAAGAGTGTCCTTCACATCATT[C/T]GTCAA AAACAACAAGAACAGATGAATAAGGAAGCCCAGTGCTCTTTTGAGATAGAGCCTTCTTCAGAATCA CCTCCC
953a	26	T	G	TTTTAAGAGTG TCCTTCACATC TGTTGTTTTTG A	...	TTTTTAAGAGTGTCCTTCACATCAT[T/G]TATATTGTATTGCACACAAACTTTTTAACTCCGTCAA AAACAACAAGAACAGATGAATAAGGAAGCCCAGTGCTTTTGAGATAGAGCCTTCTTCAGAATCA CCTCCC

ID	Pos	Allele		Sequence
VI-14631	82	G/A	---	TGAATTCAATGGACAGTTTTGCCTCTGTTTAGTGAAACCCTCACAAGCACTCTGCATAGTCCGCTTTCTGTCTTCTTTAAC[G/A]TGCCTGGTTCCCTCTGCCCAAACTTTAGGATTGGGCCTCCTCAGGCCTTGTCCTGA
VI-6053	24	A/G	---	ATCACCACCGTGTCTCAAGAACAAC[A/G]TCTTCAACTCATATCCCCGGGACTTTGTCAACTGCAGTACACTTCCTGCATTGAACCTGGCTTGGCCAGTTGGAACCACGGAG
VI-15964	99	T/A	GCTCTCTGTCC CCTCTGC / GACTTCTCCAC CCTCTGC	AGCAGTGAGGGGTATATCGTGTGTATTAAGCTCATCTCTGTCCTGGAGGTA[T/A]GCAAGAGGGTGGAGAAGTCTTGGCAAGGGGAGGTAGTAAGCTCATCTCTGTCCTGGAGGTA
VI-12075	103	G/A	AGCAGCTGGG AGGCAC / CCCCTTCTTC TCTTCCTTC CCT	CAGCTAAAGGATCACTGCAGCTAAATACAGATAGAAGCAACAAAGCCAGGCAAATACCCATCAGAGACAGTAGTGACAAGAGCAGCTGGGCACGCGGGGGAGGGCC[G/A]GAAGGAAGAGAAGAAGAGGGGGAGGAG
I-12179	96	G/A	GGAGGTACGG TGGAGGTCA / TCGAATGACCC TGTAGATGC	TAATTTAAAAACACGCCCTTCCCACATAGTCGTGAGGTACGGTGGAGGTCA[G/A]GCATCTGCACATTTTCCTAGAGGACATGAATAGTGATGTGGAGGTACGGTGGAGGTCA
I-14651	49	C/G	CAAGAATCAT TCTCATTAAA TCTTTTCTGA CTTATTT	CACAAATAGTGAAATTATCTGAGCAAGAATCATTCTCATTAAAATTGT[C/G]AAATAAGTCAGAAAAAGATCAATATCTCCCCTGCTTCAAAAATGACACTCCCAATTTTCAGCAGGTAACCACTGTTA
-14666	105	T/A	---	AATGTGGACTTTCAAACAGGGTTTAAACTAATACTAATCTAATACAACTTCTACAACACATTCCAGAGCATTATAACAAGAATTATTTACAGGCAGCTAAT[T/A]AACCATGAAAAGAAAAAACTTG
13473	31	C/T	---	ATCTAGATGTCAGCAAATGGGCTGAGACTG[TC/T]TTGTCTGGTAGATGCAGTGTTTGTGTATGTTTCTACTCTATTACAAAATTAACAGAAAATTAACAGAAATATGGCTTGCCTTTGTGCAAATGTTTATATCACAGTC
13967	103	A/C	AAAAGACTAC AGATACAAGG AAATAAAAA TG	AATTTAATAGCAGCTCTGTGTTGTGATTTAAAGAACAAGGAAATACAAGGAAATAAAAA[A/C]CACTTTAGGAGATGAAAAACACAAAAAAAAATAAAAAGACTACAGAAGGAAATAAAATATGTCATTCAGCAGTCATT
4408	60	T/A	GCAGACACAC TATTACAGGCT AG	TTAATATTTCAGCAAAGTTATTGCAACAGGTTGAAAATGCAGACACACTATTACAGGCTG[T/A]AAAGTAACAAAATGAGTTTTACACAGCATTTGAAAATAAACACATACTTATGGGATTTGTTGAATGA
3683	47	C/G	---	TTTGTGTGTTAAGAACAGCATTTTGAAAATAAAACCTATCGTTCATGGTACATATTGATTGTCGTCCCCATG[C/G]TTTACAGCCTTTTAAAT
)b	63	C/T	CATTGAGATAA AGCACACTTAT CAC	TTAGAAAACTGATAAAAGCAACAACACTTTGGGGAAAGCACCAGTCCTTTGTGCTA[C/T]GTGATAAGTGTGCTTATCTCAATGAAGCAACCCCA
335	22	G/A	---	ACATGGCAGATACAGAGCTGTC[G/A]ATCTTGAAGACGAACACCACTGACCAGGAAATGCCACTTTTACAAAATCATCCCCCTTTTCATGATTGGAACAGTTTTCCTGACCGTCTGGGAGCGTTGAAGGGGTGACCAGCACATTTGCACATGCAAAA

WI-16002	59	T	C	GATAACATAA AATGATCATG AGAATTTC	CCAACATTTTAAAAACCTATGACTGGTCATTGATAACATAAAATGATCATGAGAATTCAT[T/C]GTTA AAAGTCAAGAGGAGATGGCTAATGCATGCTGGGCT
WI-15361b	101	A	G	GCCATCTCCTC TTTGACTTT · CCCACTTGAAC TCAAGTCATC A · AAACTAAAAC CTTTGTGCCTA AAA	GTGGAATTTATTAAGCCATCCCACTCAATTTCCTTCACACTCAATACTGTTGAACAACAAGATAACAT CTTCTTGCTCATCCCACTCGAACTCAAGTCATCA[A/G]TTTAGGCACAAGGTTTTAGTTTTCTCGG GAAATCAAGTTTAACCA
WI-14759	73	T	C	GCGTTTGACTT TCCCACACTGC GTGCGG · CTAGGAGGGT GAGGTGTAGA TAT	TGAGTTACAACAAATGAGCAACAAGTTAGAAAAATTGGTTTATTCAAACTTCCTAGCGTTTGACTT GTGCGGT[T/C]GTACTCAAATGGGGACGGGCAGTGTGGGGAGGGATTGCAACCAGAGTTCATACTG CAA
WI-12535	50	A	T	GCTCCACGAGA AGAGAGGAA	TCCCTAACATTTATTTCAGGTGGTGACTAGGAGGGTTGAGGTGTAGATATT[A/T]CTTCCTCCTCTC TTAAAGACCTGCCCTCC
WI-13805a	112	G	A	AAAGGCACAC CTCAGCCTGCC GGGGAA TTGACC	TTCCATTCATTATGCTTGGCTTTACCAATTTTTATAGCTATTGGGAGGCAGGAAAGGGAATTTTGGC CCCAGAAACCATGAGATTTGGGTCAGAAAAAGGCACACGGGGAA[G/A]GGGTCAAGGCAGGCTGAG AGTCACATTCCAGACCTC
WI-12340	18	T	C	...	ACACAATATAATTCCATT[T/C]CGAGTGATTAAAACCTTTTTGTTGTTTAGAACCAACAAAACTAC AAGAAAACATTTCAAAACCTTTTTCAAAGGCTGA
WI-14808	52	T	A	ACCCACCACA CTACCCTGT GAGGCATCACA ATGTTAAGATT TT	CTTTGAAACACTTAAGCAAACAGTTAAAAGTACCCACCACTACCCTGT[T/A]AAATCTTAAC ATTGTGATGCCTCTGCATCAATTTT
WI-14816	29	A	T	...	AGTTAAAAAAAATCGAGTCAGCATTTTGTATCCAAGCCCCTGAAACACAAGAAAAACTGGAAG TCAAATGCATTTATTTTGTATCCCAAGCCCCTGAAACATGAAAAATATTTACTAAGGAATGTTG
42c	71	G	T	...	ATTACCAGCTACGACTTTC · CCGTGTTTCATTGAAGGCTATTAGGCAAACATTTTATATTGCAAGCTCAT
42b	70	G	T	...	CCGTGTTTCATTGAAGGCTATTAGGCAAACATTTAAATGTCATCATCCATGTGAGGGCTCTAGATC ATG[G/T]TAGGTGATTGATAAACAAATACGATCCATAA
2a	45	C	T	GCTATTAGGC AAACTGAACA TTTTAAA	CCGTGTTTCATTGAAGGCTATTAGGCAAACATTTAAATGTCATCATCCATGTGAGGGCTCTAGATC AT[G/T]TAGGTGATTGATGAAGGCTATTAGGCAAACATTAAATACGATCCATAA
173	57	C	T	TCTAGAGCCCT CACATGGAT · GGATACAGCA GTAAGAATA · ...	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGT[C/T]ATCCATGTGAGGGCTCTAGATC ATCATGTTGAGGTGATTGATGAAGGCTATTAGGCAAACATTTAAATACGATCCATAA CACCTAAATCATTCTAGAAACTGGGACATACAACAGTAAGAATACAAAAAATCCTGC[C/T]CTTATA GAGCATACATTCTAGAGAGGTGGGAAAGAGGCAATAAATA

Name	Pos	Allele 1	Allele 2	Probe	Probe	Sequence
WI-14836	28	T	C	…		TCTTTGGGAGGGATAGAGGACAGAGTGTT[T/C]GTTGATTTTCGTTGGTTTCGGTTGGTTGTCATT GGTTTTTGTTTGTTTGCTAATTTTC
WI-14856	60	A	T	TGGTGACACG GAAAATACTT AA	TTTGTTTGCTA CTTTTACAAA CTTT	ACATTCCTTATGATAGCAACAACTAAATATGATGGATGGTGACACGGAAAATACTTAA[A/T]TAA AGTTGTAAAAGTAGCAACAAAATTGAGTATATACTATAAGTGATAGAGGATGTATATGAAAAA GGCTATAAAAGCTCCAAAA
WI-14863	61	G	A	…		ATGGCAATTTACTTTATAGCAATGAACAAATATTTGTCAAGGGCAAATATTTTTGTCTG[G/A]AG TTAATAAGTTAATATCTTTTACCACAAGCTAGAGGTCAACAGTACCACTATTGATTGCCACT ACCTGGC
WI-14867	46	T	C	GACATTCCAA GGCTCTCTAAC A	TGGGGCTGCAG ACACTC	TTTTAATTAAACGTAAAAAGGCAGGACATTCCAAGGCTCTCTAACA[T/C]GAGTGTCTGCAGCCCCA TTCGCTTTGAGATGTGAATGTGTTAACCCAGGGTGGA
WI-14733	98	G	A	CCAAATTGAC AGATATTCTGC A	GATGAGGTCAG GCCATTATT	ACGGAGTCGTCTCTGATGTATTCTTGTCAAAAAATGTTGCCTGATTCTAATCATGAAAGAACAATT AGAAAAAATCCAAATTGACAGATATTCTGCA[G/A]AATAAATGGCCTGACCTCATCAAAAACATCA ATGTCATGAAAACACAAA
WI-14898b	79	A	C	…		TTTTGTACCTATTCCCTGTTCAGTGCATGTACAGGAAGAGTTGTCTCATGTACAGGAAGAGAAA ACTTTCTCCAT[A/C]AAGCTGCCTGCGTGCACGTTGCCTGGGCTTTGCTAACCCCTGGTGCTGCATCT GCCTGTGTTCTGTCTT
VI-4898a	50	A	C	CATGTACAGG AAGAGTTGTCT CA	AAGTTTCCTT AGTGGCACCT	TTTTGTACCTATTCCCTGTTCAGTGCATGTACAGGAAGAGTTGTCTCAT[A/C]AGGTGCCACTAAGG AAACTTTCTCCATAAAGCTGCCTGCGTGCACGTTGCCTGGGCTTTGCTAACCCCTGGTGCATC TGCCTGTGTTCTGTCTT
I-14907	48	G	A	GGCACACATT GGACTCTGAC A	TCTGCTGCAAG GGGAAT	TGGTATTTATTTCCGACATTACTGTAGAGGCACACCCATCAATGTGACTGACTCCTGCAGCAG ACATTTGTGAAGCTGCTGTGGTCGGCACACATTGGACTCTGAC[G/A]ATTCCCTTGCGACGAG CACGATGCTCACGTGTG
I-14911	52	G	C	CCAATACATT CAGTTCCTGGT CA	CAAACCAGGA AAAGGACCTT	CTAGAATCTGGGAAGTCCAAGCTCAGTGCACCAATACATTCAGTTCCTGGT[G/A]AAGGTCCTTTTC CTGGTTGCAGAACAGATACCTTGCTGTATCCTCACATGGCAGAGAAGAGGAAGTAATCT
-14913	88	C	A	…		CTGATGCTTTGACACTCTGGGGCATTGCTGTCTGTCTGCA[C/A]CCTGCACGTGCACTTCTCCTGGACCAGCCAATTTC TAGTGATGATAGTAGAGGACTCACA CTACACCTCCAACCACCT
14914	66	G	A	CTGGACACAG TTTTCTCTAGC A	CAAGCCCAGGA CAATAAATTC	ATTTCCCTGATTGGCTGTGTCGTAAAGCCTGTGAAGTCATGCACATCTGGACACAGTTTTCTCTAGCA[G/ C]GAATTTATTGTCCTGGGCTTGATGGCTTCACAGC
14926	49	T	C	…		GTTTATTTTCAAAATGACAACATCCCAGATTGAAATGGGCACTTAGCGAA[T/C]ACTTGTGGACCACA AGACTTGTCTGGAGAACATGTTCAAATTTTCAAATAAAAATTTTCCTTAATCAGGTCCA

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-65-

'I-16083	89	C/T	ATGTTTAACA CAAACATATC AAGGAT	TGGAAAAGAGATT CCAGCC	GCATCTTTATTACCACAGAAACTCATTTATGTCCTAATCATTGTTAATATATAATATATAAGCATGTT TAACACAAACATATCAAGGAT[C/T]GGGCTGGAATCTTTTCCATTCTATAGAAAGCACTAACCATC CATTAAAGCAG
'I-14930	55	C/T	GGAGGAGTCC CTCATGGAT	CACAACCAACC AATACCGC	CAGTTCTGTGTTCTGGAACAGCTCTCCTTTCCACAGGAGGAGTCCCTCATGGAT[C/T]GCGGTATTG GTTGGTTGTGGTGATTTGGGGAGCACGAGGAGAGCAA
'I-14946	47	T	C	...	TCAATACTGAAGGTGTCAAAGTGGTCATTTGCCCCCAGACATAACA[T/C]CTCTAAATCATCCTCTA GATCCAGGGAGTCATAAGGACACATTAAAGGGGTCCCAAGTACTTTATGGAAAGGATT
5987b	80	A/G	...	...	ACATTAAAACAGCACAATAAAGGGTCCCAAGCTGCCGGTTGGTAGTGCCTTCCACTATGTGAGGACAC TAAGAAGATGGTC[A/G]TCTATGAACCAGTCATCTATGAACCAGAGTTGGTGAGTGCCATGTCTCTTAAACCTCTCAGC
5987a	32	C/T	CACAATTAAA GGGGTCCCAA	GGAAGGCACTA CCAACCTC	ACATTAAAACAGCACAATTAAAGGGTCCCAAG[C/T]GAGGTTGGTAGTGCCTTCCACTATGTGAGGA CACTAAGAAGATGGTCATCTATGAACCAGAGTTGCCGGTGCCATGTCTCTTAAACCTCTCAGC
'I-14948	56	T/C/G	AGGGAAACTG CTAACTTGTCA ATCAGTTGTTG TCG	GATGATCTTAC	GAATAAAGTTCTTATTGCCGTTCCTTCAGGGAACAGGGAAACTGCTAACTTGTCAGT[T/C]CCAACA ACTGATGTAAGATCATCTTCTGACCATAGCGAACCTGTAAGGCTTGCTGTTCCCTCCAGCTGA
-16100	52	A/G	CAAAAGCTA TTTTCCTACAC GTTGA ATATTAC	ACAGGAATGTC AGAAAACAGT	TTGTGTTAAATTCATCAAGGAATTGACAAAAGCTATTTCCTCACACTTGAC[A/G]GTAATATACTG TTTTTCTGACATTCCTGTTATCAACTCCTCTGAAAATC
14958	83	A/G	AATAATTTAT CTCTTTCTTTT CAAGGG	AATGCATTCAT TTGGGTTTTT	GTGATTGATCTGTAATTATTGGGATTATTTATTCAACTCTAAAATAATTTATCT[A/G]AAAAAACCC AAATGAATGCATTTTCAGTTTCTCCAGGCCTTGAACTGC AGCAGACAAAATTCAAGGA
14976	35	C/T	GTTGATTGCT TCGTTCAAAG AGC	TCAAACTAAAT CTTCCATTCTA	TATTTTTAATTGGTTGGATTGCTTCAAAG[C/T]GCTTAGAATGAAGAATTAGTTGAGGAG GGGCAGGTTTGGGGGTAGGCTCAGCGGGGCCACAAGAAGATGCCCATCTCACACCTGGAG ACGTCCATGAGCACCTCG
4981	31	G/T	TCAGTGGTGTT CACCTCTGACA TATTGGATTTT TAATACTTAGC ATAAA	TAATTGATTCAGTGGTGTGTTATTGGATTT[G/T]TTTATGCTAAGTATTATGTCAGAGGTGGAGAAT AAAGAGGAAAAAGAAGCAAGTGTGGCTCGCATCAACGACCTGATCCTTGTCACAGGAAGTTTTTGA GAGCTCCACAAA
4992	80	C/T	TGCATTAAAT GAAGCTCAGAC AGCTTTCCT	GCTATGTGCTC AGCTTTCCT	TGATTACATTTTTAAAATCATGCTACCAGCCCATCTAAGCACCACTCTGCATTA AATGAAGCTGCAGIC/TJAGGAACACACAGGCCTCAATAATTACAAATGGCGGAAAGAAACGTA
002	72	T/A	GACAGAAAAA GACTCAGACT	...	AAATCTTCTTTCACACAGTTAGGCCTCAAATGGGCTCTCCTCCAAGGCTGGACCTGAAATGCCTTCTTGA TTTCC[T/A]TCAGTTTCACACACAATAACAGTGATTGGAAGGTTATAGAAATAAACAGATGGATAGACAG
200	90	G/A	GACAGAAAAA GACTCAGACT GTCTAA	GTTTCTAGTTC TGCACAAACTT CA	TCAAGCCAAATATCTGCAACAATAACATGTATTGAAAGGTATA[G/A]TGAAGTTGTGCAGAACTAGAACTAGAAACAAAAATCCACCT AAAAAGACTCAGACTCAGTCTAAGTAG[A/G]AAAAGACAGAAACAAAAATCCACCT

ID	No.	Allele		
CACAATACTT CATGTGACCTAT CAGAAATAA	68	G/A	CACTGGACATA TTCCCTACCTG	ATTTTGTTGATGTGGTTAAATCTTATCTCTTTTTTTATACACAATACTTCATGTACCTATGAAATAA[G/A]ACAGGTAGGGAATATGTCCAGTGCAAACAGAGGACTCACACCTGTGCATAGACAGCACC
AAGGGACGAT TTAGTATCTAA AAACA	91	A/T	GGCATGTCCA GTGTTTT	CATAAGTTGCATTTATTCACGTCCCAGGGACGATTTAGTATCTAAAGCTACTGTGTACAGTAATCAGGACTGGAGAACACTGGGACATGCCCCCCTGAATTGCAAGT CTAAAAACA[A/T]CAAAAAAAACACTGGGACATGCCCCCCTGAATTGCAAGT TGGAGTTCGTAAGAATCTAC
CCTGCCTTAT ATTGGAATTTC A T	100	C/T	GGGAGACCATG GGTCTCT	ATTTGTTGTTTATTTAGCACCTGGCAAATTTCCCTGCCTTTATATTGGAATTTCTA[C/A]AGAGACCCATGGTCTCCCCAAGTGAGGAAGCC AGGGCACTCAGCCTTC
TGAATGCTTCC AAGTACAAAT ACA	38	T/A	TGAAAGTATGT TGTATATGGTA TTGTGA	TTTGGTGCTACTTTGTGAATGCTTCCAAGTACAAATAAACCTACAAAATCACATTGC TTCAATCACAACTCAAATCA[T/A]CTCACAATACCATATACAACATACT
TTTACTTTGTT GTCATTTTTAT TCTATTG	40	A/C	CCATAAGGTCT CACACTTTTAT TAT	TGGGATACCCTTTACTTGTTGTCATTTTATTCTATTG[A/C]ATTATAAGAAAAGTGTGAGACCTT ATGGCTTCTGCTTATTGGGCAATATGCAATATAATATTGTGTGTTGTTAAATTTATGCAT
TCTGGTGATGC AATTGAAATA A	35	C/T	GCTGCCAATTA CATTAACTTAC AA	TCTAAGATTTTACTCTGGTGATGCAATTGAAATAA[C/T]ATTGTGAAGTTAATTGGCAGCATT GCCCAAAGTTTAGAGGACTATTTCTTAAACAAGACAGTGTCTGACATTTATTTCAGGT
AATGCACAAA ATCTTGTCTCT TC	88	T/A	TCAGATTTTTA CATCTCTTTCT AGCA	TTTTTTTATTGCATTTGAGTGCTTATTATATTGGGAATTATTGGAATTGTAAAATCTGACCTAGTTGAACAGTGTT GCACAAAATCTTGTCTCT[T/A]TGCTAGAAAGAGATGTAAAAATCTGACCTAGTTGAACAGTCTT AATGAACTCATTGTCCAT
CGCACTCTAA ATTAGAGATA GATTTT	58	T/C	TGCTCGTGGTG AATAAGATG	CGGATATAATTATGTACCGCACTCTAAATTAGAGATAGATTTTTCTGATATACATT[T/C]CATCTT ATTCACCACGAGCACCAATTAATAA
...	17	G/A	...	GCAGAACCAATTAATAA[G/A]AATCTGCAAGTTCCCCAAGAACTCTGATAAATTGCACAAGATG GCCCTTAAAATCGATACTAAAGGAGAGAATAAAGGACTTAAAAGGACTGCTTGATGTGACAGTCACTGGT
...	81	T/C	...	TGTAGTTCTTCAAAAAGACATGTTGGCAGATAGCCAGGCCATACTATGTGTCTGCTGCTCCCAACAAGTATCACTGGT GCACTAAAAAAAT[T/C]GTGTGCTGCTTTGTATCCCAACAAGTATCAGAATACTGT
TGAAGATTAA CCCAGAGTCGC	97	A/C	ATCTGGTATTTC	AATTGTGTGCAATCTGGTATTGTGTATCCCAACAAGTATCAGAATACTGA[A/C]TCTCTTCAAAATGTCAATAAATACAGCTTTTCAAATTAAGTAATATAATACAGCTTTTTCATTGAAGCTT[G/T]TACCT
GCAGCAAGAT TACATCAGTA ATGT	59	G/T	CTCCAAATAGC CTAGAGTATAG TAAGGT	CATGGCAGCAAGATTACACTCAGTAATGTCAGTAATATAATACAGCTTTTTCATTGAAGCTT[G/T]TACCT TACTATACTCTCTAGGCTATTGGGAGTGTTCCCCAC

ID	No.	Allele 1	Allele 2	Flank (left)	Flank (right)	Sequence
WI-15100	74	G	A	...	...	TCTTATTCACAGCCAAGAAAAATACCCAATTATTTCCAAATAAAGCAAAAATTGGAACAGAGACTGGA GTGAGAAC[G/A]GGTTCCACCACCAAGCCCCTCAGACAAGAGATGGACAGCGGCAGCTGGTTCTGGGGT GCATTTCTAGTTGGACTTTAT
VI-14492	92	A	T	CCTTTATTTC CCAAAATATAA TAATTACT	GTCACCATGTT ATATTTCTTT TAAGAC	TGGTACAGAATGTTAATTACAGCAGGGCAGTGATTCCAGTTAAATAAAATTAAAAACCTTTATTTT CCCAAATATAAAATATAAATTAA[A/T]GTCTTAAAAGAAAATATAACATGTGACAGCTTT
I-2002c	89	T	C	...	...	TCTTTAATTTATCGGAATCCTCCCCCACT[T/C]GCCTCCCTGCTCTCTAGAGTGGGGACAAAGTGGGGGTGAGAAG
I-2002b	68	G	A	...	...	TCTTTAATTTATCGGAATCCAGGACACAACTCCTCCCCCACTGCCTCCCTGCTCTCCCACTGCCTCCCTGCTCTCTAGAGTGGGGACAAAGTGGGGGTGAGAC AC[G/A]AGACAACTCCTCCCCACTGCCTCCCTGCTCTCTAGAGTGGGGACAAAGTGGGGGTGAGAC AG
2002a	30	C	G	TCGGAATCCA GGGACACAA	TGGTTTTTGGG TGTTTTTCTT	TCTTTAATTTATCGGAATCCAGGACACAA[C/G]AAGAAAAACACCCAAAACCACCCAAAACCACATGGAGACAG AAGACGAGACAACTCCTCCCCACTGCCTCCCTGCTCTCTAGAGTGGGGACAAAGTGGGGGTGAGAC AG
5116	96	C	T	GGGAGCCCTA GTTGCAGTAA ATGACA	CCTGAATATGC AATTATTTATT	TTTTCATTTATTTTCCAGAAAAAGAAATCACATTTCAGTAACAACTTACATATAGAATTAAACTTTG TTCTGGAATGGGAGCCCCTAGTTGCAGTAA[C/T]GTGTCATATAAATAATTGCATATTTCAGGATTTTG TGAAATAGGTGGGGA
2578	37	C	T	GGCCTAAAGG AATGGGAA	TCAAGCGACCA CCAACAC	GCAAAAGCAAAGCTATGGAGGCCTAAAGGAATGGGAA[C/T]GTGTGTGCATGGAGCAGAAGTCTTCCTGGTCGCCTGATACTTGGT GCTTGTGTGCATGGAGCAGAAGTCTTCCTGGTCGCCTGATACTTGGTTAACTGCACTAAT TTGGGCAAACTGTCATTC
153	40	A	G	CCCTTATGTTG AGTCAGTGTC T	AACCTCAGATA AGTGCAGTGTC	ATTTCACGTTGGCCAAGATCTCCCTTATGTTGGCATTGCA[A/G]AGACACTGCACTTATCTGAGGTTA GAAAAATGTAGTCTTAATAGCCCTCTTAATGTGTAGCAAGGCAATTACCATTCCTAA
215	84	G	C	TGGCTTTAGAA TCAAATGGG	CCAACAGGGGA AAAAGTCA	TTTAGAATCAAATGGG[G/C]TGACTTTTCCCCTGTTGGTGAAACTCTGTGAGGGTTTGGCA
25	80	C	T	C	CTTGAGGGACCT AGAAAGCAAA C	TTTGATTGGCA TAATCACTCC	AGGAAAGAGTGGTAAAGCAAAGGCGATCATTGGATGGAATGATTATGTGTCACGAGCACT.TGAGGAC CTAGAAAGCAAA[C/T]GGAGTGAATCAAATTGCCAATCAAATTGGAAGGGCTATGTGAAGGTATGGC
32	51	G	A	...	...	AATTTGCTAGTGCAATGGACCCAGAATTGGAAGGGCTATGTGAACTACTACACA[G/A]TATGCACCACCAC AGCCATGTCAGTGTCAGTTCAGCTTTCTTGTCATTCAGCTTTCTTAAAAACACTCAAAAGGCTGCA
3	55	C	T	TGTTAGTGACA GACAGATAAG CTTAGGATG	TTGCTTAAGGG CAAACAGAC	TGACTGTATACCCAATTGTCTGTGCTTAATGTTAGTAGTAGCAATTACAACTCACTGGGAGAAACAGGCAGATAAATAGGATG[C/T]GTCTGTTT GCCCTTAAGGGAGAGAAACAACAGCATGCAAACAGAGATAAACAACAAT

ID	No.	Allele	Sequence
VI-15182	49	C/A	GAGACTGCCCTGTGACACAACTAGCTAGCTGCACAACCAGGGCAAAATA[C/A]TGCTGGATTAACCCATGTAATGGGTTACCTTTATTAGTAATCATGGGTCCCTCATAAGCATGGTCCAGATCCG
VI-15198	38	T/C	GTGGACCTTCTACAAGTACCATGGGCCCTTGGCACTATGATATGTTGTCTACACAGT[T/C]CTACTCTGCCTGACGGATAAGTTCCGACTCTCTT AGGCAGAGTAG ACTTATCCGTC
I-12601	42	T/C	TCAAGTGGTAAATAGCCATTTATTGAGCATTTATTCTTGCTT[T/C]CTACTCTGCAGTTCCCTAGAGACTAGTCCGACTCTCTT ACATGTTGTAGAC GTTGTAGTCTT
-14510	104	A/T	ACAACATTACGACCCATCTCTCAAGAGGAAGTCTGGTATTATGGAAAAACATTTGTCATTCAGAT TGGCAAAATA TGCATAACAA T
15239	57	T/C	ATGTTGAGAGTAAATATGCCCTACATATTTAGTGAAGTACACCCAGATATTTTGGGGAGAAGAG TTGTTTGCTTTT[T/C]GTGGCAAATATAAACTGGCA TAAACTGGCA
2634	52	T/C	CAGTGTGATGACATTTCAATGGGAAAAGATTGTTGCAATAAACACCATCAT[T/C]CTGAGGAAGCCTTTCTGAGGTTGACGTTCCCAGCGAGT GGACCTTATCT GTGGACTCAGG CATTTGCAAT AAACACCATC A
...249	34	T	ATGAGTTTATAAACTGGAGACAGCGCATCATATGAACTGTCTAGCAGTATTA[T/C]GCTATTAGCTATGTTACAATTTGTCCTGAAGGTGTAAACTAAGATCC GCATCATATG AACTGTCTAGC GGACAAATTGT AAACATAGC AGT
159	28	C/T	TGTTTGAAGGGCTTGACACAAAAGTTCACACCCAGAAAGTGGTGATTCCTGA TGAGGAGGCACAGGCTGGGGTCTTCAGGT GGAAAGCCAG AGATTTTTAAC AAAGTTCTAA AA
...48	41	A/G	CCACCATTCTTGGCTCT[T/C]TTGTTAAAAATCTCTGGCTTTCCTGGCTGG CTGTCCGGGGAAGACACCGTGCAAATGC[C/T]AAAGTGCACTGAGGA GGAGGAGGGTCTGTGACTC AAGACACCGT GCAAATGC CCCTCTCCTCA GTGCACTTT
...84	64	G/T	CCAAACCCTGGAATATTTATGAATCTAAGAGTCCAGACGCAGTTCATCCACGAGATCTGC CCTAGTGGCAT AGTGGACATCC T TTGCTACTAAA GGAAGAAATGCCTAGTTGCATTAAGGATGGAAATGCCTAGTTGGCATT[A/G]GTAGGATGTCCACTTTTAGTAGC
...0	75	G/A/GA	TCCATTTAGCTTGTCTTGTTCCATTAACCATGCTAAAACATTCAGTAGAGCACAGCGGACACAGCGGACACTGTCATAAGTGGAACAAGGATGAAGCT CATGCTGTAA GGAACAACAA GGACTAAATGG ACAGCTGTGTC AGCCTAAATGC
...0	75	G/A/GA	TTTATAAGCTGAATGAAAGAGGTCGACACGCGACACTGTCATAAGTGGAACAAGGATGAAGCT[G/A]GCAAGCTCCCTGGAGAGAGAAATTAGCATAATTCTT AAAGGATGAA GCTAATCATG TCTCTCCAGGG AGCTTGC GA
...39		T/C	AAGGTTTAATGGACTCACAGTTGGCTGGGAGGC[T/C]CACAATCATGGTGGAGGCAAA CATGGTGGCTGG GAGGC CATGCTTCACCAT GATTTGTGA
...123		C/T/C	TATTTGAGTATTTCATCCATGGCACCATCTTGGCTTCTCCACTCCCTATACATTCTCCAGGGTTGAGGTTCTACCC CCATAGGTTGGCATT[T/C]CTCACAATCATGTGTATCTTCAGTTGGCATTCAATAGCCTATC[C/T]AACTCCATGT AGTTGGCATTC AATAGCCTAT TGAAACTCCCA CATGGGAGTT GGGAGTTTCATATAA

I-14528	62	T	G	TAAAT AATTAAAA	TATGCTTATTGAAGAGAAATAGGCTATTAATATATTTAACTTTTCTGGATGGTATAAAT[T/G]TT GAATTATAAATTTAATTTTATATAAGTGCTAATCGAGACATCACTGGTATAATTGA
I-15347	74	CT		GACTTCAAAG GAAAAGAACA AATTT	TATTCTTTCGGTTTCGGATGCAAACAAACAAAATTTAAAAGAAAATGTGACTTCACCAGTGGTATAATTGA
I-14546	95	C	A	TCACTCCCCA AGTCTTTG	ACAAATTT[C/T]CAAAGACTTGGGGGGAGTGAAGGCAGAGCCTGGTGACGAGGTCTGCAGA CG
I-15353	37	G	A	CCAATTTCTAG TGATAGTAGA GGACTCA	GTATTTTCTGATGCTTGACATCTGGGGCATTGCTGTCGTCTCTAGAGAGACTACTTCTCCTGGGACCAGC CAATTTCTAGTGATAGTAGAGGACTCA[C/A]CCTGCACGTCAACCTTTCATATACAGATCA
-14580	100	G	A	AAGGTGCACGT GCAGG	TTTATTGGCTGCTGTCTCTGTAATACAATGTGGTGAAAAC[G/A]TCTTAATTCAGGCACCATCTTCCACCTTG
8540	73	T	C	CCGACCAAGAT CCCTCC	CTAGTTATTATACACATCCCATCTGTCTTGCA[G/A]AGGAGGGATCTTGGTGGCTTAACA
1039b	97	T	C	GCCCTTCTTT GCCCTTA TCAGGCAC	CCAGCTGGAGGTGGAATAAATGCGGCAACCACAGAAAAACACAGTACACACAGGCCTGCATT
39a	87	T	C		AAGTAGAACACAATAGAATCATCAGAATGCACTACGCACACGAGTAAATACTG TTTGGTAAAACTTGTTTCAGTTAAATATGTA[T/C]GTGTCCGTGCATGTCAGGACACAACCAAGCC
4	107	C	A		GACCAGACACTCTGGGTTGAGATGATGATTTTAATGCCGCAGCCGACACCCACA AAGTAGAACACAATAGAATGGCTCAAAAATATCAGAATGCACTACGCACACGAGTAAATACTG
	32	G	A	GGGAACATCA ATGCAACAAG	TTTGGTAAAACTTGTTTCAGT[T/C]AAATATCAGAACCAAAGCTTAAGGACACAACCATGCAGAAAGAGCAGGGA GACCAGACACTCTGGGTTGAGATGATGATTTTAATGCCGCAGCCGACACCCACA
	87	T	A	TTTGTGGCTTG AGTTTACAAAT T	CACAACATTCCAGAAGTTTTCTGCAGCCATTCATAAGGTTTCTCCCC[C/A]AGTATGGATTCTCTGATGATTAATA ACGATTTCCCACACTTCGGCTAACAAGAATGGAAGCTTCCCCCTTGTTCCCGATTCAGGATGTTTAAT TTGCTTCTCTCTTTAAAACTCTGTGACTTTT

ID	Pos	Var			Sequence
-6192	91	A	G	GACTGCTAAG GATTTAATTTG GAT	TGAAGTGTTAG ATGGCTAAGTA TTAAAA	AAGAGGAACAAATTAGCTCAGTCCAACATGATTGGCAGTTGGCATATTCTAGTGAAGCAAGCAAGTGTTCT GACTGCTAAGGATTTAATTTGGAT[A/G]ATTTAATACTTAGCCATCTAACACTTCAAGCATAAC
-6194	105	T	A	CACATGGCAA TGATAATAAA GAAA	TCTATCCTCAG AGTGTAGTCTG CA	AAGTGATGTGTCCTCACAAATACATTTCTCAAACTCAAAACATCTGAAAATATCACTGAACTT GTCACCAAGAAGTCACATGGCAATGATAATAAA[T/A]AGAGACTACACTCTGAGGATAG
						AGCTCTAAGAGTAAAACAATGGAATTTGGAAAAAAATAGGAGTAAA
1-6213	164	C	T	---		CATATGCTGCTTTATTTCTGTAAGGATACACTGAAACTGAAACGTTAGATGATAATAGCTAAGAATGT AGAAATGAGGCATCAGCTTCTCTACCACTCCTACAGAATGTTAGTATGTATTGTCATTACATGTT ACTTTTGATATTGTCTCATTATACTATGT[C/T]ATATAATAATACAGTAAGTAGGTGATCC TGCATTTCAGGTAAGCGGTGTAGGTGGAAATCCAGATTTCCTCTTGAGGAAA
6217	131	C	T	---		CGGGTTAAGAAATACCTTAAATTTAGGTAAATAAAGCTCAAGGAGGTGGGGGTGTCATCGTCGTGGTG TCAGTCCTTCTGCCCCCTGGCTGTCAGTGTCGCTCCAGGCCTTGACAAGCAGCTCATTCAAG[C/T] GGCCCACCATGGCCCTAGGGTCGTCAACAAGTCCAGCAATCCAGCAATCATGGCGTTCTCGTATCTCGATCC AC
3238	175	G	A	---		ATAGTCTTTATTTGTCAACGAAGGCTACACGGGATCACTTCTGTTGTTTTGTTTTTATGCTTTTTTTTC TAGAAGGTATCTACACATCTGCATTTATTTACAGCCTGTTGAGAAAAAACTTCTCAAAATT[G/A]GTTCCAGATTCAAGATACAGTGTTA GAAACACAAAGTGTTGAGAAGCCAGAGTCTCCAGTGTTGGTCATCCAGGAAAATGATT TCCACATGGTAAGGCCAGAGTCTCCAGTGTTGGTCATCCAGGAAAATGATT
272	86	C	T	GCATTTATTCA GGGAAAACTT TAA	CTGTTTTTGGA GAAGACAAAG AA	CTTGATTTAATCAGGGCTTTGGGGTCATAGGGGGATTAGTCACTGTCACAGTGTCATAATAATGCATTA TTCAGGGAAAACTTTAAT[C/T]TTCTTTGTCTTCTCCAAAACAGCTGCTGGAACACCTCAAATTAA GGGATGTTCATCTCAAAACACCTTTACTGAAACTTGATTCCTTGGGCAGGAAGGTCTTTACTGTAG
03	96	G	A	CCCAGAGAAG CTCTGTCTGC	CAGCCATGGCT TTGCAG	CAGAGGACTTAATGCAATGCCTATTCGGGCAATAAATGAATACTTGATGCATTCATACAGGCAAGAA TCCCAGCATCCCAGAGAAGCTCTGTCTGC[G/A]CTGCAAGCCATGGCTTTGCAGGTGCAGCATCAGGGAAGCT GGTGCAGTTCTAGTCTCGCCCTCCGAATTCCCTGCCCGAGTTCCGATTCCCTGCCCAGTTCCCTGCCC TCTG
5b	193	C	T	---		ATGCTTTTGCATGATTCTAATTATTGCCTTTTCAGAGCTCTGCTGGTAAAAGTGGGGTGCCATACA AACAGTCCCTTTCAGGTCAACCGTTGTCTCCATGCATCCTGCCAATCAATCACTGTAATGTCCATTGTCCA CTTCCCTTTACATTCTTTGGGGGA
	187	T	C	---		ATGCTTTTGCATGATTCTAATTATTGCCTTTTCAGAGCTCTGCTGGTAAAAGTGGGGTGCCATACA AACAGTCCCTTTCAGGTCAACCGTTGTCTCCATGCATCCTGCCAATCAATCACTGTAATGTCCATTGTCCA AACAGGTCAACCGTTGTCTCCATGAAAAACTGCTGATAG[T/C]AGTGTCCTGGTT CTTCCCTTTACATTCTTTGGGGGA

-6375		GGTTTATTGCA TATGGAAATC AA	AATGTGAGATC TT.ATTCTAAC CTTTTT	AAGGTTTATTGCATATGGAAATCAATAG[A/G]TATCTTTACAAAAAGGTTAGAATAAAGATCTC ACATTGTAAAGGCACATATGAAATTCATAACCTTTATAGCAAGCACAAGGGCAGTGAGACATCAACAA
	28	AG	AA	TTGTGTCTCAACAGATGAAATTCATAACCTTTGTTTTCTGATAAGACAATTCAAACATACAAATCAAT TACAACAAATGTGCTTATCAGCTCCCCTCCCACCCCTATATTTAA[T/A]GCAACTGACAGTTTTGAAG GACACCAAGACAATAGGGCT
-6409b	112	T A	...	...
I-6409a	73	A T	...	TTGTGTCTCAACAGATGAAATTCATAACCTTGTTTTCTGATAAGACAATTCAAACATACAAATCAAT TACAAC[A/T]ATGTGCTTATCAGCTCCCCTCCCCTATATTTAATGCAACTGACAGTTTTGAAG GACACCAAGACAATAGGGCT
-6523	165	GCTAATCCAGT AGAGACTGAA G T GCTG	AGATGCTTAGG GAAGGTTGATA CAGC	CTAATATAATCCTGGGCACATGGATTCCAAGAGAGATTTGCAGCAGATTCATTATAGTTACTTAA CAGCTAAATAAGGGTGTATTTAACTTACTTACAGAGTCACTAAATAATGGAGGGGAAAGGAAA GAGTAGGGCTAATCCAGTAGAGACTGAAGCTG
6554	195	C G	...	TCTCCTAGCCCTATTAGGCTACACTGTAGTCACCTTCTATGAGAGCAAGGGAACAGGAAGATGGGC TCCTGGAGTCCAAACAGGATGTGGACGTCCCTGGTAGTTCTTCTCTTTCACACAACTTTCCCTGAGA ACTTTCAGAAAGCATAAAGCTAAAACTCTGAGAGAAAC[C/G]CTG
558b	68	C T	...	ATTGTAATTAAAATTTACATGGGCCTATTTATTAAGGACATTGTGTAATGTTTCCACTTTGTTTTAAA [C/T]AATTACAAACATGTGGCTTAAAATAATGTACAGATCAAGTTGAAAAATGGGCG
58a	42	G C	...	ATTGTAATTAAAATTTACATGGGCCTATTTATTAAGGACATTGTGTAATGTTTCCACTTTGTTTTAAA AAACAATTACAAACATGTGGCTTAAAATAATGTACAGATCAAGTTGAAAAATGGGCG
29	75	TCTTTTCAGAG AATAAAAGTT T C GTCATA	TGACACAGCAT CCATTGCT	AACCAAACAAACTAAGAAATGGGAAAAGAAAATGGCAGGTGAAGAACTCATTGT[G/C]TGTAATGTTCCCACTTTGTTT AGTTGTCATA[T/C]AGCAATGAAGTTACTGTTATAAAACAGGAGCTCTTTCAGAGAATAAA ATCGTGAGCCAAAAC
134		CAGACTCTGG AGCCACAGC	T C ...	CTGCCCTGAACCAATCAGATTTAGTTAAATCAAATCAATCAAAACTCCAGCTGTTTCTCTTGTCTTT TTACTTAGCAAGGAAAACTTAGTGAATGCTACTTGACAAGAAGAAAGTCATTTCTCAAGCACA[T/C]ACCCAAAACTTGAAGGTGGGCCAAAGTCAAAATAAGGGTGGGAA ATGAGAAAGATGTGTGGGCCAAAGTCAAAATAAGGGTGGGCCAAAGTCAAAATCTGGTTATATTTGATGTTGCCAAT
106		ACATAAAAATA TTGCAGTGTAT C T TAGCC	TGCTAAACACA TGGGCACGGT TAGCC	TGTTTAGCAAATTATAGCTGGTCTGTGTATAACCAGAAGAGAGCGGGTATCTGG

ID	Pos			Seq 1	Seq 2	Sequence
VI-6690a	28	T	C	AAACACCACC ATTATTAAGG AGAG	GCTGTGTTGG TAGTTTTCCT	TGCTAAACACCACCATTATTAAGGAGAGT[T/C]ACTAGGAAAAAACTACCAAAACACAGCATGTGAAAC AGTGGGCACGGTGGTAAAGGGCACGACTCTGGAGCCACAGCCGGCTAATACACTGCAATATTTTA TGTTTAGCAAATTATAGCTGGTCTGTGTATAACCAGAAGAGCGGTATCTGG
NI-6770	53	A	G	CAAACCCCAA AACATCACA	GCTTTTGGAGT GTATAATAGTA TGAATAA	GATGTTTAATGACACAGATCTCCAAAGTAATCCAAACCCCAAAGTAATCAACTACTTCAACTGCAATCC ACTATTATACACTCCAAAAGCAAAATACTTCAACTGCAATCC
VI-6686	151	A	G	GCATTCTTCCA ACTATTCCAAT GTT	AAAACAAAGA A	ATTCTGTAGGCAAGGTTCAGCAAATCAGCTAGCACTAATCTGACCAAATGGGTGAGTCAGCCTCA TCACAGAGATTTTTTTTTTAATTTAGATGAAATTCACATTAAAAACATGTAACTCACTCACAAGGAC TCCAAAAACAAAGAAT[A/G]AACATTGGAATAGTCACTTACAAGGAC
I-6761	32	C	A	GATCTAACAG CTGCAGAATG G	AAAGCTGGG AAGGAAGAAG	CCTGAGAGGCAGATCTAACAGCTGCAGAATGG[C/A]CTTCTTCCTTCCCCAGCTTTTGTGAACAAAAC AATTCTCTAGGCATCAGAAAGCACTGAGTGCAAAATGGGTTGTTCAGGTACAAGGTCTC
6844	225	T	C			TAAAATACTGCCAACTGCATTACGTCGTCCACTCTTGCATCATTAAAACAAAGGGTATTCCTCCTTG GTATTTCAAATGATGCATTATCACAATAAAGAAGTTAGAACTTAAAATGCACCCTGATTAATTATG TAAACTGGTAATTGTTTAAAAGCATAATAATTGGTTCCTTCTTCATAAAATGGAAATTTAAA TATTTCTTCTGATAGTCTTGAGGT[T/C]ATCATTATGAGTAGTGCAAAGTGTG
824	112	A	G			CGGTTTGCTACACTTAATGGTGTTTTTTTAAGGGATTTTTTCAGGTGTTGTCAGCAACATCAA ACAAAAGGTACTGAGTACTCCACAGGGTACAGAGTGCTGCCAA[A/G]CACCTTAGAAAAATTACAT GACACGGAGAAAATGCGCCTCCTCTTGCTCCTTGAAGAGTTACAGTCTAGGGATTTGACAACTCACAGT CTTAGGAACTGGGCAAGTAAGGCAAATTCTTCATCCCCTAGAGCTATTGTG
389	139	T	C	GAAAAATGAG ATGCAGTTAA AATTC	TCACTTTGTGG CTTTTAATTAT TCT	GTACAAAAAAGCTGAGAAGGAAGAGCCAACATTCTGATAGGTACGGACAA AAGAGCTCCTTCAATCAAAGGAGTTACATATTAAAAGCCACAAAGTGAAACTGTTTGTCTGGGCCCTATGTGTTGTAGATT CTCT
11	216	T	C			TCCCCAGCTCATATTTATTTGGCACAGAGTGGCACTCAAATATCTGATGAACTGAA AAGAGGTCTCCAGAAAACTTTGCCTTCCCGAGGAGAAGTCCAACCATATAAAATGTATGAT CAAGTCCCAGAAACTTT[C/T]CATGACATTGGACAATAAATGTTTCAAAGCACACTGGTTCC
3	112	G	C			GCCAGTCTCTAGTAGTCTCTAGGGACATGACCAGGAGGGGAGCATACCGCCCGTTATTCCCAGAT[G/C]AAGATTTGGTGGAAGGAG AGGTGGCCATACTTGGGTGAGCAACGGGATACCGCTGTTCCCAGATG ACCATGACAGATGACAACGGAACAGTTTCTCAAAAACAGAGGTATGA
	74	C	T			AAAAGCTTTAAAAAAAAGTGGTGTCTATCTTTAGAAAACACTTTCAGCAAGATCAAGTAGCCCAGCT ACAGCCCTTC[C/T]GGTGCATCTTAACCCCTCCTTTT

ID	pos	allele	left flank	sequence
VI-9617	37	[G/T]		TGCTCTTTTATTCACGTTTCACAACACACGCCGTG[G/T]TGGCACAGTCTACCAAAGTGCCGCGAG CGCCACGCTTGGGCCGGAAGGTCTCATTCGTTCGTCTCTATGGCACAGTCGATTGAATTGGGATGGCCAG CTCCAGAATGTTCCACGTGGGGGCACTCTGTGGGCAGAGGCTGAGCCCTTGCCCACACTGGCACCA AGGAGGTTGCACGATGCAGCTGCAGTGGGTCCAAGCGGGTGTGCTGTG
I-9657	121	T/G		AATGCTGGAGAAAACATCAAACATTGAGTTGACATTTGTTTGCTGAAGTATAGCTACCATCCACTAT CATGAATTTTGTTTCATTACAAATGATAGAAAAGCCAGATTCTCAAATAAAG[T/G]ATAATTCTT TGTATTAAATAAATGTTTATAAATGTTATGAAGCTCATTACATTAATTAATGCTTTGATATAGATTTGAGG
119b	114	G/C	AAAAATTAAC CCTCCCAAGTA[G/C]CAGGTGTGGGA T	CAGGGTCTTGCTCTGTCTCCCAGGCTAGAGTGGACACAATCAAGACTCACAGTAGCCTCAACCT CCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGT[G/C]ACCACCACCACGTGGTTAA TTTTTTAATTTTTGTAAAGATAGGGGTCTCACTATGTTGCCCCGTCTCAAAAACAAACAACTAAC
19a	51	C/G	C[C/G]	CAGGGTCTTGCTCTGTCTCCCAGGCTAGAGTGGACACTATGTGCCCCGTCTCAAAAACAAACAACTAAC ACCTCCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGTGGGACTAGCCTCA ATTTTTTTTAATTTTTGTAAAGATAGGGGTCTCACTATGTTGCCCCGTCTCAAAAACAAACCAACTAA C
3112	71	C/T	TCATAAAGAC TACAGACTTA[C/T]AGCTTTTT GTGTATTATAT GGAAAAAG	ACAGGAATCTGAAAGTTACCAAGGCAATTTCCCTTTAGGATCATAAAGAGTCAATTTTCTAAATATCCTTAAAAAAGAACTACAGACTTAAGCTT TTCAGTAGTGTTATGTAGAGTCACACTATACTGGCAAAAATATTTATTAATTGAGGGAATAGGCCAAT TT
988	36	C/A	TGGTACGTGCT CTCAGTACAA[C/A] GTTT	TGTTAACATTTTTATTGGTACGTGCTCTCAGTACAA[C/A]AAACAGCATCAGTAGTGTCACTTTGAT CTTTATGGAAACTGTTTGTGACCATCTTTATCTTCCCCTGTGGATGAAGTAAGTATAATATGTACAT AAAAAGGAATTTTAGCTTAGTAGAAAAGAAAGCCAAGGTCAGAAGTATGAATGATGTATGCACACAAGT
7	87	A/G	CATTATTAAAC CCCTTTGCAGA	TGCTATTCATGACAGACACGTGAGAGACAAATATTCTTATTTTACAGATGGAAATAGACCCAGACATTA TTCAGTACTTAACCACTAATATTTCCATTTTAACACCTATATTTAAGTTTTCCATTTTCTTAATAGAAAATGA GCAAATATCACACATATATTTCCATTTTA[G/A]ATCTGCAAAGGGGTTTAATAAT
		A/G	CCATATACAT ATATCAAGGT[A/G]AAAGTCCA GCCATAGGAA ATGCTGTTTTT AGTTGTGTCCA	TGTATAAAAAATCCAACTTGTTCCACAAGTACATATGTCCTATGATTTTATGCATACATCCATATAC ATATATCAAGGTAAAGTCCA[A/G]TACAAAAAAAAACAGCATTCCTATGGCCAGTGTTCTACAGAAGT AAGACTGTGCAAACTTTATCGTATAGTCAAATGAGATTGCACACTACAAGGCAGCAGGATGAGGCAGAAGCA

12611b	50	G/C	--		GTCCTCAGGCCCTTCTCTGGCTGCAGAGCCGTCTTCTCAGGTTGCCTGTC[G/C]TCTCCTGGCCTCTAG TCTTCCCTGCTCTCCGAGGTAGAGCTGGGTATGGACGCTTAGTGCCCTCACTTCTCTCGTCTATACCT GCCCCATCTGAGCACCCATTGCTCACCATCAGATCACTTTGATTTTACACATCATAATGTATTCACCA CTGGAGCTTCACTTTGTTAC
12611	34	T/C	--		GTCCTCAGGCCCTTCTCTGGCTGCAGAGCCGTCTT[T/C]CTCAGGTTGCCTGTCTCCTGGCCTCTAG TCTTCCCTGCTCTCCGAGGTAGAGCTGGGTATGGACGCTTAGTGCCCTCACTTCTCTCGTCTATACCT GCCCCATCTGAGCACCCATTGCTCACCATCAGATCACTTTGATTTTACACATCATAATGTATTCACCA CTGGAGCTTCACTTTGTTAC
1172b	179	C/T	TGAAGAAATG GCTGATACCA	ATGTGCATTT TCACTGCAG	TGAACGTGTGTGGTTAAAACTAGGCAATTGGTTAAAAATCAATTTAAAAAACAGGCAATTGGTTAAAACAGTG ACCACACTCAAGCAATGAGAGGGCTTCTTGAAGAAATGGCCTAGAAACAGTG AAAAGAAAGACAGCCTAGAAACAGGCCTAGAAACATGTTCTTGAAATACCATTTCTGCTTTC CATGATGAGCCTGGAACATGTG
172a	17	C/A	--		TGAACGTGTGTGGTTAAAA[C/A]TAGGCAATTGGTTAAAAATCAATTTAAAAAATGCA GTGACCACACCTCAAGCAATGATTATCCCTAGCACTCAGATTATGTTCTTGAAGAAATGGCTGAGAAACA CATGATGAGCCTGGAACATGTTGT
77	35	G/C	GCAGATTGGA AGTGTGAAAA	CACTTACATTT CTGAATATTTA GACTCTT	AGAGGCAGATTGGAAGTGTGAAAAAACCCTTGCATCATGGAACATGTTGT AAATGTAAGTGCTGCCCTCAACTGTTCTTTACCCACTGTCTTGCAAAGAA[G/C]AAGAAAAAAATGAAAGAGAGTCTAAATATTCAG TCCTTTGCAAAACCCTTGCATCATGATGAGCCGAGTTAATTTGAAAACTAGATTGAAT
1b	141	G/A	--		TCCATGGTTTGGTTGCTACTGACTTTGTTAGCCTTACTGCCCACTATGCATTGGAACATTCCCATATTC CAACTAAGCAGGAGGTTCACAATAAACAACATAGGCTCTTTATTCCTCTTCATTAATTTTCTT TCAC[G/A]TTATTCCCTCACCCTGAACGCCCTTCTCCTTCCGTAGTGACATTTAAAATCCACTTTAC ACATTCGGACC
a	126	T/C	GGCTCTTTATT CTCCTTCTTTC	CGTTCAGGGTG AGGGAATAA	TCCATGGTTTGGTTGCTACTGACTTTGTTAGCCTTACTGCCCACTATGCATTGGAACATTCCCATATTC CAACTAAGCAGGAGGTGTTCACAATAAACAACATAGGCTCTTTATTCCTCTTCATTAATTTTCTTTAC CTTTCACGTTATTCCCTCACCCTGAACGCCCTTCTCCGTAGTGACATTTAAAATCCACTTTCA[T/C]TAATTTT CATTCGGACC
114		G/C	ACATACATAT CCATTATACA ACAGAAAAG	GACCTTTCTT TCCAGCCC	GAAGGCAGGACTGTGTTTTGGAGGACAAAAGTAAATCTTTTATATCTTTATTTTTAATTTTATT TTTTCAGGCATAGAGATTGAGAATTTCAGTATATCCATTATACAACAGAAAAG[G/C]GGGCTGGAAAAGAAAG GTCAAGTGAGAATTCAGATATTCTTAAATGCAAGGCTGACAAATTTGGGCTTGATT

NI-478	46	CT	GCATGTCTGTG TTACTCTATTT TGTTC	AAATGCCACAG GTGGCT	AAACCACTGCAACCTTCAAGCATGTCTGTGTTACTCTATTTGTTC[C/T]AGCCACCTGTGGCATTTC CAAAATATGATAATCTCTGCCACCATACTGCTTAAACAACAAATAGAATCTGGCAGCAAAATATAGC ATAAGCTTACTTCTAAATCAAAGGCTACCATCAGTACCTTAGCACATTTAAAAAATAAAAACCAAC ACTGCCCA
NI-533	29	TC	ATCACAGCAG AGTACCTTTCT AACT	CCTTCCAACCT CTACACAATCT T	AGCCATCACAGCAGAGTACCTTTCTAACTT[T/C]ATAAGACCCTGTGTCCAGTTAATCCA CTGTTCTGTTGTGGTATAATGACCCTGTGTCCAGTTAATCCA
II-601b	112	TA	...	...	TCACTTATCTCTCTTTTTGTGGTGAGAACACTTAAAAATCTAAGAATGATCAATTTCAAATAAAGATGG TAGTGAGCGAACAGAAGAGGTTTCATTGATTGACTCCTAAACTGAGTAC[T/A]CAAAAACGAGCAGGTGCT CACAGTCAGGAAGCAGGTGCTGAGTACAGGAT
-601a	74	CT	...	...	TCACTTATCTCTCTTTTTGTGGTGAGAACACTTAAAAATCTAAGAATGATCAATTTCAAATAAAGATGG TAGTGAG[C/T]GAACAGAAGAGGTTTCATTGATTGACTCCTAAACTGAGTAC[T/A]CAAAAACGAGCAGGTGCT CACAGTCAGGAAGCAGGTGCTGAGTACAGGAT
863	107	AG	CTCCTTCACAA CCTCACCA	CTTCCCGGTAA GCCAAGT	AACAAAAACAGACACCCTGGGCTTCCTCACCAGTCCACATGGTGCCAAACAATCCCACATTCCT ACATCCTCCCCACTGGGCTGCCTCCTTCACAACCTCACCA[A/G]ACTTGGCTTACCGGGAAGCATAAA GCCAAAGCATTAGTCTTTATTGCAACATGGTCTGGCTGCAATAC
19	36	GA	ACTGCTTGCTT GTTGATTTAAT C	TTATTCTAATC CCACATGACAG C	ACTCACTGCTTGCTTGTTGATTTAATCAACACGATTGCTAACAAAGCAGATTCTTTTTCAAGCTGTCATGTGGGATTAGAATAAAATA AACACAAAAATGAAAACACGATTGCTAACAAAGCAGATTCTTTTTCAAGCTGTCATGTGGGATTAGAATAAAATA AATAACTTCAA
1	37	AT	...	...	TGCATTCATTATGCACCAAATAATAACTTCTGTACAT[A/T]CATTATTGTATTCATTATCACAAAAT TATGAGTGAGGGATGATTGTTATCCCTATTTACAGATGAGAACACTGAATAATGGTAGTGACTTAGAAGAAGTATCT TTCCCAAAGTCACAAAGTTAGTGACAACTGTACAAC
1	70	GC	CAGTATCTGA AGTTTTTGTCT CCCA	AGGAACACCTA CAAAATGACTT CT	GTTCTGCATCGATCACTGTACAACCGGGATTCGAATCCTTTCTCCTTTGAAAACAAGGC CTTCCTGACCTGTTTGCAGTGGATACTGTTTTTGAAGGCTCTGTCTGTGCTACGTTTGCTGTTCCATTTTCTCATTTTGTCTCC CGTTCTTAAGGGAGGCGTTTTGTAGGTGTTCCTGGGCGTTTTATCAGATGGCTTGCAGAGTTTACAGATGGCTGTGTGGTCTGAAGTTTTCTAATACACTGC ATGAGAGTGGCTTGCTCATGAAGGTTACAGAAATTGGACAGAAACTGGCATGTTCCAAGGAGAGGAACAGCATGGAGAAGA AAAATCATACTCTATCCACGTGCCAAACACTGGCAATTAGTTTTGTTA[A/T]TTACTAAAACACAAATGT TTAACTTGGGGGTCCACAAACAAGGATATGTTGGCAAATGGTATTTCTGTGATG
178	AT		...		CTATGTGTATTCCAT[G/A]ATCGAAAAGGAAGTTCATCTGAGAGAGAGGTAGAACAGGTCCTA GAACCTCAG[G/A]ATGCAAAAGCAAACAGACTATTTGGATAAGTTCACAGACCCTATCTCACTGACCCAAAGGTA AAAAAATAAAATAAAAAAGTAAGAACTTACATCAGATTGTGCATTTCTTATTTCTATTTGCCACCCTGTTTGT
76	GA		...		TAGGAA

Clone	No.						Sequence
WI-5791a	44	C	G	---			CTATGTATTCCATCTAGCAAAAGCAAGACTATTTGGATAAGTTT[C/G]ACAAAGATGATGAGAACAGGTC CTAGAACCTCAGGATCGGAAGGAAGTTCATCTAGTCCATAGACCCTATCTCACTGACCCAAAGGTA AAAAAATAAAAGTAAAGAACTTACATCAGATTGTGCATTTCTTATTTGCCACCCTGTTTGT TAGGAA
WI-5406c	120	C	T	---			CACTCTGCTGTTGTCCATGGGTGCCACAGACTCTTCCAGAGAGCCACTTCCACAGATGCAACAGGCC TTTTGAAGGAGCCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAACC[C/T]TATGAGCCCAC ACTTCTCATTTCCTTAGAATTTCTTGGACTCTGTGAAGAGGAAGGAGAAAAGAGAGGCAA GG
WI-5406b	118	C	A	A	CCAGGATGTC AAGGTGAGAA A	AATGAGAAGT GTGGGCTCAT	CACTCTGCTGTTGTCCATGGGTGCCACAGACTCTTCCAGAGAGCCACTTCCACAGATGCAACAGGCC TTTTGAAGGAGCCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAA[C/A]CCTATGAGCCCAC ACTTCTCATTTCCTTAGAATTTCTTGGACTCTGTGAAGAGGAAGGAGAAAAGAGAGGCAA GG
WI-5406a	42	A	G	---			CACTCTGCTGTTGTCCATGGGTGCCACAGACTCTTCCAGAAG[A/G]GCCACTTCCACAGATGCAACAG GCCTTTTGAAGGAGCCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAACCCTATGAGCCCAC ACTTCTCATTTCCTTAGAATTTCTTGGACTCTGTGAAGAGGAAGGAGAAAAGAGAGGCAA GG
WI-5798	48	G	C	TG	TTTATTCTCCC TTGTTTTCTTT TG	ACTGTTAGAAA ACCAGTATTTT TCAAT	CCATTCCTTCTTCCTCCCTCCCTTATTCTCCCTGTTTCTTTG[G/C]ATTGAAAAATACTGGTT TTCTAACAGTGTGCTGGTATGGATACTATGTTATAACATGCATAGTTCTATATGGGTATCA
WI-5415	54	T	A	TTT	TCTTCATGAAT TCATCTTTCAG TTT	GGACTAATTCA TGATCCGATCT	CCTGCTAATAATAATTAAGCACGATTTGTCTTCATGAATTCATCTTTCAGTTT[T/A]AGAATCGGAT CATGAATTAGTCCAGGCTTTTAGTTGTAATCGAAATTGGA
WI-5437	41	C	T	G	TCCCAGAGAA AAATCCAAGA G	AGTTTCTAAAC ACAAAATATG GTTTAAG	TGTTTTAACCCAGGCAGACCTCCCAGAGAAAAATCCAAGAG[C/T]CTTAAACCATATTTGTGTTTA GAAACTCCTGTGCCAACCACTCTGATGTGAGTGAC
WI-5481b	131	A	G	G	TGTCATTTATG CTGCAGTCG	TTACTTCCAGG CTCCAAGTATT	AAGCCAATTCACATTAGTTGATGAATTTGACAGTATCTAATGCATGGGCATCTGTTTCAAC TCTCTGTTTTTCAAGAGGTAGTATCTATTTTGTCATTTATGCTGCAGTCG[A/G]A ATACTTGGAGCCTGGAAGTAAAGACCTATTTTCACAATTA
WI-5481a	29	G	A	AATTT	CCAATTCAC ATTAGTTGATG GATACTGTAAA ATT	CCCATGCATTA AACTCTGTTTTC GATACTGTAAA ATT	AAGCCAATTCACATTAGTTGATGAATTT[G/A]AATTTTACAGTATCTAATGCATGGGCATCTGTTTC AACTCTCTGTTTTTCAAGAGGTAGTATATGTCTGAAAAATCTATTTTGTCATTTATGCTGCAGTCG[A/G]A ATACTTGGAGCCTGGAAGTAAAGACCTATTTTCACAATTA
WI-5492	38	T	C	---			TCATGAGTCTCTTCTTCACGAGATGCTTAAAGTCCCA[T/C]CAAAGAAGAAGGATCCCATGGCCTAAT GAAGAGTGTACCTCCACCTTAGGGATATTTGCAGACCAA

ID	Pos	Allele 1	Allele 2	Flanking seq 1	Flanking seq 2	Sequence
I-5826	134	T	C	---		TATTTTTTTTCTCAATTCCTGGAGCACCACCATGTGCTCTTCTATTCATTTCATGCTTCACATTTATTTTTTTTCACTTAGTTAAAATGCTTTTCCCTTGATCTAGCAATGGCCAGTTTATACATATTCTTTAGT[T/C]CCTTGGTGCATTTACTCTTTACAC
I-5546	40	C	T	CCCAATACTTTTTCAGGGTGAA A	CCTGTATTTTA GCAAACATGGG	CCTTATAAACCCAATACTTTTCAGGTGAAAAAAAGGGAAAA[C/T]ACCCATGTTTGCTAAAATACAGGAGTATAACAGCATGACATGTTAAGGGAATTACAAATGCTTGAGTGTAAATTCTGATGTGGGAAATATTAGAAAAATTAAGCGAGAGAGGCA
I-5552	97	C	T	GGCACCAGCCT TTTTAGAGT	CCCAGG	TGTTTGTTCTGCACCTCCCCAACAAGTGGTCAATGAGCCTCAAGGGGTTTGATTGAGCGGGTATGGGTGGGGCTATCGGCACCAGCCTTTTAGAGT[C/T]CCTGGGCAATTGTGTCACTAGTGTCAGA
-5836b	161	C	T	---		TAAGTTGATTTAAACACTCTGTGCCTCAATTTCTCACCTATAAAATAAAAGATAATAGTATCTAAAAAAAGAGAGAGAATTAAAAGTGGATAGACATGAATAACTCTGATGATACTGGTTGTATCCCTGAATCCTGCAATATACACACATGATTCAATGAT[C/T]CCATTTTGAAAATTAAGCTTTTGAAATTGTTTCCAATGATG
I-5573	58	C	T	GTTCATAAGG AGGTGGGGA	TGAACAGTTGG AGAGTAATGTG TC	TCGGGTATTAGGATGCGTTCACCCTGATGATGGGCGTTCATAAGGAGGTGGGA[C/T]GACACATTACTCTCCAACTGTTCATCAGAACACTTCAACAGCG
I-5850b	134	G	A	---		CAGGACCTTGGAGCCTTGTCTGTTTGTCCTTCCACCCTCACTCTTTCTGCCTGCCCATGGGTGGAGCCTCTCTCAGGCTTCCTCCTGATCCACGCGTCTATCTTCTATATGGGGCAATATCCAATGTCCCATTC[G/A]TTTTGCCATTTCCTGTATATCAAACAGAGAAGCAGAGGGTGG
I-5850a	92	C	T	---		CAGGACCTTGGAGCCTTGTCTGTTTGTCCTTCCACCCTCACTCTTTCTGCCTGCCCATGGGTGGAGCCTCTCTCAGGCTTCCTCCTGATCCACGCA[C/T]GCGCTCTATCTTCTATATGGGGCAATATCCAATGTCCCATTCGTTTGCCATTTCCTGTATATCAAACAGAGAAGCAGAGGGTGG
I-5612b	125	A	T	CTATTAATGA GCATCGTGTCA TTC	TTCTCTTGAGA AACCTAAAAC ACTG	TGCCTGATTGACACATAGTTATCTGACAGTAAATCATTCTAACATCACAAATATCTATTTCTGCCTGTCACACTAATTTGCAAAGCATTCAATTGATTGACTATTAATGAGCATCGTGTCATTC[A/T]CAGTGTTTTAGGTTCTCAAGAGAATTATGCTGTTCCTGTAACTCAAGTA
I-5612a	44	T	A	---		TGCCTGATTGACACATAGTTATCTGACAGTAAATCATTCTAACA[T/A]CACAAATATCTATTTCTGCCTGTCACACTAATTTGCAAAGCATTCAATTGATTGACTATTAATGAGCATCGTGTCATTCACAGTGTTTTAGGTTCTCAAGAGAATTATGCTGTTCCTGTAACTCAAGTA
I-5636	26	A	C	GCCAATTTTAT CCGCAATAAA	CATCGAGGACT TTGGGAA	TGAGAGCCAATTTATCCGCAATAAA[A/C]TTCCCAAAGTCCTCGATGGAGGCATTTCAGAATCGGGGCAGGGGAGGCAGGAGGTGAGAAGGTGAGACAGAGATGTGAAGAAC

			TTAGAAACCTCCATTTATTCTGCCATGGTACATCTTTTTAAGAATCTTTTTTTTCATTTATGCATTC ACTGACTCACTCACTTGCTCTATCATCTTTAAAAA[C/G]AAATATTAATATTTTATTTACAGAGGAA CTCAGAAGCCAGAAAAATGACCAAGACACAGTCCAGTCTCCATCTTCAAAAGGTCACAGTCCTTCA GAGAAGACAGACAACTAAATAAATTCCAGG
II-5865c	103	C	G	---
			TTAGAAACCTCCATTTATTCTGCCATGGTACATCTTTTTTTCATTTATGCATTC ACTGACTCACTCACTTGCTCTATCAAAAAT[T/A]AAACAAATATTAATATTTTATTTACAGAGGAA CTCAGAAGCCAGAAAAATGACCAAGACACAGTCCAGTCTCCATCTTCAAAAGGTCACAGTCCTTCA GAGAAGACAGACAACTAAATAAATTCCAGG
II-5865b	99	T	A	---
			TTAGAAACCTCCATTTATTCTGCCATGGTACATCTTTTTTTCATTTATGCATTC ACTGACTCACTCACTTGCTCTATCAAAAATTAAACAAATATTAATATTTTATTTACAGAGGAACTC AGAAGCCAGAAAAATGACCAAGACACAGT[T/A]CCAGTCTCCATCTTCAAAAGGTCACAGTCCTTC AGAGAAGACAGACAACTAAATAAATTCCAGG
II-5865	165	T	A	---
	CATAGCCATGG ATAATATTAT GACAGAAAAA	CCTAGTAAGTT TCAGTCATTTG ATATGT	CTCAGACACATTCATTTTCATTAGTTGTTAATTTTTGTGTATTTCATAGCATGGATAATATTATACAGAA AAAAAATT[T/G]TACATATCAAAATGACTGAAACTTACTAGGTAGCAATTTGTTTGTCAATTTGCT
II-5874	76	T	G	
	CAGCCTCTCAG TTTTTCCATC	GACAGAAAAG AGAGTAAATT ATGAAAAA	CATGGAGCCGACGTTCAGCCTCCTCCAGTTTTCCATC[A/T]TTTTTTCATAATTACTCTCTTTCTGTC ACAATGTTCTGCTTCGTATTTCAACTCTCATTGCTGATGGTAGTCATAAAATATGGGTGATTC AGAAAATAAGTAAATG
II-5752	36	A	T	
			TTAGCAGAAAACAACAACAAAAAATGTCACAACACTGCAGTAAAGAAGTGTTTCCCGATAAATA[C/G]C CATTAGGTATTAGATAAGCATCCCATAAAACATTGTTGAAAACGAAGCCGAGTTTCGATTCACACA GTTGTCTGTTTTAACCTCTCTAAATCCCGATAAATAGCCATTAGGTATTAGATAAGGTATTAGATAAGCGTCCCACGAAA CATTGTTGAAAACGAAGCCACGTTTTCCGATTCACACAGTTAGTTCTGTT
II-5760b	61	C	G	---
			TTAGCAGAAAACAACAACAAAAAATGTCACAACACTGCAGTAAAGAAGTGTTTCCCGATAAATACCCAT TAGGTATTAGATAAGCATCCCATAAAACATTGTTGAAAACGAAGCCGAGTTTCGATTCACACAGTT GTCTGTTTTAACCTCTCTAAATCCCGATAAATAGCCATTAGGTATTAGATAAGC[G/A]TCCCACGAA ACATTGTTGAAAACGAAGCCACGTTTTCCGATTCACACAGTTAGTTGTCTGTT
II-5760	187	G	A	---
	TTCTCACCATG GGGATCTTG	GGGTGGGGATCT AACTTGCA	AATATCTGGCCTTTTCTTCTTAGGAGGAGATTTCTCACCATGGGAATCTTCTCAGTCTTCCTTGCTG CCCACCCTCACTATTGAGAAAGTGTAAGAGACTAAAGTGAAGACTAAAGTGCAAGTTAGAT
II-5944	52	A	G	
			GAGTTTAATGAATCCTGTTCCCCTCCTAAAAACCTCCTGTTCCCCCAACTTCACATTCAGCAGATATT CTTTCATGGGTTATTTGCCCAAGTCATGGCATGTAATGTGATCATTTCAAGAGTGTGAG TAATGCTTGGTA[C/T]TTGCTCTGTGCCGTATCTGCTCCAATCACCCATTCCACTTATTTCCTATTAT GCTGAATGAAACGGTTATATTACAG
II-5967b	148	C	T	---

ID	No.	Allele		Sequence
VI-5967	165	C	T	GAGTTAATGAATCCTGTTCCCCTCCTAAAAACCTCCTGTTCCCCAACTTCACATTCAGCAGAGATATT CTTTCATGGGGTTATTTGCCCAAGTCATGAGGAGATGCATGTAATTGTGATCATTCAGAGAGTGTGAG TAATGCTTGGTACTTGCTCTGTGTGCCGTAT[C/T]TGCTCCAATCACCATTCCCACTTTATTTCCTATTAT GCTGAATGAAACGGTTATTACAG …
VI-6093	53	G	C	GGGTAAGATCCAGAGCCACCAGGTGAACTCGCCGGTATTGAAGTCTTTGGGCCA[G/C]GTCTGTAATG ATCTGACTTCTCCCAGAACCCCCTCTTCTCTGGAAGTTCCAACTGTGCACTGAGCCCATTGTGAGGGA GCATTTGAACCAAAACCCAGCGACACTGCTGACATTTGACTTTCAGCAAACCTTGATTGACGGGTGAC ACACCATGCTTCGAGAAGGAATGAGG …
VI-6141	80	T	C	GACTCTGTCTCAAGAAAAAAAAATTGAATAATTATTAAGCACTTCTTAATTAAGCAT CTACAAGGTACTTA[T/C]CACTGTTCTGTGGGTTTCAATCCTCTTCACCTTTAGACTTCAGGAAATT CTTCTTAATTA AGCATCTACA TGAAAACCCCA CAGAAAAATGCATGAAAACAGGATTGTTACATGCAGAGAAATAGGGGGAGATAAAATTTGTCTTT AGGTACTT GAACAGTG CTC
VI-6450	45	T	G	ATAGGACAGTTTTCTTCCAATGACTTATTCTATATCTTGTCACA[T/G]AGAAGTACCACACATTTCA AACAAGAGCCAGGCTATGCCCAGGTGGGATTATTTCACGGTCATGGTAATGTCATGTAAGACTA CCAATGACTT TTGTTTGAAAT TTTTTACTGGCCTTCTTTTATGCATAAAACAAGGTATTGTCTATTCAACACATGTGTCAATACAG ATTCTATATCT GTGTGGTACTT TGTCACA CT
VI-6461	88	C	T	CAGTTGTCATGTCCCTCTGGTACTAGATATAGTCTTTATAGAATATGTGGTTTAGAATAAAGCCACA AATTATTCTATAAAACAACA[C/T]AAGGAACGAGGGCTCAAAAGTGGAACAAAACGGCCTTAGTTTC TAAGTGGAAGACTAAGACGGATATAGGAAAAATATAAATCCGTGACCTCTTA …
VI-7466c	141	G	A	GAAACTATCCTTAGTGGTGCCACATTTCTATTTCTGATTCTTGGTCACAGAGGGGACTTTCTGGGCT ATGAAATAGTCTATTCAGTGAACTAGTTATCATAAAGACATGCAAAAACCTTTCACAGTCTTTGT CCTGG[G/A]AATATCTCACAAAATTAATTATAAATTGGCATGGCGACTTTCTGATTAGCCTGACAGG TTTTCACAGTC AGTCGCATGCC TTTGTCCTGG AATTTATAATT ATTGTTCCTTT ACTGAA
VI-7466b	80	T	C	GAAACTATCCTTAGTGGTGCCACATTTCTATTTCTGATTCTTATTTCTGGGCT ATGAAATAGTC[T/C]ATTCAGTGAACTAGTTATCATAAAGACATGCAAAAACCTTTCACAGTCTT TGTCCTGGGAATATCTCACAAAATTAATTATAAATTGGCATGGCGACTTTCTGATTAGCCTGACAGGA GACTTTCTGGG TGTCTTTATG TTGTTCCTTT CTATGAAATA ATAACTAGTTC GTC
VI-9814	104	C	A	TGCTTTTTAAAAATAAACAATGACCACCACCTGACACCATAGTCTGTCTCCACGTCTCCTC AGTAGAATAAGACAGGACTTTGCTGGCTGTCTATCT[C/A]TTCCTTCAGAAGAGCACTTGGCCCCT CATAGGCATTCCATAGATATTTGTTGAATGTGCTTTTTGCATATTGATTCCTACATTTGATACA TTCTCAGGAGGGACCATTTGGCCTAT …
VI-9720b	55	A	G	CCTCTAACAAGAAAACTTGACTTCCTCAACTCAAAATACCCTTCTCTAATAATTT[A/G]AGTAACCA AAATATTCCTTCAAATAAATTAATCTTTAATTAGAAGAAGCAACAGTGTTAGAGGTAGTACATTCA CCACC …

	Position	Variant	Sequence
I-9720a	47	A/G	CCTCTAACAGAAAAACTTGACTTCCTCAACTCAAAATACCCTTCTCT[A/G]ATAATTAAGTAACCAAAATATTCCTTCAAATAAATAATCTTTAATTAGAAGAAGCAACAGTGTTAGAGGTAGTACATTCACCACC
I-9825	123	A/T	CACGGCTCTAAGGCAGGATGTGGCTTATGAGATACTTGCATTGTCTGTCTGCACACCTTGAATCTGCCTGCTGGCTCCCTTACTTACCTCTCTGTCATGTGCAGATGAGGCTCAGGGTGCT[A/T]GAGGATTAGTAAGATCTCTTTCTAAAGACAGGAGAGATTATTACAGAGAAGAACTCACCAGGGTTAGTTTGCATTTAAGAATTGCCAGTCTTTGTCCTGCATCCATCTTGAACATTAATCCACATG
I-9748	74	C/G	CCACTTCAGTAAATCAATTGTAGCACTTATTTCTAAAGATTTCTAATTTTTATATGTTACCCTTTGTCATT[C/G]TCAGACCAAGTACACATGTTTCACACAGCCATCTTTTTCCTGGAATCTTTCAGAATTACAGTTATGATGTCCTTTATATTCCCCA
VI-9943	91	T/C	TGAGGCTATGATGGCAGATTTGTAGTGACTAATACTTATTAAGCAATTTCAATGTTGTGGGCACTGTTCGTTGTTGTTTTATATCCATCTTC[T/C]ATTTAATTTTCTACTGAGCAGAAAAAAATGTATACATTAACCTTTGCTCCCTATTGTACCTTTAATATTGCATTTCACACCTTCTCTTTTGTCATTAGGGAAGGGGCCCTTCACAGATCCGTCAGCTCAACACTGCCTCCT[T/C]AGTGAGCCTGTGAACCACCCAAGACGGCTGGGTCATCAGTGTCATCCTCTTCCGGACAACTATCTTGTTTAAAGAAAAAAAGAGTGTCTTTGAATGTATCCATTTTATCCCCAAATAATCTTGTTTAATAAATTCCTTATTAGGCCAAATCCAATGTGCTGAAATATCTGCCAAGCATGTCATTCTACACAAAGGGATTTGCAAA
VI-9891	39	T/C	CTCAGAATTATTCAGATCTTCCCCAAATGTCATGATTCTGTTGTCTCAACATCCTATTTTTCTCAAACATTTATCTAGCCTGTA[C/T]AAGTCATCCAGTGAGGCTGTTATTCAATCTATGTGAAATTTTGAGCAACCCACAGGATTAGAATTAGCATCTTATTTTTGTACCCACATTA
VI-9897b	84	C/T	CTCAGAATTATTCAGATCTTCCCCAAATGTCATGATTCTGTTCTCAACATCCTATTTTTCTCAAACATTTATCTAGCCTGTA[A/T]CAAGTCATCCAGTGAGGCTGTTATTCAATCTATGTGAAATTTTGAGCAACCCACAGGATTAGAATTAGCATCTTATTTTTGTACCCACATTA
VI-9897a	83	A/T	CTCAGAATTATTCAGATCTTCCCCAAATGTCATGATTCTGTTCTCTCAACATCCTATTTTTCTCAAACATTTATCTAGCCTGT[A/T]CAAGTCATCCAGTGAGGCTGTTATTCAATCTATGTGAAATTTTGAGCAACCCACAGGATTAGAATTAGCATCTTATTTTTGTACCCACATTA
VI-9935b	115	C/A	AGATAACCCTGGAAAACTAGAAGAAATTAATAACGTGTTGCACACCTCACCAGAACTGGAAGGAGTCTGACTGTGTTCTTATGGGGTGCTTGGACTGGCAGGGGAGTTCAGACA[C/A]AGCCAAGAAAAGCCTGATATTAAGAGGCACTTGCATTAA
VI-9935a	42	C/T	AGATAACCCTGGAAAACTAGAGAAAATTAATAAACGTGTTGCA[C/T]ACCTCACCAGAACTGGAAGGAGTCGGACTGGCAGGGGAGTTCAGACAGCCAAGAAAAGCCTGATATTAAGAGGCACTTGCATTAA
NI-9983	146	C/T	CCTGTTAGGTGCCAGAGTCCATGCTCTTGGCCACACAATGTTAGGCTGCGTCTGCCTCCCCATTTCCTTTGTCTTGATTCCCCAAACCCAAGGTTCTCACCCAATCTGATCAAATGCTGACTAGGTCGTCTGGTCAGGGTAAAGCATTATGA[C/T]AGACACAAGACAAAGAGGTAAAGTTGCTGTCTCCTCAAGAGAGAGAGAGACATAAAACAAAATGGATCTGGAACTAAGTAAGCCTTCGAGGAGGGAGCAAAGG

NI-10019	139	A	T	TGATGTAATGC TATGTAGCAA ATCT	TTGATTACTGT GCTTAGGGGA	ATATCAGTGGGGTTGAGTATACAGCAATCTATTTGTTTATTTATGTGTGCTATAAATCAATGGTTCTA ACATTCAAATAAGATCTTTTGCTTCTCTGCTCAGATGCTTCAGTGAATGCTATGTGTAGCAAAT CTA[A/T]TCCCCTAAGCACAGTAATCAAGGCCTTCACCCCA
NI-10020b	122	T	A	GCGAGAAAAG AAATCATGAC TTT	GACTGTTAATT TATTTAATCAT TAGTCTGG	TTTACTTCATTGTCATCTTGACTCGTATTAAATAAATTATGTTAACTGGCTCTGAAAAGAATTTAGGC ATGCATAGAGAATAGCAGTGTTTTATTGGCGAGAAAGAAATCATGACTTT[T/A]AAAAATACC AGACTAATGATTAAATAAATTAACAGTCCTAGGGTTCCGGAAGTGGCCTAAAGCACGTAGTAGCCCT CCTTAGA
NI-10020a	39	T	C	TGTCATCTTGA CTCGTATTAA ATAAATT	AAATTCTTTC AGAGCCAGTTA AC	TTTACTTCATTGTCATCTTGACTCGTATTAAATAAATTA[T/C]GTTAACTGGCTCTGAAAAGAATTTA GGCATGCATAGAGAATAGCAGTGTTTTATTGGCGAGAAAGAAATCATGACTTTTTAAAAATACC AGACTAATGATTAAATAAATTAACAGTCCTAGGGTTCCGGAAGTGGCCTAAAGCACGTAGTAGCCCT CCTTAGA
WI-10064b	170	C	T	CCTTTAGATAT ATTGTGATTGT TTTACATG	ACCTTTCTGAA GCCAGATTTC	TCTGAGTCTTTCTGAGACACTTGCCATGGTCAAGGGTAGCAGGATCAGGGAAGGCATTATAATAAAT ATAATTTGCAGAGCATCTCTCCTATGCACCAGATATTGTGGTGACACTCTGTTAATCCAGTATCC CTACTCCTTTAGATATATTGTGATTGTTTTACATG[C/T]GAAATCTGGCTTCAGAAAGGTTAGGTGTT T
WI-10064a	54	C	A	GTAGCAGGAT CAAATTATATT TATTAT	GAGATGCTCTG CAAATTATATT TATTAT	TCTGAGTCTTTCTGAGACACTTGCCATGGTCAAGGGTAGCAGGATCAGGGAAGG[C/A]ATTATAATA AATATAATTTGCAGAGCATCTCTCCTATGCACCAGATATTGGTGACACTCTGTTAATCCAGTA TCCCTACTCCTTAGATATATTGTGATTGTTTTACATGTGTTTACACTGGCTTCAGAAAGGTTAGGTGTT T
WI-10289	29	T	C	TCTCCTGTCCC CAAACTCTT	ATTCTTGTTGT ATTGAATGGAA TTAA	CCAGGGGATTCTCCTGTCCCCCAAACTCTTA[T/C]TTAATTCCATTCAATACAACAAGAATTTATAGAA TATGCACCACCATGCCACAAAGACACCCTTATATTAGT
WI-1319	40	A	T	TGGCACTTAG AACATAGTTT ATTCTTT	GCCACACACCC CTATGGT	AAGAAAATCCTTGTGGCACTTAGAACATAGTTTATTCTTT[A/T]ACCATAGGGGTGTGTGGCCTATCT TTTACCTGGCATGGCTTTAGGTCCTGTGTATCTTTTGCCACAAAGAGTCGTGTTCTGAC AGTCTTATGATCTCTATTTTAACATTAACACTGGTCAGATGTGTTTAAAACTTGTTGAACCTGCAGC
WI-10316	104	T	C	CTGTTGATTTT CTACCTCTATT CTCTT	GCTTTGGAATG TATCCAAAAGT TT	AGCAACGTGTACAACTTAGTGAGGTGTAAATCAGAAGCATCTATATTATTCACCAGTCACCACCCTG GACTATAGTCTGTTGATTTTCTACCTCTTA[T/C]TAAACTTTTGGGATACATTCCAAAGCAT CATGGTCACTTCCAGTTATGAAAAGGATGTTTAAAAGCCCAGCC
WI-2572	61	C	T	…	…	AGTGAGTTGTGCACAATTTGGAGACATTCTGTGACCCCAAACTTAAAACACTTCTCCCCACA[C/T]AC AAAGTTAACACTTCAGTTACCAGGTGATGATTGAGCAGA

ID	No.				
VI-10368	31	C / T	TGAAGCAACC AGGTCTTGTT	CAAGATATTAT ATTTATTCTCT AAGAGGGG	GAGGAACTGCCTGAAGCAACCAGGTCTGTGT[C/T]CTACCCCTCTTAGAGAATAAATATAATATCTT GAGATAGGGAGGAGGAGCAGCCTGAGGACAGTCTGGGTTTGTTCTACCCCACTGGAAGCAGAATATCC TTCAAAGCTTTTCCAGTGAGTCATGTTGCTGCTAAACTATATGACCCTGATGGATTGCCTTTCAGGG T
VI-10391	32	A / G	CTGTCTCAGGT ATGACTCCCA GA	GGGAGTTAGGA GTCAAGAAGTT	CCTCCCGTTCTCTGTCTCAGGTATGACTCCCA[A/G]TCAACTTCTTGACTCCTAACTCCATCTCGGTG TCTGCTTCCCAGGGGACGCATCTGACACAGCCTTTGCTTGCTGTGACAAACAGAACATTGCAGAGAAG TGATGCTGCGTGACCTCCAGGATA
NI-10567c	146	A / C	GTTACCCAGA GTCTTCTAATA GCAA	TGCCGGCTTCCA GTAGCT	AGCGATGAAATTTATATGTTATGCCTGACTTAGCGGGGTGCTCAATAAATATTATTCTTTTTCATATT TCCAATTATTAATAACTAGAATTTCACCAACAGAATTTTAAACATTTAAGTTACCCAGAGTCTT CTAATAGCAAC[A/C]AGCTACTGGAAGCGGCAAGAATTTAACCCT
NI-0567b	82	A / C	...	...	AGCGATGAAATTTATATGTTATGCCTGACTTAGCGGGGTGCTCAATAAATATTATTCTTTTTCATATT TTCCAATTATTAATT[A/C]CTAGAATTTCACCAACAGAATTTTAAACATTTAAGTTACCCAGAGAG TCTTCTAATAGCAAAAGCTACTGGAAGCGGCAAGAATTTAACCCT
VI-10567a	60	C / T	GGGGTGCTCAAT AAATATTATT CTTTT	AAAATTCTGTT GGTGAAAATTC TAG	AGCGATGAAATTTATATGTTATGCCTGACTTAGCGGGGTGCTCAATAAATATTATTCTTTT[T/C]TCAT ATTTTCCAATTATTAATACTAGAATTTCACCAACAGAATTTTAAACATTTAAGTTACCCAGAGT CTTCTAATAGCAAAAGCTACTGGAAGCGGCAAGAATTTAACCCT
NI-11153b	84	C / G	CAAACTTCAA ATTGCTTAAG TACTTTA	AAATCCAACA GTCAAGGTCTT C	CGTTGGGAATATTCTATCTCACCTAAATTATGCGTGATTAAAATATACATTTAACAAACTTCAAA TTGCTTAAGTACTTTA[C/G]GAAGACCTGACTGTTGGATTTTGAGTTTTCTTTATTTCTTAATA AAAACATGCATATTTAAGTTGTCAGCAAGATGTACTTATATGTTAATTATCTGATATCAGCATCCCTT TATGTATT
NI-11153a	33	C / A	GGGAATATTTC TATCTCACCTA AATTATG	GCAATTTGAAG TTTGTTAAAAT GTAT	CGTTGGGAATATTTCTATCTCACCTAAATTATG[C/A]GTGATTAAAATATACATTTAACAAACTTC AAATTGCTTAAGTACTTTACGGAAGACCTGACTGTTGGATTTTGAGTTTTCTTTATTTCTTAATA AAAACATGCATATTTAAGTTGTCAGCAAGATGTACTTATATGTTAATTATCTGATATCAGCATCCCTT TATGTATT
NI-2616	125	T / C	CACAAATGTA ACAAGAATTG ATCC	CCATGGCTGTA GTCCCAGT	GTTGTGAAACTCCAGTATCATTTCCCTCAAACCACGCTTAAATCACAAATCACTTTTCTTTCCTGTA GAGCTCAAACTCAGTCAGTGAATGAAATTGCTGCACAAATGTAACAAGAATTGATCCTA[T/C]ACTGGG ACTACAGCCATGGAGAAAAAGCAATGTAGTCAGCAAAATGTTAACAG
NI-11163	58	C / T	CAAGTGAATT ATGACCAAAA TGAGA	TGTCTCTTTCA TTTGAGGTTTT T	TGACTCAAAGGAAACTCAAAGTTTCACCAAGTGAATTATGACCAAAATGAGA[C/T]AAAT TTGTTAAAAAAAAACCTCAAATGAAAGAAGACAAAATAGTTCAAAGATTCAGGTTCAATATTTGT
WI-10656	59	T / G	...	...	ACCTACAAAATAGGGATAGTCATGGTGTTTGGCAGACTTTCTTTTCTTTTGT[T/G]CTCTA GAATCCATTTGCTTTTGGCCAGCATTCCCTCCCCATATTTAAGGAGAGAATTCACCTTTTCT CTGTTGGGATGATCACAGTTCTGCTCTTCCCAATCCAGAGGCACGTACTATTCACCCCATGGGGTCAT AGAGAGGATTAAACAGGGTGATGCCTGCAATGGGAATATTTGAAACC

ID	Pos				
II-1169b	154	T	G	TTAACCAAGA GTTTTTCATTC TTTTT	CTAACTTAAAA ATCCTCATTCA AAATATAA	CAGCATAGAGGCTGTTAGTGACCTTGAGTTAGATTTTCTCTATCGAGAAAGCAATAAGTGAAAGTAA CTGACTTGAAAAAAAGAGCAGACA[T/G]TTATCATGTTCTGATAATTTTTTTATATTTGAATGAGGATT TTAAAAAAAGAGCAGACA[T/G]TTATCATGTTCTGATAATTTTTTTATATTTGAATGAGGATT TTTAAGTTAGCAT
II-1169a	95	A	G	AATAAGTGAA AGTAACTGAC TTGAAAAA	AAACTCTTGGT TAAAAAGCAC TACTT	CAGCATAGAGGCTGTTAGTGACCTTGAGTTAGATTTTCTCTATCGAGAAAGCAATAAGTGAAAGTAA CTGACTTGAAAAAAAAATTTAAGCCT[A/G]AAGTAGTACTTTTAACCAAGAGTTTTCATTCTT TTTTTAAAAAGAGGACAGCAATTTATCATGTTCTGATAATTTTTTATATTTGAATGAGGAT TTTAAGTTAGCAT
II-10685	25	A	G	---	---	CAAGTGCTTGGACCTTGGATAGGTC[A/G]ACCGGCTGGAAGGTTGGACAGTTGTTGGTTAGGTTGGAG ACCAAAATTCAGTCATCCTGTAATATAGATCTTGTCCTTTGGGTTACCACTAGGGGTCACTAAAG AGAGATGGGAGACAGCAGTCTCAATCTTGTCTAAATAATTCCAAATAGCCATGGGTTTGGACAAAATAC AAGGTTAGTGTCTCTCTAACTTAATGGGCATA
II-10686	133	C	T	TGCCCCTGTCC AAGG	CAATCTCTAAA TTCATGTGTAG ACACA	AATAACCTGTGGCACATAAGGCAAATACTGAGCCCCATACAGAGTGTTTATGTTAATATTATGAAA AAAGTCAAGAGAACAAGATGATAGTTCTGCTAGAATACTTGAAATCTGATGCCCCTGTCCAAGG[C/T]TGTGTCACACATGAATTTAGAGATTGAATGAAAATGGCAAAATTCAGAAGAGGG
VI-11175	77	T	A	AAATGATTCTT CTGTTCTCACA TCTGCTCAAAG TTCTTTTTGAA A	AA	GGTAGGATGATTCTAGAATGCCACTTTACAGCCCACTGAAATATTGCCTCCCAAATGATTCTTTCTG CTCAAAGAG[T/A]TTTTTTAAGTTATCTACTTATTTATATTCTGCTTTTTCAAAAGAATGTGAGA ACAGTACAAAAATGTGTTCAGTAGCAAATTAAAATTAAAAGTAAGAAAAGAAGAAGCCAATT TGGGC
VI-10694	144	A	G	TGCAAATGCTT TATGAGTTTTC	GGCATTTTGTA AAGGAGGAAA	TAGAGAGGTCTTTCAGTTTCAGGGGTTGGAGGGGTGGTGAGATTCACTTCTTAGAAGCACTGGC TATGTACAGAAAGATAAACTCTGAGAGAGAACTCAGTTCTAAAGTGTTCAGTCTTTGCAAATGCTTTA TGAGTTTTC[A/G]TTTCCTCCCTTTACAAAATGCCATCAATTCCTCAAGGAAAAAAAAGCTTTCT T
VI-2716	23	T	C	TGAATTCATCC AGAAAAACAG C	TCTCTTTTCTC TCTTGTTGTCA TTC	GTGAATTCATCCAGAAAAACAGC[T/C]GAATGACAACAAGAGAGAAAGAGAATAAAGGTTTTGT ATACGACAAGTGGCTCAAGCAATTTCTCTGTCCCAGTGCATGGAGCAGTG
VI-10719	115	T	C	TGACTCTCAAG GCCATTCTAG	GCACTGCCAGC AGCC	CAGGCCCAACTCTGTCATTAAGTGTTTAGAACAGACACCTCAGTCACACAAAGTTTCTCTTGTATGT GCCCACCATAAACAGTTACTGGAGGATGACTCTCAAGGCCATTCTAGT[T/C]GGCTGCTGGCAGTGCTT TTCCAGCCTGCTGCCCATAACTAA
VI-10721	40	A	G	TGGCTCTGCTA CTTGCCA	GAAACTCCCAC ATAAATAAAT CTCA	CAACCAATTCAGATTTAATTTTTGGCTCTGCTACTTGCCA[A/G]ATGAGATTATTTATGTGGGAGTT TCTGAAGATTCCCATGGTAAATAGTATTCCCTGCTTAGGTTTGAAGAAGTGAA

ID	Pos			Flanking	Sequence
VI-1204b	88	T	C	---	GCACACGAAATTGATTAATATTGGCTGACTTT[T/C]ATTTAAAGTAACATAAAGGTATTATGTACATTTAAGTGATCAAAAAATTTAATTGGGAAGAGATTTAGTGAATCAGAAAATAAGTCTGAGGAAATTATTCAGAAGGCAACACATC
VI-1204a	80	T	A	GTAAAAAGGG TGAAAAGAAA AACTT / TGATCACTTAA AATGTACATAA TACCTTT	GCACACGAAATTGATTAATATTGGCTGACTTTATTTT[T/A]CACCTTTTAATTGGGAAGAGATTTAGTGAATCAACATAAAGGTATTATGTACATTTAAGTGATCAAAAAATTTAATTGGGAAGAGATTTAGTGAATCAGAAAATAAGTCTGAGGAAATTATTCAGAAGGCAACACATC
VI-10732	80	C	A	AAGAACAATG GCTGTGTCTTC CATAACAGAA ATTGGTTCACT CTTTAA	ACATGTATTTCCTTAGTGGTCAGCCTTCCTTACCCCCAGAATATCCCTGGTTATTGCTGTGTCTTCATTGGTTCACTC[C/A]TTAAGTTCTGTTATGCATTGTCTTGTGTATGCATTAGGTGTTAATCATTCCACACCACTCTGTTTAAACTGTC
VI-11206	127	A	T	GGTTGTGTTTT CTGTATGTACA GAGTGACAATC ACTC CTAATGGTTGG	TAGTCTTTTCTTGTACGAGTGTCATAAAGAATTACCACTCTGTCACATTTGTAAAGATAGCACAGAGAGAAGCATTACAGGGCACAGCAGCAAACATGAGGTTGTGTTTCTGTATGTACAACTC[A/T]CCAACCATTAGGATTGTCACTCTCATATAGACAGAATTCAGTGGTGATTGAATTGAATTCCACACATGGAATAAGTCTA
NI-11215	68	C	T	---	GAAAAAAAGTTTAATTGGATTGCTTAGTTGTCTTAAATTTGACCTACTTTCAGATTTATTTAGT[C/T]ATTTTTTCTATAATATTTCTTGTAAGTGATGGATTTCTATAAATTAAGGAAACAGATATTTACACAGAGAAGACAGGATTGCTTGAATTAGTAGTAACATTCTTTATTCCAAGCCCCATCCCACCATGTTTT
VI-1219b	89	G	A	GAGAGAATAT TCCAAAAAGT AGAGAAA	ATGAAAAATGCATTAGAAGAATTGGGAGGAATATTCCAAAGTAGAGAAAAAGAGACAAAGAGATGAAAAATAGGA[G/A]AGAAAGTGTAGAAAAATTAGAGGACCATTCTATACAGTCCAATATTTGAATAATAGTTATTCAAAAAAGAGGCAAGAAAATGAGGGGAGAAAAATCCACAAAACATCTC
/I-1219a	18	G	A	---	ATGAAAAATGCATTAGAA[G/A]AATTGGAGGATAAAATTGAGAGAATATTCCAAAAAGTAGAGAAAAAGAGACAAAGAGATGAAAAATAGGAGAGAAAGTGTAGAAAAATTAGAGGACCATTCTATACAGTCCAATATTTGAATAATAGTTATTCAAAAAAAGAGGCAAGAAATGAAGGGGAGAAAAATCCACAAAACATCTC
/I-1222b	136	G	A	CATACCACTGC CCTGGTAGCCA AGTTGTGA GGCTGG	AGCCACAGTGGAATCATTTACACTACCGAAATCAGCAAATGCTAAAATTGGGGCTTGGATTTTGTTTTGTTTTTCCATAGACCCCACGTTGAACTTATTGTTAAACATTTACCAGCATTACCACTGCGGCTGG[G/A]TCACAACTTGGCTACCAGGAGAACCTTGACAGACTTCGTAATTGCTTTCACAGGCTACTGGAAAGCC

ID	No.					Sequence
I-1222a	25	C	T	A	GCCACAGTGG AATCATTTAC	TTTTAGCATTT GCTGATTTCG	AGCCACAGTGGAATCATTCATTTACACTA[C/T]CGAAATCAGCAAATGCTAAAATTGGGGCTTTGGATTT TGTTTTGTTTTTCCATAGACCCCACCGTTGAACTATTGTTAAACATTACCAGCATACCACTGCGG CTGGGTCACAACTTGGCTACCAGGAGAACCTGACACAGACTTCGTAAATTGCTTCACAGGCTACTGGA AAGCC
I-10775	39	C	T	CACTC	TTTATGCCATA TTAATTCATTA	CTAGATGTATT TGCTAAGAAA ATATGATG	TTGCAAGTTGTTTATGCCATATTAATTCATTACACTC[C/T]ACATCATATTTCTTAGCAAATACA TCTAGACACCTGGCACTCAGTAGGGATATTCCTGGCACGATAATCATTGTTATCATTAGACATTGCA GGAACCACCATATGGATGGATAAAATGTGTTGTTTAATGAAGGCAAGCAATTA
I-11226	165	A	C	...	...	TTGCATGCATTTATACGAAAGGAATTAAAATATCTTCCTTATAGTTGAATTTAAGTAAAAATAAA GTTATACATATAATACAAAAAAGTGTAAGTATAGTAACAAATGAATTAGAAAAATTGTCAGTGGTTGC TAGTACAGGAATCAAATTTGGACTATGAACA[A/C]GACATAGTTGCTAAGGATATTCCACAAATTAT TTCATGA
I-10778	62	A	G	GCAAGGGGAGG AACATTTACA G	CTGGTGACATC AGAGATGGAC	CAGTGGCTGGCTACTGACAAACGTAACATCGTGGCAGGTGGCAAGGGGAGGAACATTTACAG[A/G]G TCCATCTCTGATGTCACCAGCAGGGCCAGGAAGGGTTGATCTGGAG
I-10789	21	C	T	GGGACACACT GCTCTAGACC	TTGAGGGGACCC TGGGA	TGGGACACACTGCTCTAGACC[C/T]TTCCCAGGGTCCCTCAAAGGTGGGTGTAGAGGCCCTACTGCCCT GCCCTGGGGACGCAGAGGCCTTAGTCCTCCTGGGGACAGTGAAAGGGCCACCACC
I-10810	58	C	T	CATCTTCATGG GCAGGAATT	CAAACCCTAAG AAACACAGAA ATG	ACAGAAAAATGCCTAGGTCTTGTAGCAAGAGAGAAAGCATCTTCATGGGCAGGAATT[C/T]CATTC TGTGTTTCTTAGGGTTGTGGCTGGCCATCAGTTCAACTCAGCCCCTGTCCCCTGATCCCAGCAACATT TCCGTAACTACCCTCTAGAAGTCATGCAAAGAGAAATGATGA
I-10828	23	T	C	...	...	GGACCAAACAGAATTACTTGGCA[T/C]AGGGTTTCTTAAAACTATTTCTGCAGAACATTAGTAAAGT TAAATAAGGATGCAGGCTACCAGGGAATCAGGTACAGTTAGGGAACATGTGGATGAATATTCTTAGTAGAG GACTTCTCAAAAGGCTATAAATATTTGGATACATTAGCTTCATTATGAATCTCAAAAGGAGCATGTAGT AGGGCATATCTAA
I-10832	91	G	C	CATTAATCTGC AGGCTCTCC	CCTAACTGCAG GTGACTTAGAA A	TATGCCTTCCCAAGCGAGCCATCCACGCTGCTCTTAGCACAAAAAATAGAATACATCATTCTGAATG GCACATTAATCTGCGAGGCTCTCG[G/C]TTTCTAAGTCACCTGCAGTTGCTCTCGAGACACTGTGTA TACCATATAAATCTGATTTCTGAGCAGGAGGAGCAGGGCTGCCGTGAAATAC
I-10834	96	C	T	AGAATTAACT GTTCAAAAGT GTGTTAAT	TGGCCCTATAA AATTGGTATTA AG	GATTTGAGTATTATCAAAATTGCCCAAGACCATTAACAAGATTAATAGTTAAAGCCAAAACTATA AAGAATTAACTGTTCAAAAGTGTGTTAAT[C/T]CTTAATACCAATTTTATAGGGCCACCATTAACTT CTGAAGAAAGGTCAGCATATGCAACTAAATTTCTAAAGTCCAGT
I-2287	24	T	C	...	...	GGATGATGTTCTGTGGTCCCTTTA[T/C]AAGCCTCTTGCATCCCAAATGTGTAAATTATTTATTCT TGGTATTTCTCGCTTACCCATAGTCACCTGTCAAGTGTTCCACCCT

ID	Pos	Allele 1	Allele 2	Flank 1	Flank 2	Sequence
VI-2296	81	A	G	TGTTACTTTGA TTCTTTGCTCT GA	GCAAATCACAC	TGGAGGGTTAGAAATGCAGGTGGCATCCTAGAAAGGTCTCAGGCTTAGAATAAGTTGTTACTTTGA
VI-2300	77	G	T	GGCACAGAAG	AGCTAACTGG	TTCTTTGCTCTGAC[A/G]CCAGTTAGCTGTGTGATTTGCAGAAGGTTACATTGTTGTTG
VI-2371	55	G	T	GTCTTGTTCTT CCCAGCTTCT	CAAAGATTGAC AGCCACCAC	TTTCATCATGCTGTCTTCCCTGGAAATTTCCTTTATTTGAGCGGGGCAGGTGGTAGGCACAGAAGC CAGTCATAC[G/T][G/T]TGCTTAAAATTGACCCAACCATTACTAAGAATAGCATTCA
VI-2395	122	A	C	GAACATATTT GTAGAAAAAT TACTATCCAA	TCACCTTCTA TTTATTCTGAA TTCA	CAATGATCCCCAACATTTCCAGGGAAAGGTCTGGTCTTGTTCTTCCCAGCTTCT[G/T]GTGGTGGCT GTCAATCTTTGACATTCCTTGTCTTGCAGCTGTATAATTCCAATCCTTGCCTCCAGCTTTACATGATGT TCTCTCCGTGTCTGTG
VI-2437c	192	G	A	---	...	GGGGGCACAATTTAGCTACAGTGCATATTAAAAAGATAACATAGAATATCATAATAACTTGGTTAC TGAAATCTGAAAACTTAGGATGAGTGAACATATTTGTAGAAAAATTACTATCCAA[A/C]CTGAATTC AGAATAAATAGAAAGGTGAATCATCTTATATCATTAAAGAAGCTAAATTATTAGTAACAATCTTTA CATTTACACAAACCCA
VI-2437b	179	G	A	---	...	CACCAGCCACCACCTACAACCTCCTGTGGGGAGTCTGGCTTGATTATTGGGGACAAAATAATTT CAGCTTGAAGAGAGATTCCAATCACAACTTTCTAAATAATAGACACCAAAAATTCCCAATGCTCTAA ATAGATGGACTCAACCCCTTCTCTGCAAGAGGCAATCGAC[G/A]AACATCACAGTGGGGCTGTG GTGCCAAGGACGCATTATG
VI-2437a	128	G	A	---	...	CACCAGCCACCACCTACAACCTCCTGTGGGGAGTCTGGCTTGATTATTGGGGACAAAATAATTT CAGCTTGAAGAGAGATTCCAATCACAACTTTCTAAATAATAGACACCAAAAATTCCCAATT[G/A]CTC TAAATAGATGGACTCAACCCCTTCTCTGCAAGAGGCAATCGACGAACATCACAGTGGGGCTGTG GTGCCAAGGACGCATTATG
VI-2440	71	G	A	GCAACCTACT GACAATTTAA TTTTAGTT	AACAACTCTGC TATTGGTCTCA C	CAGTAGGAAACGGGTTCTTCCTTAGACCCTCCAGAAAATAATGCAACCTACTGACAATTTAATTTTA GTTG[G/A]GTGAGACCAATAGCAGAGTTGTTACCTGCAGAACT
VI-1356	123	T	C	TGTTTAGGAA ATAATGACAA GAAAAA	TGGTTACAACT GTACCAAACAT G	CTGTAACCTACACACATCCTCCTGTAACCTCTAGGTTACTTGTAATACAAAACACAATGTAAATGCT ACATAAATAATTGTCATATATTGTTAGGAAATAATGACAAGAAAAAAGCC[T/C]GTACAT GTTTGGTACAGTTGTAACCAGCCATTTTCCCCAATATTTTCAATCCACAGTTGGTTTAATCCACAG AAACCACGAATG
VI-2886	46	C	A	CAGAGTCTGG GGGAGAAGA	TTGCCATGCTT TATCTCGTT	ACAGTTAAGAAAAGGCTGCAGCCGTTGCAGAGTCTGGGGGAGAAGA[C/A]AACGAGATAAAGCATG GCAAAGACCACGCTGAAAGTATCCCAGGGTGCTGTATGTGCACATAGGAAGAGATCACTTACCTCAGCA TAGGAGGAGGGCTAGGCAAGGAAAAGGTGTCAGAAGAAACAGAGAGGCGTT

ID						Sequence
VI-2906b	77	T	A		---	CCTGAACCTGGAGCACTTCCCTCCCTGGACACCTTCATTCTTGCTGGTGAACTTTGCTGCTGGAATGCTC TTTCCCTCG[T/A]GAGCTTTGCTGGCTTACTTTTCTTTTCCTTAGGTTTCAGCTTCAAAGTGACCT CCTTAGAGTTGGTTTGCTGACCAACAAA
VI-2906a	50	A	C	GACACCTTCAT TCTTGCTGG	AGAGCATTCCA GGCAAAGT	CCTGAACCTGGAGCACTTCCCTCCCTGGACACCTTCATTCTTGCTGG[A/C]ACTTTGCTGGAAT GCTCTTTCCCTCTGAGCTTTGCTGGCTTACTTTTCTTTTCCTTAGGTTCCAGCTTCAAAGTGACCT CCTTAGAGTTGGTTTGCTGACCAACAAA
VI-1736	175	C	T		---	TACTCCTCATTCCTCATGTCCCTAGACGTACTCAGATTTCCATGCCCTGAAACATTTATTTCCTAAAT TAGATTTCCCACCCCCAGCACTATTTACACAGAAAACAGCATGGAGCAGTTTGGAGTCTGGCTCTTAGA GAACTTACTTAAGGACAGTGGTTTTCCATCTGTCTTCCA[C/T]AGAGATCTAGGGTGTCTTTGGAACC ACCTTGG
VI-1851	136	G	A	GCATTGAATT AACTATAGAT GTGTTAAGTA	CACTAGCAATG TTAAACTGAAG TTG	AATACCCCACGTCCTAACACCATCACACTGATCATCAATCAGGTTTAACATATTAATCTGGGGAGG ACACAAACATTTAGACCATAGCATTGAATTAACTATAGATGTGTTAAGTAATTAATATTAACATGGTA CA[G/A]ACAACTTCAGTTAACATTGCTAGTGATTCCATGTGGATACCATGTACCTTCTTACATCATG TGA
VI-3000	62	G	A	CCCAAAACAC AGAGACCCC	GCCACTATAGG ATTGACTAAGA CTCA	CTGATGTTTGGGAAGCACTGTCTTACATCTCTAAATGTCACCCAAAACACAGAGACCCC[G/A]T GAGTCTTAGTCATGTTCAATCCTATAGTGGCAGTACCTGAATCAGTGCCTGGTGCATAGTAGACACT
VI-1754	177	G	A	TTTTCTCCCTT CTTAAAGAGA TAGTC	AAAGTCGAATT GCCTCTGG	ATGGATCTGCTCAATTATAGTCCCAGATAAACAGCCCTTCTCCCGCCACCCCGGATTATTTACT TAAGGGTTTAGCAAATTCACCTGACAAAGAGTTAGGTTTCAACATTGACCCTCATAAAGTGATTTT TTCTCTTTCTCTGTTGTTTCTCCCTTCTTAAAGAGATAGTC[G/A]CCAGAGGCAATTCGACTTCTGT AGCCACAAGATT
VI-3167	37	T	A	AAATTCAACC ACAGATCTAT TAGATTC	TGTGATAGTTT TGAGATGGGTG	ACAACACAGCAAATTCAACCACAGATCTATTAGATTC[T/A]CACCCCATCTCAAAACTATCACATCAA AGAAGCAAGGAGGACATATTACTGGTGAGGAAGCCAAATTCAA
VI-3208	140	G	A	GTGGAGTGGGC AGATAAAGA	TCACTCAAACT AGGGCTTGG	CAAGCACACATTCAGGCAGTGGGCAGTGGGCAGGTAGGAGGATAAGTGGATCAACCCCCTTGCCGCAGCAGAGAGGAGGAAG AAGTTCAGACGCGTTGGGTAGGAGGATAAGTGGATCAACCCCCTTGTAGGGCAGGTGGTGGGGCAG ATAAAGA[G/A]CCAAGCCCTAGTTGAGTGACACTGTGTGGGATTCAAG
VI-1775	47	C	T	CCTGCATGGTC TTTTCTCTG	AGTTGAGATTT ATGACAATGAT GTAAA	ACTCCACCAACAGTTTTGTGAGCCAACCCTGCATGGTCTTTTTCTCTG[C/T]TTTACATCATTGTCATA AATCTCAACTGACACATCAGTGTCTGCCACCCCA
VI-3402	55	G	A	AGCATATTCA TTGATTTCCTT ACAT	GAGGACTTAAA AGGGAGCATTT G	CTGCCCCTTTACATCCAAAGCCCAGTTACTCGAGCACATATTCATTGATTTCCTTACAT[G/A]CAAAATGCTC CTTTTTAAGTCCTCAACTTTTAAAGCGGAAGCATGCACAAATAGATTTCCTTAGGA

Clone	Position	Allele 1	Allele 2	5' sequence	3' sequence	Context sequence
NI-3416	33	C	T	CCAAGTTGTA GCATTCAGAA GTC	ACGAGCACAA CTACCTCTAAG AG	TCTGGTTCCTCCAAGTTGTAGTAGCATTCAGAAGTC[C/T]CTCTTAGAGGTAGTTGTGCTCGTGTTAAAA TATGTTTTCAAGATAGTAGTATCTCCCTGTTGTCTCCAAACAAGTGTACCAACAGCATTGTTAAG GAAATGTGCAATGCTTGCTACCTGCTGACGCAACATAATTAAATCCCATTGCCTAAAAGACCAGG
NI-3453	70	C	T	TTCTTAGGCCC ATCAGAGAA	TCAATTTTCCC CATGACTTC	TCCTATTCCTACAACAACAGAAATTTAACAAATTGAAAATCAGCTACTCTTCTTAGGCCCATCAGAG AATT[C/T]GAAGTCATGGGGAAAAATTGATGCCCATTCCCACTTCCAGAGCCATCATCTGTAAAGAC AATTACAGTTACCAGGGACACAATCCCACTTCCAGAGCCATCATCTGTAAAGAC
WI-3474b	109	G	A	---	---	CATGCTAGGTAGATCTGATCATGAAGTTGAACAAACTTAAATCATCAAGTGTGTCAACTGGTTTGA GTCAGTTTCCCTAATTTAGCACAGTATTTTAATGAGGTGGT[G/A]TGGGAGAAATTGATGGTTGCG TAGTTGAGTTTCTGTCCACC
NI-3474a	90	A	G	AGTCAGTTTCC CTAATTTTAGC AC	CAACCATCAAT TTTCTCCCA	CATGCTAGGTAGATCTGATCATGAAGTTGAACAAACTTAAATCATCAAGTGTGTCAACTGGTTTGA GTCAGTTTCCCTAATTTAGCAC[A/G]TATTTTAATGAGGTGGTGTGGGAGAAATTGATGGTTGCG TAGTTGAGTTTCTGTCCACC
NI-3502	79	C	T	CCTGGGTTTCT GGATGTCT	GGGTGACCCTG TCCTCA	TTTGACCCCATCACATGAGAATAAAACCATAGAAATGGTGGAAAAATAAACGGGAGAGACCTGGG TTTCTGGATGTCT[C/T]TGAGGACAGGGTCACCCCAC
WI-3600b	146	G	C	GGTTTCTAACC TGGATATAAA CATCT	CCAGTGCAGCC TTCCAT	TCACGGCCAAGTTCTGCAGCAGTCCTTGACTCCTGCCTGTTTCCAGAGTCTGATTATCCATGCCCTG ATAGTTCTGTGAGCCACCTAAACTCGTTCCTGCTTATCCAGAGGTGGTTTCTAACCTGGATA TAAACATCT[G/C]ATGGAAGGCTGCACTGGATGAGGTCACAAA
WI-3600a	78	T	G	CCATGCCCCTG ATAGTTCTG	GGAAACGAGTT TAGGTGGCTC	TCACGGCCAAGTTCTGCAGCAGTCCTTGACTCCTGCCTGTTTCCAGAGTCTGATTATCCATGCCCTG ATAGTTCTG[T/G]GAGCCACCTAAACTCGTTCCTGCTTAGTTATCCAGAGGTGGTTTCTAACCTGG ATATAAACATCTGATGGAAGGCTGCACTGGATGAGGTCACAAA
WI-3678	125	G	T	---	---	TAAATCATGCTATTTTCACAAGGTAATCCACTCACAATAGGCAATTGATGTGATCTCTTTCTGTAA GAAAAGCTCTCATGCTCTTCCTGAACCTTCTACTTGTGCTGTTATGATGCACCT[G/T]CCTTTGG ATAGATGGTTGATAGGAGATGGGTTGTAAAGACACAATTTACCTTGTGTGTTTCAGGCAGAAATAG ACTCTCTCTGTGTAATCACTGAATGAGTTCCAAAGCCTTTATGTCTTAC
WI-3687	67	A	C	---	---	AAAGCGATGTTGAGATACCACATTCCATGAAAAAGTAAAAACACACACAAAAATATGACATAAAA T[A/C]AAAAACTACTATAGTTTATGAAAATGACTTCCAAAATTCAGAGAAAAGTCACTTAAACAGG ATTCTCAATTCATTCCAGAATACTCCTGTCATTCTTAACTTTGACTGCACAG
WI-3735	72	T	C	CCTCAGTTATG TATCAAATGA AAAAC	GGCTCACCAAT CATTGTTTT	TCTAAAATGTGAAACCAAAGAATCCTGACACGACCTAACTGCCAGTCCTCAGTTATGTATCAAATGA AAAAC[T/C]CACACCGGTTCAATGAAAAAACAATGATTGGTGAGCCATGCCCCTTTATTTAATGAAA GATCTTGGGCAATTAACTC

ID	Pos	A1	A2	Left probe	Right probe	Sequence
WI-1819	51	C	T	---		GAAAAGCAGGAAGCCAGGCAGGCAGGACAAACTTTGAAAAAGTCTTCAGCAC[C/T]TTCGTGGGATCCG AATTTTAGTGTGATTGGCAGGCAATGCGCAGGGGTAACATGTTCCAGTGTTTAACTGCACAGAATTGC CAGATTAGCGATTGTTGACTTGTCCAATTAATGAAATGTGAAAAAAAAGGGTGGTAACTGTT AAGCCTGCTGCAATGTTTAGACACGATGTTTAGGGGGAGGTGGAATACC
WI-3746	116	G	A	---		GGCCTATTCACATGACACTGGGCCAAGATCTTGTTCCCTTCTTCAATAGATAGACTAACTAGAAA ACTGCCCTGGCCCAGGAGAAGATGGTTGTCTTCATCATCTCTGTCTCTGC[G/A]GCCCCAGGATAAAGCA GGCA
WI-3867	49	T	C	ACAGTCATTT AGTCTTCCTGA CAA	TAAGATAACC ATACTAGGTAC ATCCG	AGCAATGAGTTAACTCCTTACATGAACAGTCATTAGTTCTTCCTGACAA[T/C]CGGATGTGTACCTAGT ATGGTTATCTTATCTGACAGACAAGGACACTGTGACACAGAGATTGTTACTTGAACAAAGACACAGT CATTAAGTGGAGAAGCCAGCATTCTAATCAGGCTCAGTGATCTGCCAAACCAACCCTTCTGCTATAG CATC
WI-3898	25	A	C	TGACCAATGTC TTTAGAAGCA G	TCGTCGGTGTC CTCTCC	CAATGACCAATGTCTTTAGAAGCAG[A/C]GGAGAGGACACCGACGAGAGACACAGGAGGAGTGAG GTGAAGATGAAAGCAGTGTGACGCAGCCACAAGGTGAGGAAGAGACAAGGGTTGCTGGCCACT
WI-3901	114	A	G	---		GGACCATTGTCCCTCAGAAGTACATTCAAGCCCTGACCGGTGTCTCCTAACACTGTGACCTCAGGCA AGTCATGTCTGCTTCCTGAACCTCGGCTTCTCACCTGACAAGTGG[A/G]TATCATGTGCTACACTGC AGTGTTTATAATGCTGCAT
WI-4019	99	C	T	TGATTCTTCTC AAGACTCACA CC	TCTAGAAGCAA TGAAGGATGG	CTGAGGAGATTGATGCTACTTTACCTGAGGAAACTTTTATACCTCCCCTGAGTTTGTTGCCTTGCAA GACATTGCTGATTCTTCTCAAGACTCACAGC[C/T]ACCATCCTTCATTGCTTCTAGACCTATAACTAG ACTCAAGTCCCAGCAGCCCCTTAAAGGTAAGGTACAAAGTGTGACCCCATGGGGAGGTATGTTACGCTA CAAAAGAG
WI-4091	33	G	A	CCAAGAGCGT CCTATGAATC A	AACAGCAATA ACAGGAACAA ATG	CCACTCCCAGGCCAAGAGCGTCCTATGAATCAT[G/A]CATTGTTCCTGTTATTGCTGCTGTTCACAGAGT GGCAACTCTTGCAAAGGGAGGGGGTACAAAGTGAATTTTAGATGCTGCAGGAGACGAGAAGGGTC
WI-4160	84	A	T	TTGAGGTCTTA GTCATTGCATG	TGAGTTCCTAT TAAGTGACAAT ATTGTT	TAATTCACATTGCTCTTGTTGTGCATTTATTGCTTCTTATGTAAACAATCACCACATTGAGG TCTTAGTCATTGCATG[A/T]TGTATAACAATATTGTCACTTAATAGGAACTCAAGCATAGTATGTGT ACATTTATTGCTAACAGCAG
WI-4168	117	A	G	CCTATAATTTA GCAACAATAT CAACAGAA	TGCAGGTAGAA TTTTCTAATAT AGCC	TCCTCTTCTGTAATAGGAAGTCTGATTAGATGCCTTTGAGGTTGGCTTCTAAGATGGTAATT ATCTGTCCAAGTTTTGTTCCTATAATTAGCAACAATATCAACAGAA[A/G]GGCTATTAGAAA ATTCTACCTGCATCCTGACGTTCTTCATGATACT
WI-4168	32	A	G	GGTGAGAGTC AAATTGATAC AAACA	ATTGCCAAACA GATTTTCAGA	CGTTGCTGGTGGTGAGAGTCAAATTGATACAAAACA[A/G]TCTGAAAATCTGTTTGGCAATCTATTAAAGG CAAATATATACCAGCAGTGTGGCTCTAGCAATTCACTGCTGGCATTACCTAACTAACACTAAAATGAT

ID	No.			Seq A	Seq B	Sequence
/I-4177	68	T	C	TGAATAAGCA CGTATTAAATT TACCTA	AAGGCAGCAA ATCATGATG	ATGCCTGCGGATATACTTTCCAAATGACTAGTAGTATGAATAAGCACGTATTAAATTTACCTATTATATT A[T/C]CATCATGATTGCTGCCTTCTTTCCAAATTTACTACAAATTGTATTGTCACATGAGGCACATG ATCCCATTAACCCAAATAG
/I-4199	51	A	C	CTCCCCAAGTT AGTCAATATA AAAA	ATATGTTGATT AGGTATAACA ATATGTGTG	GCCATGAGCACAGAGGCTGAAACCACTCCCCAAGTTAGTCAATATAAAAAAA[A/C]CACACATATTG TTATACCTAATCAACATATAAATGTTATGATTAAACAGTCCACAGCAAACAA
VI-5163	24	C	T	CTGTCACTGGT CTGCCTGT	AAAGGAACAC AGGAAACAGAC C	TTCTGCTGTCACTGGTCTGCCTGT[C/T]GGTCTGTCGTTCCTTTCAATGTTCAACTGCTTGTAT CTGTGCCCACTAAGGTATCAGGTTTATATGGCACAGGATGAGGGGCTTTGTAGACCAGAGTTTTCTT GGAAATTGCAACATTTGGGCAT
NI-4250b	117	A	G	---	---	TAAGTGCATTAACTGTACAAGTCCACAAATACCTCTTCCACCAAGTGCTAAAGCAGTTTAATAACA GGTTCAATATGAGTCTTGTGAAACAGGGGTGGGAAGGATCCTGTAAAAGG[A/G]TAAATATTGTTTT CCATAATAATTGAAGATGTG
NI-4250a	94	G	T	TCAATATGAG TCTTGTGAAAC AGG	CTTTTACAGGA TCCTTCCCAC	TAAGTGCATTAACTGTACAAGTCCACAAATACCTCTTCCACCAAGTGCTAAAGCAGTTTAATAACA GGTTCAATATGAGTCTTGTGAAACAGG[G/T]GTGGGAAGGATCCTGTAAAAGGATAAATATTGTTTT CCATAATAATTGAAGATGTG
NI-4255	68	G	C	TGCTCCCCCAT CACCT	GGCCTACTTCA AGTTGTGTAAG G	TAAATGTCCTGGGGAGATAATAGGAAAGGTCCCATCCCCTGATACCTTGGTTGCTCCCCCATCACCT [G/C]CCTTACACACTTGAAGTAGGCCCCATCCAAACACTGGTCAGAAGAGTAATACTGTCGAC
NI-4256	57	C	T	---	---	ACAGCCCTCTTCAAATGCACAATCAAAAGCACCAGTAAAAGCAGAGGCAAAATCTGG[C/T]CTCAC CATTGGAAAAGTCTTCTGAAGGATAAGGGAGTGAATGACCATAGGGCAGGACCGGAAATGG
WI-4325b	71	C	T	---	---	AGTTCACTGCCTAGATGAGTAGACCATGTTGTCTTGTTAAATGTACATGGGCAGGAC[C/T]GGAAA TGGGATGCTACTATAGATAATCTTTTTAAATGACTCTTCTTGGTCTCTTCAAGATATCACCAGCCAC CCAGGACACTGCCATATCT
WI-4325a	58	C	T	---	---	AGTTCACTGCCTAGATGAGTAGACCATGTTGTCTTGTTAAATGTACATGGGCAGGAC[C/T]GGAAA TGGGATGCTACTATAGATAATCTTTTTAAATGACTCTTCTTGGTCTCTTCAAGATATCACCAGCCAC CCAGGACACTGCCATATCT
WI-4347	158	A	G	---	---	TGGGCAGAAGTCGGGTATGGCAAGTCAGGGTGGGTTAACTTGGATGCCACTTCTGCCTGTCACTTCT CTAGACTCTTGACCCTGCAGGAGGATCCCTGCCCTCTGAGTTTTATCATCTCCCACCTCCAGCCCAG GGCCCTGTATCTGTTCAGGCCCC[A/G]GAATCGTCCAGGACGCTCCACAACTGTGGGAGGTAGGAATGACGA G
WI-1936	117	T	C	---	---	CCAGTCTAGGCTGCGCAAGGACTTCAATTCTGGGCAAGTCCTGGTTGTGTGTTAGGGTCAGAGGCAGCG ACCTGAGGGGACCACACAAAACCAGTGGGACCACCAGGGGTACTTGTATCACC[T/C]CTCCCGCAACCCCA AGCAGCACAGCTTGCAGTCCAGGAAAGACTCCTTACTTCCACTTGGACACACAACTTGGA AAAGAGGACTTTGACACACTTGGA

ID	Pos	Allele 1	Allele 2	5' sequence	3' sequence	Sequence
-5204	54	C	T	...		TAGATTTGATTGATGACAATAGGGAAGGAAGCCTTGTTGTTAAATTGGGTTTTGAAGAA[C/T]GAAGAAAAATGGAAAAGGGAAGAATTGACAGAAGAATTGGAGAGAAACCAAGAGAGAGTTGTGGGGGCAGCAAATCCCAGTTTGACTGGAATATAGAGTGATGTCAGGGTTG
-5215	70	A	G	GGACCTTAAT ATTTAACAGA CTCAAAAA	AGATAATTTTG TAAAGATAGTT TTCGC	TTTTCCCTTATTTATTTAGGAAGCAAAAATGTTCATACAGGACCTTAATATTTAACAGACTCAAAAATAT[A/G]GCGAAAACTATCTTTACAAAATTATCTCCATAGCAAGTAGACATTTTAGCACATTTCCTGTAGTCAAGGTTTTAAAGGCCAAATGAAGTTGACTAAAGACAAT
-4448	112	T	G	TTGTATCAAA GAGATGGGGT ATATAA	AATTAAAGAA ATCTTTACATG ATATAA	CCCTGAAATGTGCTTTGCTTCCTCCTCCCAACTCTCTAGGGAACTTTTCCATGTCAGGTGAAGGTTTTGAAGAGTACTTAATTAACTTGTATCAAAGAGATGGGTATATAA[T/G]AAAGAACCATGTAAAGATTTCTTTAATTAGTGAATTCATCAGGGCTCTTCCACTGTCTATCAGTAAA
-4456	49	C	T	AGTTGAATTA TTCAGAAAAT TATAGTTCC	TTTCCTGTTAT GCATGAACTG	ACACATTTCATTTGCTTAAGTTGAATTATTCAGAAAATTATAGTTCC[C/T]CAAGTTCATGCATAACAGGAAACACCAGGTTGGGGCAATTGATTGAATTGT
-4461	49	A	G	TCACTGTTATT TTAAAATTAT CCTTCC	TTTGACCTTTC ACCAATTTCA	CTGAAACTAATGAGGTGCTAAATCACTGTTATTTAAAATTATCCTTCC[A/G]TGAAATTGGTGAAAGGTCAAAGAATGAAATTCCCACTTTTAGATTTCTGGAAATTTATTGCGATGATAATGCAATGGGC
-4465b	75	G	A	---	---	CTACTGGATTTACTTTGCTCAAGCCAGACAACACGAAAGTATCACCTTTT[G/A]ATTCTCTCTACCTCACCTCAGGGAATC
-4465a	41	A	G	AAGCCAGACA ACACGAAAGT	GGTGAAAGATT ACTAACTGTTT TCTTT	CTACTGGATTTACTTTGCTCAAGCCAGACAACACACGAAAGT[A/G]TATAAAGAAAAACAGTTAGTAATCTTTCACCTTTGTATTCTCTCTACCTCAGGGAATC
-1949b	160	T	C	GAGTGAATAA ATGAATGCCA CTAATC	TGAGAGGTGGG GACAAAAA	GGGGTTAGGACCTCGAGATCTTTCAGAAAGCACAATTCAAACCATAATGGCAGTGCACAGGTAACCAGTGGTGAGATGCTGCTGAGTTCTGAGGTCAAGGCTGCTGCCATGGTCATGGTCAGATATGTTGAAGAAATAAAGGAGTGAATAAATGAATGCCATAATCTC[T/C][C/G]CTGTGTTTTTGTCCCCACCTTCCCACACCTTCCCTGGCACA
-1949a	86	T	G	CAGTGGTGAG ATGCTCTGAGT	CCATGTCAGCA GCCTTG	GGGGTTAGGACCTCGAGATCTTTCAGAAAGCACAATTCAAACCATAATGGCAGTGCACAGGTAACCAGTGGTGAGATGCTCTGAGT[T/G]CAAGGCTGCTGACATGGTCATGGCTGAATATATGTTGAAGAAATAAAGGAGTGAATAAATGCCATAAATAAATGAATCTCTGTGTTTTTGTCCCCACCTCTCCACCTTTCCCTGGCACA
-4529	64	T	C	CCAAGTAAGT CTATCATTCTG AAGATG	TTCTAAAAATA ACACTTCCTGA AAA	TGAGAGAGTTTTGGATTATTCATCCTCTGCAACACTCCAAGTAAGTCTATCATTCTGAAGATG[T/C]GAGTTCTTCTTTTATATCCTATGATTATTTTTCAGGAAGTGTTATTTTAGAATATAAACTCCTGGGTCCCATCCAGGTCTAGGGTCATCCATGGGCATGGGCCCTAGGATCATTT

ID	Pos	Allele 1	Allele 2	Primer 1	Primer 2	Sequence
WI-4540	110	A	G	GCACCATGTGG CATCC	GACAATGCAGC CATGCA	AGCTTTTCCTTTCTTAAAAAATTGGTGTGCCATAGTACTGGCTTCTGTGTGCATCAGGAGAGCAAGCCTAT TGCTCGGTAACAGTACTTTGCAATAAGCACCATGTGGCATCC[A/G]TGCATGGCTGCATTGTCCAGTC AAATGAGAGACAACTTCCTAT
WI-4582	226	T	C	---	---	AGCAAGCATCTGGCAAGCCTCGGTGTGACCAGAACATTAAATTCACCAAACACCACCTGCTCCAAATGT CCATGTTAATGCAATTATAGAAGACTCCAGTAGCATTCAAGGCCAGTTAACTTATTCCTGTACACA AATAACTTTATGGGAGACAGCATTGTAATTCAAATCAATAAATGACTCGGTTGGCTGTACAAGCAT AAACAGAAACGCTTGCAAAATATGGT[T/C]CCTCCTTGCTAGAAACCATTGAT
WI-1965	105	G	C	GCCATTGAGG AAGTGTTTAA AG	GAATGGGATGGG TCATCTCTCT	CAAAGGTTAGTTTAACTTGGGGGGCAAACACAAAGTTATGAGTACTCAATAACCTATGTTCAAGGG TAACCAACACCTTTTGCCATTGAGGAAGTGTTTAAAG[G/C]GAGAGGATGACCCATCCATTCCTGG GCTTCTTATATGACACCATACTATTCCCACAGATGTGGAGTCATTTATTTGGTTGGTGATGACAGT CATGG
WI-5248b	99	C	T	CACTGTTTTCT ATTGACCGTAC TTTG	AGAAAAAGAG AAGAAGGGAA AAA	TGTTTAAAAACCATACAGTTGTGCTGCTACGTTGTTGTAGAGCAACCCCAGAAAAATTAAACGCCTAC CATTTTTCACTGTTTTTCTATTGACCGTACTTG[C/T]CTTGCTTTTTTCCCTTCTCTCTCTTTTCTG CCCTCTTTAACTATT
WI-5248a	38	G	C	AGTTGTGCTG CTACGTTGTT	TTTTAATTTTC TGGGGTTGCT	TGTTTAAAAACCATACAGTTGTGCTGCTACGTTGTTA[G/C]AGCAACCCCAGAAAATTAAACGCC TACCATTTTTCACTGTTTTTCTATTGACCGTACTTGCTCTTGCTTTTTTCCCTTCTCTCTCTTTTCTG CCCTCTTTAACTATT
WI-4596	69	T	A	TGAAGCAGAA AGCACTGTGA	CAGGAGATGGG CCTAATAATG	CATTGGTGGGTCCAACTTCTCGGTGACATTACTCTGTTGACTTGCTCTGAAGCAGAAAGCACTGTGA C[T/A]CATTATTAGGCCCATCTCCTGCGAAGCCTGCCTACAGCAATTGTAACATATGGCATTGGG ACATATCTCTGAGCCCATCAACTATTGACAAGATTCTCCTTTTAACAA
WI-5252	119	A	C	---	---	GAAATAGGGCAAAATTAAGACTTCAATAATTAAGAAGTCTTGGGAAAAGGATTTGTGATGATCATTG AATCTGTTAAATACAGAATTAATACTGAATACCTGTCGTGATCATTGCTTT[A/C]TACCATGTACA TATTATATGAATTAACAATGTAAAATAGTAATGACTAAGAAATATTGGGCCCT
WI-4606	61	A	G	GCAATGCTAG AAAATTATGC CT	TTAGGTGCTTA AGTTGTCTACT TGG	TGCAAAAAGGAAAATGATAACCAGGACTGTGTTCAAGCAATGCTAGAAAATTATGCCTA[A/G]C CAAGTAGACAACTTAAGCACCTAAGGCAGAATGAAAGTTTCTCTCTTGTCATTCAGTAGTCCTCTATTCA ATTACCATTTATCGGGGTAATTAAAACACTGGAAGTAATGCGAAAGGCTAATTGTTAGATTATGATAAT TACACGTCTTTGCTATGCT
WI-5257	77	C	A	GAGGCATGAA GCAAAGAGG	CCAGGGGCAGA TGAAAG	CAATGAGAAGTTACCAGATGCGGGCAAATTAAGCATATGAAAATACCAAGTGTTGGCAGAGGCATG AAGCAAAGAGG[C/A]CTTCATCGCCCCTGGTGGGTTTTCAGTAACTGCAACATGTCTTTGCCTCC CGGATGAAAGATACCCTTCTATGACTCAGCAATTAAACACTGGAAGTAATGCGAAAGGCTAATTGTTAGATTATGATAAT GCAAAT
WI-4649	50	C	T	GAGACCATTCT TTTCCGAATG	TGTACTAGGTG TACTTACACAGA AATCATC	TCACTGTTTAGAAATTCTTCTTCCTCAGTGAGACCATTCTTTCCGAATG[C/T]GATGATTTCTTGTA AGTACACCTAGTACATCTATGAGCACACAATTAACAAGTACTTGCTACCTGAATTTGTATTTTTTAA AAAATCCTCCCAATATTG

-4650	148	A	G	GCACAAAGAA AGTATAAGTT GTCTCTT	CTGAAGTGTTA AACTGGATTG G	AACTGTGTGGTATGTAGTATTGTTTGTGTATTTTCTGGAGAGTCAGTTACTCTCACTAGATCATAAAGGG GACTTGGGAACCAAAAGTATCTCAAGACATTTAATCCTAGAAGCACAAAGAAAGTATAAGTTGTCTC TTATATTGCTTTT[A/G]CCAAATCCAGTTTAACACTTCAGTAACGTT
-4677	82	T	C	TCCAAAGTG ATTAGGTGAA AAA	TTTCAACAGTG TCATTATTCAA CTT	AATTCAGATTTGAACATACGTCGACATTTGGAAAAAATTGTCCAAAGTGATTAGGTGAAAAT GAGTTGAAATAAATG[T/C]AAGTTGAATAATGACACTGTTGAAAATGATGAATCTGCTTTCAATTCA CATGGAAAGGAGGACTAGAACACAGCAGGTTTTATAGGGGAATACTCAT
-4698	135	C	G	---	---	ATGATGTCTATCATGAGGAATTCTGTAGAAAATTTCACCTGGCAATTGATTCAAATAAAGTTTGTCC TCACCTGGGAAACTGCTTATCTTGATGTCAGTGACATTCTTTCTTTTGACGGAGGAAAACTTCAA[C/G]TTCGAGAAGGCTTAGATTATATCGCTGAAGCCCATTCTG
-4722	88	G	A	TGCACTATGG AACACCACAC G	AATATGGAATC TGCATTCAGTT G	CTTCCCATTCTGCCCAGTTAGATGACTGCCTCTCCACCAGCCTAGAAAAAGATGGGGAGATTTATTTC TGCACTATGGAACACCACAC[G/A]CAACTGAATGCAGTTCCATATGAATACTGGGAAATCAGTGA AAG
-2020	145	C	A	---	---	GCCACAGTAAAGAGGAAAATGGAGCCATGTAACAGAGGAGCTTCTGAAGATCAGTGTATTGTCA TAAAGGTCAGTGAATCACTTTGATGGTTGAGATTTCAGAAAACGTGAAATTATTGAGTAACCATGGG TCAACTACTGAT[C/A]CCAAAACAGCAGTGTTGTCTAAAAAATATGATAGTTCTTCTCCTGTCCACC GCAATGAAAAGGAGTT
-2028	176	T	C	TGTTTACGTTC CCTGTCTCATC	GGTTGGAAACT CAAATTACCTA GAA	GACTACAGGCGCACAGACAGGCATTGTGTGGCTTGCACAGGTGTTTGGTTTGTTGTTTAAGTTAGATT TGAATCCTTTAAAGAAGAAAGTGGCCTCTCAGTTTACTACAGACCTCATCATCTCCGGTTCTCTTG CACCCAGTCCACTTCACCTTCACGTTACGTGTTCCGTCTCATC[T/C]TTCTAGGTAATTGAGTTCCAACC TGTGG
-2033	183	T	C	GGGTGCTAGA ACTAATCCCTC A	CAGTGGTTCCA CGTTCTCC	ATGTGTATGAGCTCCACATTCGCCAGATTCAACCAACTATGGATAGAAAATATAGTATTCCCAGATGG GCAGCCCAAGGATCAGAGGGCTAATTTTAATTTTCCAAGGTTATACAGGACCAGTGTTGGAATTTT AGCATTTCTGGGGTTTGGCATCCATCAGGGTGCTAGAACTCCTCA[T/C]GGGAGAACGTGGAACC ACTGATATACCAAT
-4745	131	T	C	---	---	TTATGGATACATGTTTCTGGTGGAAGGACAAGAGTTGAAGCAAAAGGACAAAGGAGATCAACTGGG TAGAATAACTCATCGATCCCACCAGCCTCCTTCCCACCATTCTCCACCACTTCTCTACTTCTGA[T/C] AGGCAGAGACTTATATGGAAAAAGGGA
-2034	150	T	C	CCACAGTGCA CCAAGGAC	GGGTAAAGAT AGAGTGCAGGT CC	CCACGACTATGTCTTCAGAGTCCCTGGTACTGACAGAGGCTTGAGGACGAAGGCTTGAGGACCATGTGGCGCCAAGA CCTCCTTCTGCCGGTTCAGTGAAAGACGATGAACTCCTTCATCTTCTACAGCAGCTGGACTTCACCA CAGTGCACCAAGGAC[T/C]GGACCTGCACTCTATCTTACCCCTTCCGACACCAGAGCTGAGATGCC ACACTCTGAGTG

ID	Pos	A1	A2			Sequence
I-2038	155	C	T	TGTGCTTTAAA GTGTGTAAGT ATTAATTAG	AITTCCICTG AAAGAAACAT CA	TCAGGTGACAAGAGAAAAAGTCACATTCTTCAATCACTCACCATTGTCTGTTATTGTCTCTTGCAGTGT ATCCAAGGATGTCACTTTGGAACTCGTAGATCAGAAAAACTGTGCTTAAAGTGTGTAAGTATTA ATTAGATTTCTATTTGATA[C/T]TGATGTTTCTTCAAGAGGAAATTTGTGTAAGAGGATTCCCATT TGCAITTCCATTGGC
I-4782	113	C	T	GATGCAGAAG ATAACTAGAA AATGC	GAACTCTCTG GTTATTTTCT GTTC	TCATTGACTTTTAGAGTTCCTTCAGTCTTATTCTTTAGGAAAAACTAGGCTAGGAGAA CACAATTCAGGTCTCTCCAGATGCAGAAGATAACTAGAAAATGC[C/T]GAACAGAAAAATAACCA GAAGAGTTCATTATGGTTTTTTCCAGAACGATTAC
I-4788	65	A	G	GCATAGAATC ATCTTGCTAAG TTCC	GGATAAAATT AAAATTTTGGC ATAA	AGGAGAGTTTGGCTCTCTTTCCGGACTCTTGGAATTCAGTGCATAGAATCATCTTGCTAAGTTCC[A/G] TGAAAAAAAATTATGCCAAAATTTAATTTATCCAAACTTAAGTCGAGATTATAATTGATATTT AAAAAACTATATTGAGTCTTCTAAAAAAGATGGCGTATCACTCTA
I-5300	38	T	C	TCCCAGAGAC CACTTCATTC	CTACTCTTCT ATTTCATAATC CAAAA	CTTACTTCCAAAGTGTTTCCCAGAGACCACCACTTCATTC[T/C]TTTTGGATTATGAAATAGAAAGAGT AGGTGTTATTATTCCTCTTTTACCAAGGTGAAATTGAGGCTCAGAGACAAGGTAGATGATGAGCCCA AGGTCAGTGACAGAGCCA
I-4818b	121	G	T	TGATAATGGG GCCCTGTT	CCTTCCTTTA TATGTATGCCA GA	TATAATGTTTGTTCCATAGTTGCCATAGACTAGGTTATGTCCACACATGAATAAACAATCTTATATA ATAATTTATTCAAGAAGGAAAATATACATATGGGGTGATAATGGGCCCTGTT[G/T]CTCTGGCATA CATATAAAAGGAAGGCTAA
I-4818a	43	A	G	TTGCCATAGAC TAGGTTATGTC	CATATGTATAT TTTCCTCTTG AATAAATT	TATAATGTTTGTTCCATAGTTGCCATAGACTAGGTTATGTCC[A/G]CACATGAATAAACAATCTTAT ATAATAATTTATTCAAGAAGGAAAATATACATATGGGGTGATAATGGGCCCTGTTGCTCTGGCATA CATATAAAAGGAAGGCTAA
I-5317	139	T	C	TTCCATTTCTG GTAGCAGGT	GATGCAAAGA AGAAATGAGTC C	TTTTTCCATTTTGTTGATTCTTTTGTCTGAGCCCCTTAGATCTCCTTAAATTAATAGCAAGGTTAAT AATATAATAATGATGTTATATATTACAATTCAACAGGAATTCCATTTCTGGTAGCAGGT ATA[T/C]GGACTCATTCTTCTTTGCATCTATTTCTTTAGGTTATTTGCAGCCCGAGATCTACCCAGG
I-4888	56	G	A	GCAAGATATA AAGATTAAGA AAAGATAACA CA	CAATTCCACTA CCTCATTTATT CA	AAATGAGTAACCCAAGTTACTCGGCAAGATATAAAGATTAAGAAAAGATAACAAGA[G/A]ATGAAT AAATGAGGTAGTGGAATTGCTTGATAACTGGAGTAGTGCCTT
I-5328	44	A	G	---		AACATTTTTAACCATGCTACACATTTACAAACACTGAAAAGACAG[A/G]AAAAAGAATATTTTG CCTCAAAAGCTCTTAAGAGATTATGTAATAAAAGAAAATATGAATCAGAAAGAATCAGAAAGGAAAGAAAT AGAAACACGTGATACTGGAAGGAG
I-4897	93	A	G	---		GCCTTTTGAGTTAAGTCTTTTTGAGTGTGTCTTTTTTTTTCCCCCACTAGGTACTCTCTCGGCCCAAAT CCCCAAAAGAAGAAAATAAGCGCTTGG[A/G]GATAAACACATCTTC
I-5345	29	G	A	---		CCCTGCTATAGGTCAGTTTAAAAATCCT[G/A]CCTGCTATGTTGCTTGTTGAAGCCACATCCACT GAGGTATATTCTGTCTGCATTTCTATCACTCAGTTTCAGATCCATCCATCAACTTGCAG

Clone	No.	Allele 1	Allele 2			Sequence
WI-5370	143	T	C	AATAAGAGATGG TACCTTAACTA ATAAAAACAA	CAAAGTTGGTA CAGAGAATTC AAA	TGCATGTTACTTCTTGGAAATCATAAAGGGGATCTGAGAGCCTACAGTGATATGGCAACATTAACCAAT CTTTTTGAAAATTACCTGTATCCCATCATGGTTCATTTGCAAAAAAATAAGATGGTACCTTAACTA ATAAAACAA[T/C]T[C/T]TGAAATTCTCTGTACCAACTTGCTTTC
WI-9711b	423	T	A	---	---	GATCTCCTTCATCCCTCCAGAAGAGGAGAAGAGGAGAAACACAGAGAGAAACGCCTGGTGCAGAGCC CCAATTCCTACTTCATGGATGTGAAATGCCCAGGTGAGGAGACGGCTTGCTGTAGTGGGGAAAGCAC TGGACCTCAACAGTTGGAAAATGTTGTAGTGTCTCGTATCCTTGAAGCTGTGCAGCAGCTT CAGTTTCTTCGCCTGTGGAAAATATTTCCCTGATACTCTTAAAATTTGAATG
WI-9711a	390	C	A	---	---	GATCTCCTTCATCCCTCCAGAAGAGGAGAAGAGGAGAAACACAGAGAGAAACGCCTGGTGCAGAGCC CCAATTCCTACTTCATGGATGTGAAATGCCCAGGTGAGGAGACGGCTTGCTGTAGTGGGGAAAGCAC TGGACCTCAACAGTTGGAAAATGTTGTAGTGTCTCCTGTATCCTTGAAGCTGTGCAGCAGCTT CAGTTTCTTCGCCTGTGGAAAATATTTCCCTGATACTCTTAAAATTTGAATG
WI-9702c	345	G	A	---	---	GGAGGAATTTCAGGGTGAATGGACTGCTCCCGCTCCTGAGTTCACTGCTACTCAGCCTGAGGTTGCAG ACTGGTCTGAAGGTGTACAGGTGCCCTCTGTGCCTATTCAGCAATTCCCTACTGTATGTATCAGGAT AGAGGTGAATCAAGCTGATATTTGCAACTTCTCAGTTTATTCTAACTTTAATGATCTCTGTGACTT TTATACTAGCTTTAAGAGGTTTCATTCCAGTGTGCTACAGCATCTGATAG
WI-9702b	344	C	T	---	---	GGAGGAATTTCAGGGTGAATGGACTGCTCCCGCTCCTGAGTTCACTGCTACTCAGCCTGAGGTTGCAG ACTGGTCTGAAGGTGTACAGGTGCCCTCTGTGCCTATTCAGCAATTCCCTACTGGTATGTATCAGGAT AGAGGTGAATCAAGCTGATATTTGCAACTTCTCAGTTTATTCTAACTTTAATGATCTCTGTGACTT TTATACTAGCTTTAAGAGGTTTCATTCCAGTGTGCTACAGCATCTGATAG
WI-9702a	179	C	T	---	---	GGAGGAATTTCAGGGTGAATGGACTGCTCCCGCTCCTGAGTTCACTGCTACTCAGCCTGAGGTTGCAG ACTGGTCTGAAGGTGTACAGGTGCCCTCTGTGCCTATTCAGCAATTCCCTACTGGTATGTATCAGGAT AGAGGTGAATCAAGCTGATATTTGCAACTTCTCAGTTTTATT[C/T]TAACTTTAATGATCTCTGTGA CTTTATACTAGCTTTAAGAGGTTTCATTCCAGTGTGCTACAGCATCTG
TIGR-A003N21	49	C	A / G	---		TATAGTATTTAACGAAGCCTAGAAGCACGGCTGTGGGTGGTGATTTGGT[C/A]AGCATATCTTAGGT ATATAATAACTTTGAAGCCATAACTTTAACTGGAGTGGTTTGATTCTTTTTTTAATTTTATTTGGGA GGGTTTGGATTTTAACTTTTGTTGTTAAATATTTTGTTAAAATAATTAATTGGGAATACCTAATATCAG TGATTACCTCTCAATCTATTTGT
TIGR-A004V30	203	C	T	---		AGAATGGCTACTTCATAGGGCAGCAGCAGCCCACTTTGGCTAATTTTAACATCCAAAGCTAATAAAT AATCAAGAAGAAATAGAGAACATTAACAAAATAAATTATGTTCTATTTGGGAATAATAATCAG ATACTAACAGTCAGTGAAGAATAAAAAGATAATAATCACACATACCTTCTAGGTTAGTAGAGA AAAG[C/G,T]CTTCTAGGTTAGTAGAAAGTT

Clone	Pos					Sequence
GR-004W22	232	C	A			GGATAAATCAGTACAATAATGGGGACCTTAAAACTGCTGTGATGCAGGAGGAGTGGAGAGGCTGGGCAGTG CCCGAGGCAGGGAGGGAGGGACAGTGGGACGGGATGCTCAGTGGTGGAGCCACAGCCCTGGGCTCTGGA TGGGGCATGGGAATGACCAGGTTCCCACATCATGCAGCCCCCGCCCTA[C/A]CTGGAGAGTGTCTCTAAAA GCCTGCCCACCATTGGTGCTGCCCCCTCC
GR-005D24	138	C	T			CATAGAAAGGAGTCTTTGAGTATTGTACAGTTTTGAAAATTCTCTTTGAGATAATTGATTTCATATTC TGTGGCTTTCAACCTCCATTCCAACATCTTTATAGAGAAAT[A/G]AAAACCCAATTT CTC/T]TTTCACCATTAGTTTGATTATCATCTGGATTTTCACTCAAGATGCAGCTCCTAAGATTATT GTTATGTTAAATTCATAAACTCCTTCACCTTTAATAATTAAGGAAACAAT
GR-005D24	123	A	G			CATAGAAAGGAGTCTTTGAGTATTGTACAGTTTTGAAAATTCTCTTTGAGATAATTGATTTCATATTC TGTGGCTTTCAACCTCCATTCCAACATCTTTATAGAGAAAT[A/G]AAAACCCAA TTTCTCTTTCACCATTAGTTTGATTATCATCTGGATTTTCACTCAAGATGCAGCTCCTAAGATTATTG TTATGTTAAATTCATAAACTCCTTCACCTTTAATAATTAAGGAAACAAT
103735	74	C	G			TGAGTCTGAGCACGAGTTGCAGCCAGGGCCAGGGCCCAGTGGGAGGGGTCTGGGCCAGTGCCACCTTCCGGGGCC GCATCC[C/G]TGTTAGTTTCCCACTGCCTCCTGTGACGTGGAGCCCATTCTTCACTCTTTGAAGCGAGCAG TCAGCATTCTTAGTAGTGGGGTTTCTGCTTGTGGTGATGACTTTGAGATTATTCTTTGTTCCTGTTGGA GTTGTTCAAATGTTCCTTTAA
139840b	42	T	C			GGTTTGTCTGGCATAGCCATGCTGGTAGCAAGAGAGAAGAAAAAT[T/C]CAACAGCAAAACCACA CAAACCAACCGTCAACAGCATAATAAAATCCAACAACTATTTTATTTTCATTTTCATGCACAACC TTGCCCCCAGTGCAAAGACTGTTACTTTATTCAAAATTCATTGTGTATATTACTACAAA GACGGCCCCAAACCAATTTTTCC
139840	56	A	C			GGTTTGTCTGGCATAGCCATGCTGGTAGCAAGAGAGAAAAAATCAACAGCAAAA[A/C]ACCACA CAAACCAACCGTCAACAGCATAATAAAATCCAACAACTATTTTATTCATTTTCATGCACAACC TTGCCCCCAGTGCAAAGACTGTTATTATTCATTGTGTATATTACTACAAA GACGGCCCCAAACCAATTTTTCC
VI-8997	41	G	A	GCCCACTTGCT CCCC	TGTTTGTACGC AGTGCTCA	GTGGGCCATCGATCTGGACCGTCCCCTGCTCCCC[G/A]TGAGCACTGCGTACAAACATCCA AAAGTTCAAACAACACCAGAACTGTGTGTCTCATGGT
NI-7008	180	A	G			TATACCACTTCCATTTGATGATGGAATGCTGCTGTTCATGACCAACTTTATGGCTAGATGGGTCAGAA AGCACCCAGTCAGTTCATGATAGGCCAGTTCAGGTCATATGGTGACTTGATGACCCAGAGTCAAACATTCAG TTTCCACCAAAGCCCAGTAACAGGCCAAGAGAGCTGTCTCTCAAAAG[A/G]GAGTAGTTATCTGCAGA AGATGGCAGGGCCCTTGCTCCGAAAGCCTAGAGACCGCCACTGTGATTCACCT
WI-9005	26	C	T	CGAATTTGCTG GGGAATCT	TCCCAAAAGTC TTAAGAAGAA AAA	GGTCCCACGAATTTGCTGGGGAATCT[C/T]GTTTTCTTCTTAAGACTTTGGGACATGGTTTGACTCC CGAACATCACCGACGCGGTCTCCTGTTTTCTGGGGTGG

ID				Sequence
593	G	A	---	TTTTGTTGCTCTGGACACCCACTGCTCCCAGGATGAAAGGAGAG[G/A]AATGAGATCAGTTTGGA CACTTCCTCCTTGAAATATAAAGAATCAACAAGTTACAGTCATGTGGGGACTTCTCTCTCCAA
962	A	G	---	AGTGCATCTTGGGGGAAAGGGCTCCAGTGTTATCTGGACCAGTTCCTTCATTTTCAGGTGGGGACTCTT GATCCAGAGA[A/G]GACAAAGCTCCTCAGTGAGCTGGTGTATAATCCAGACAGAACCAAGTCTCC TGACTCCTGGCCCTTCTATGCCCCTCTATCATCATAGATAACATTCTCCACAGCCTCACTTCATTCCAC CTATTCTCTGAAAATATTCCCTGAGAGAGAAGCAGAGATTTAGATAAGA
059	C	G	AAGGCACCCA GCCATC	GCAGAGAAGAGAACCATGCCAGGGAGGAGAAGGCACCCAGCCATC[C/G]TGACCCAGGCGGAGGAGCCAA CTATCCCAAATATACCTGGGTGAAATATACCAAATTCTGCATCTCCCAGAGGAAATAAGAAATAAA
1063	A	C	CACTTCACTGA AGACACCAT TT	CTATCCCAAATATACCTGGGTGAAATATACCAAATTCTGCATCTCCCAGAGGAAATAAGAAATAAA GATGAATTGTTGCAACTCTTAAAAAAA
			TCTACTTTCTG CCCTTGGGT	AGCAGCCATCACATGATCTGTTTTCACCCACTTCACTGAAAGACACCATTTAT[A/C]TACCCAAGGG CAGAAAAGTAGAACTTACTATTCATTAAATGTTGACACAATTGGAATTGTC
079	T	G	---	AAGGGGCATTGAGACTATAAAGCAGTAGACAATCCCACATACCCATCTGTAGAGTTGGAACTGCATT CTTTAAAGTTTATATGCATATATTTAGGGCTGCTAGACTTACTTCCTATTTCCTATTTCTTTTCCATTGCT TATTCTTGAGCACAAAATGATAAATCAATTATTACAATTATACATCACCTTTTGACTTTTCCAAGCCC TTTTACAGCTCTTGGCATTTCCTCCTGCCTAGGCCTGTGAGGTAACTGGGAT
074	A	G	GGTAAAAGTT CTTTTTGCTCT AAAAG	GACAGATTTT GACCTAGTTCC TT	TGGATGCCGAGGTAAAAGTTCTTTTTGCTCTAAAAGAA[A/G]AAGGAACTAGGTCAAAAATCTGTCC GTGACCTATCAGTTATTAATTTTTAAGGATGTTGCCACTGGCAAATGTAACTGT
104b	C	T	---	GGAGTTTGCCCCTTCCTAAGGGAAGGAGATCTTTATCTTTCTGGTTGGCTTGACCAGTCACGTTGGGA GAAGAGAGAGAGTGCCAGGAGAGCCCTGAGGGCCAGCCGGTTCCTACTTTGGACTTGAGAGAAGGGAGCC CCAGGCTGGAGCAGCATGAGCCCAAGCAAGAAGAGGGCTTGGGTTCTGGAGGAAGCAGATGTTTCATGCT GTGAGGGCCTTGCACCGAGGTGGGGGCACCCAGCAGCAGCATCTTTG[C/T]TT
104	C	A	---	GGAGTTTGCCCCTTCCTAAGGGAAGGAGATCTTTATCTTTCTGGTTGGCTTGACCAGTCACGTTGGGA GAAGAGAGAGAGTGCCAGGAGACCCTGAGGGCCAGCCGGTTCCTACTTTGGACTGGAGAGAAGGGGAGCC CCAGGCTGGAGCAGCATGAGCC[C/A]CAGCAAGAAGAGGGCCACCAGCAGCAGCATCTTTGCT GCTGTGAGGGCCTTGCACCAGGTGGGGGCCAGGCCCTCCACC
974	C	T	CCTGAGCCCTC AAGAACTCA	TGTAGGGCTGA GCTGGC	CATACAATGAGAGCCCTGAGCCCTCAAGAACTCA[C/T]GCCAGCTCAGCCCTACACCAGTTTCCACC TGGAGTTCATGCAGAGGGCAAAAGGCAGTGCCATGCAAGCTGTTAA
161	C	T	CCTAAGCATTG CCTGGC	GCTTACAGGAG AGACTAGACA GGAA	CTGTGAGGGTGACGTTAGCATTACCCCCAACCTCATTTAGTTGCCTAAGCATTGCCTGGC[C/T]TTC CTGTCTAGTCTCTGTAAGCCAAGTCATCTTTCCTCCCCAGTCATCTTTCCTGTTCCCAGTACATTCCA
014c	T	C	---	CCCTGTTCCCATGCTGTCCCAGTCATCTTTATT[T/C]GTGCACTGAGCTGCAACTTCT GTCTCCATCTGTGTCCAACTTATT[T/C]GTGCACTGAGCTGCAACTTCT

Name	#					Sequence
JI-9014b	44	C	T	---		CCCTGTTCCCATGCTGACCTGTGTTCCTCCCCAGTCATCTTTC[C/T]TGTTCCAGAGAGGTGGGGCTGGATGTCTCCATCTCGTCTCAACTTTATGTGCACTGAGCTGCAACTTCT
VI-7023b	206	C	A	---		TCTGAGAGAAATGACTTGTGTGGGAGACACCCTGCCAGATCCTCATGGGTTTGTGACAGACCCTGCGTGCTCAGTGCGCCCTTAAGTGCATCCCGCGTGTGCTGACTTTGAGTGGGATCAACATCTGTCCTACGGGGTCTCTTTTTGGCCCCAGTATTCATGGCACTCTACCCAAAGCTCTGGCTGGCAGCACTAAA[C/A]ACACACATTCTTGCTCTACCCAAAGCTCTGGCTGGCAGCACTAA
NI-7023a	56	A	C	---		TCTGAGAGAAATGACTTGTGGGGAGACACCCTGCAGATCCTCATGGGTTTGTGACAG[A/C]CCCTGCGTGCTCAGTGCGCCCTTAAGTGCATCCCGCGTGTGCTGACTTTGAGTGGGATCAACATCTGTCCTACGGGGTCCCCTCTTTTTGGCCCCAGTATTCATGGCACACTCTACCCAAAGCTCTGGCTGGCAGCACTAACACACACACATTCTTGCTCTACCCAAAGCTCTGGCTGGCAGCACTAA
WI-7093	54	C	T	---		CTGAAATCCCCCTCTCTGCCCTGGCTGGATCCGGGGACCCCTTGCCCTTCCCT[C/T]GGCTCCCCAGCCCTACGACTTGCTGTGTGCCGACCTGTGCCGACCTCTCTGGGCCTCAGTTTTCCCAGCTATGAAAACAGCTATCTCACAAAGTTGTGTGAAGCAGAAGCAGAAAGCTGGAGGAAGGCCGTGGGCCAATGGGGAGAGCTCTTGTTATTATATGTTGCGGCTGTGTGTTGTTA
WI-9171	62	G	A	---		ACATATCTGAAAAATGTTGAAAGCTAAGCCAGGAATAAAAGAAAGTAGAGATAAATCA[G/A]TTCTTTACAACCGATGGTAATTAAGCTTGTATTCACAAGACTTCATGC
WI-9174	47	T	C/T	CTAGGACCCC ATTCTCCTATT	TCTAGAGGGTA TATAGGACAGG ACTG	GTGTGAGACCATCATGGTGCCAGTCTAGGACCCCCATTCTCCTATT[T/C]CAGTCCTGTCCTATATACCCTCTAGAAACAGAAAGCAATTTTAGGCAGCTATGGTCAAATTGAG
WI-7753	52	A	G	CCATGTTCCGA GAAGAACAGA A	CAGAGGTCTTG AAATACAGGG A	AAGGCCAGATGCACATCCCTGGAAGGACATCCATGTTCCGAGAAGAACAGAT[A/G]ATCCTGTATTTCAAGACCTCTGTGCACTTATTATGAACCTGCCCTGCTCCCACAGAACACAGCAATTCCTCAGGCTAAGCTGCGCGGTTCTTAAATCCATCCTGCTAAGTAATGTTGGGTAGAA
WI-9186	76	G	A	CCACTTCTCCC CGCA	AAAGGGAAAG TCTGACCTAGG T	AAAGAACTACAGAGGACGATGTCCAAAACAAAAAATGGCATCACCTGTCAAAAATGGAGTTCCACTTCTCCCCGCA[G/A]ACCTAGGTCAGACTTTCCCTTCATCTT
WI-9193	94	G	A	AGAATATTGT CTGCCCTTAAAG CGCA	GGTGTGTGTGG TAGGGGG	TTGGACAAACCTAGAATTTTCTCCCTTTATGTATCTCTATCGATTGTGTAGCAATTGACAGAGAATAACTCAGAATATTGTCTGCCCTTAAAGCA[G/A]TACCCCCTACCACACACACCCCTGTCCTC
WI-9015	48	C	T	---		TTTGGATTGATATCGTGAAATCCTCAGCCGAGAAATTGGGCTGGATTG[C/T]GCTTTGGTTAATACATCTTTCCCTAAAGAAGATAAAACACAAAATCCATTCCAGTGAGCTAGCTCGGCACCAACTAAGAA
WI-7254	37	A	G	GGTCTCTGAGAG AGGAGCCAC	GGAGTGGGTGT CATTAGGGA	GGAGCCAGGAGCAGCAGGGTCTGAGAGAGGAGCCAC[A/G]GTCCCTAAGTGGGGAGACTGGGAAGAGTCCAAGGAAGGGAGGGAGCAGCACTCCTCAGCCCTGAGGCTGCGTGCCCCTCAGACTGGGGAAGAGTCCAAGGAAGGGAGGGAGCAGCACTCCTCAATGCTCAATGGCTCCCCTGAAATCAAGACAGG

Name	Pos		Left seq		Var	Sequence
JI-9231	32	G	CAGGTCCCCCA GATTGA.		CACTTGCCCAC ACTCAGAC	GTGACCCTGTGAGGTCAGGTCCCCAGATTGA[G/C]GTCTGAGTGTGGGCAGGTGTGGGCAAGTGTGTCAAAGGGGC TGCCCCCAGGAGGATGAGGCTGAGAGCAGGAGGAGTTGAGGCCGAGAAGTCA.
VI-7836	120	T C	CAAATAAACA ATGCAACGTTC C		GCTCTCAGAAC CAAGATTAGA AATC	TTGTTTGGGAAATAGAGAGTTGAGATAAACACTCTCAGTAGTTACTGAAAGAAAACTCTGCTA GAATGATAAATGTCATGGTAGGTCTATAACTCCAAATAACAATGCAACGTTCC[T/C]GATTCTAAT CTTGGTTCTGAGAGCCATTGGTTTCAGTTGTTAGCAATCCCATACCAGCT
VI-7286	65	T C A	CAGCTTCAGCT TAACTGACAG ACCAGAAAGCT TTAA		AAACAAATCTA TAACTGACAG[T/C]GTTAAAGCTTCTGGTTAGAATTGTTTCACTTGGTGATCATGTCTTTCCATGTGTACCTGTAATATT	TCCATTCCTTTTGGCCCTGCAGCATGTCATGCTCCCAGAATTTCAGCTTAACTGACAGA[T/C] TTTCCATCATATCTCAAAGTAAAGTCA
NI-7858	91	T	CTAAGCATGT ACGTGAATTTT GTAAAT		CCCAATTTTA TTAAAGTTTA CATCTAT	CAAATTCTTGGAAATATCTCAAATGTTAATAACAATATGAATTTTCTCATGCATACTATTACTACT AAGCATGTACGTGAATTTTAAAT[T/G]TATAGATGTAAACTTTTAATAAAAATTGGGGTGTGG
NI-7860	50	C G	CGTACCTCCAA ACATAATTGA		---	GAAGATTAAGGAGGAGGTGTGCTGTGTGTCTCCTCCCGCCCTCTCCCCA[C/A,G]TGGGGGAGAGACC TGTGATTGCCAAGTCCCTGGACCCGTTGGGCCTTATGGGTGGGGTGGTAGGCAGG TGAGCGTAAGTGGGGAGGAAATGGGTAACTCTCCAAACCTAGGTCTCTATGTCAGACCAG ACCTAGGTGCTTCTCTCTAGGAGGGAAACAGGGAAACCTGGGGTCCTGTGGAT
VI-9064	29	A G	GCTTGAGTGTA AGTCTCGCAGA		CAAGGCGTACCTCCAAACATAATTAATTGATTC[A/G]TATCTGCGAGACTTACACTCAAGCAATCCTGAGG AATACTGAGGGGAGGGCCTGGCTACTGTCTCTCTGCCACTCTGCTCTTG
VI-7307	128	GT	GAAATGTGAC TTCACTTTGGT GTTC		---	CACACTTGTCTGTCTTCCAGTGCTGGAGGTCCTGCGCAGGTCAGGGTCAGCCTGGGTAAGCCGGGGTTCCACA GGGCCAGCCGGGGTCTGGCCCCCCAGGTAGGCGGAGAGCAGTCCTCCCTCAG[G/T]AACT GGAGGAGGGGACTCCAGGAATGGGAAATGTGACCACCACCATCCTGAAGCCAGCTTGCACCTCCAGT TTGCACAGGGATTTGTCCTGGGGGCTGAGGGCCTGTCCCCACCCCCGCCC
VI-9274	25	C T	CAGGTAGAATT TTCTGTCCATT G		GAGGAAATGTGACTTCACTTTGGTG[C/T]CAATGGACAGAAAATTCTACCTGTGCTACATAGGAGAA GTTTGGAATGCACTTAATAGCTGGTTTTACACCTTGATTCGGAGGTGGAAA
JI-7313e	266	T C	---		---	AATTCCTTTTCTGGTAATCAGGCACATGATGAACTTTGATTAGTAGGTCTGTGATTAAGTTCTTAAAT TGTTTTGCAGTCTTTATGTTTATTATCATAGGTATAGGTGGACCTAAATTCCTTATCATATCTTTATT AATTCAGCCAGTGTATCCACCAGTTTTTGTTGTTTTATGTTTTAAGTAACCTATTATCTCTGGATTTCATG AAGGTGTAATATCGTTTTTGTTAAACTGAATAGAATTGTATAGCGATGA
VI-7313c	256	C T	---		---	AATTCCTTTTCTGGTAATCAGGCACATGATGAACTTTGATTAGTAGGTCTGTGATTAAGTTCTTAAAT TGTTTTGCAGTCTTTATGTTTATTATCATAGGTATAGGTGGACCTAAATTCCTTATCATATCTTTATT AATTCAGCCAGTGTATCCACCAGTTTTTGTTGTTTTATGTTTTAAGTAACCTATTATCTCTGGATTTCATG AAGGTGTAATATCGTTTTTGTTAAACTGAATAGAATTGTATAGCGATGA

ID	Pos				Sequence
WI-9281	68	G	A	---	ACTGGTGGGAGACTGTGAGGATCCAGGATTCAGTATTCCTGGCCCAGAGAGGCCTTGCTGCTGGCTACTGG[G/A]TGTTAGTTTGCAGTCCTGTGTGTCTGTGTCTTCCCTCTCTTATGACTGTGTCCC
WI-7848	142	A	G	GCTAACACTTT TTAAAACCGT CTC / CATTTATTTTG AAAGCTATTCA GACA	TTCTGAAAATATAACCAGCCATTGAGCTATTAAAACTGTAATTTTTAAATTATTACAAAAAATATAA AATATGAAGACATAAACCCAGTTGCCATCTGCGTGACAATAAAACATTAATGCTAACACTTTTTAAA ACCGTCTC[A/G][T]GTCTGAATAGCTTCAAAATAATGTGAAATGGT
WI-9304	70	G	A	GTATATTACA ATGATCACCG ACTGA / CCCCACAGAAC TATTGTAAAAC AA	TCACGTTTGGTGCTTCTCAGATTTCTGAGGAAATTGCTTTGTATTGTATATTACAATGATCACCGACT GA[G/A]AATATTGTTTTACAATAGTTGTTGTGGGGCTGTTTTTGT
WI-7933b	314	C	A	---	TTACAGAAACTTGCCCTGTGCCTGTGTCCCCATGCTAGGGGCGGAGGGGTCTTTCCTTCTTCTTCTTCC TACCTACCCCTTTCTTCTTGGCCAGGGCCTGTATCCTACCTTCCTTGTCCCCTGGCTGGCTGCAC AGAGGATTGCCCCTCTCTTTCAGAGCTGGCCCTCGATGCCAAATTAGTATTTTGCACAA AGTCTAAGGGACCATGGCCTGCCTGCCTTGGGGAGGAACCATAGCTCCCT
WI-7933	96	G	C	---	TTACAGAAACTTGCCCTGTGCCTGTGTCCCCATGCTAGGGGCGGAGGGGTCTTTCCTTCTTCTTCTTCC TACCTACCCCTTTCTTCTTGGCCAGGG[G/C]CCTCGTATCCTACCTTCCTTGTCCCCTGGCTGGCTG CACAGAGGATTGCCCCTCTCTTTCAGAGCTGGCCCTCGATGCCAAATTAGTATTTTGCA CAAAGTCTAAGGGACCATGGCCTGCCTGCCTTGGGGAGGAACCATAGCT
WI-7374	182	T	A	AAATGAAACTT ACGTTTTGTTG TG	CCCAGATGTGCCCATCACGTTTTTCTGAGGCTTTTGTACTTTAGTAAATGCTTCCACTAAACTGAAA CCATGGTGAGAAAGTTGACTTTGTGTTAAATATTTGAAATGAAAATGAAGAAGTACTGTATATTA AAGTTGGTTTGAACCAACTTTCTAGCTGCTGTTGAAGAATATATTG[T/A]CAGAAACACAAGGCTT GAT
WI-9343	78	C	T	CCAACAACAT CCCTCTGCCA / CCTAGGGAACA CAATTAGAGGA	GGTCTGCTCCTACGTTGACCCTTCCCTTTCTCTCTGCTTCTCTCCTCATCATCATTCCCAACAACAT CCTCTGCCA[C/T]ACACAACAACAAAACGTAAGTTTCATTTGGGCAA
WI-7386b	104	T	A	---	CTATATGTGAGAGGCGTGATATCTGGATGGAAGTTGGGCTGGATGATCTCCAAAGTCGTTTCAACTCT TAAAGACATCTTAATCCTGAAATGTAAACAATTGTTA[T/A]GTGTTTAGAATCAGAATTTGATTTTGA ACTTGAGTAATTCATCCTT
WI-9357	75	A	G	CTTTAGAAAA TCTGCTTTAAC TTGG	AAGAAGGAGCTCAGTTACGGGGTTTTTAAACCTGAAAACCTGAAGAGTTCACTTTTTGTTATTATTAT GCTCTTA[A/G]TGATTTACAGACTGATGCCAGACAAACCTTGGGAAGA
WI-9360	79	T	C	TGCTGGGCTGT GGTCCAGAAGA GCCCG	TGCTCCCGTCCCCATCTGCAGTGACCCCAGGCCACCCCCTTGAGGAGGAGGTGGGTGAACTGCTCCTT CTTTAACTTGG[T/C]ATTCCTCTAATTGTGTTCCCTAGGAAATGACTGTCCCAAG
WI-7423	107	T	C	---	TGCTCCCGTCCCCATCTGCAGTGACCCCAGGCCACCCCCTTGAGGAGGAGGTGGGTGAACTGCTCCTT GATACCAGGCCATGTGCCCATGGTATTGGTGTTCTGGGAGGTCCTGGGACCTGCCACCGTG GATACCAGGCCATGTGCCCATGGTATTGGTGTTCTGGGAGGTCCTGGGAATAAAGGCATACTGTCT

ID	Pos	Allele	Flank 5'	Flank 3'	Sequence
NI-7424	131	T A	CAAGAGAGAG AGAGGAAAGA AAAA	TGCAAAGAAA GAATGAAAGT G	CCAGGAGCACTAGAGAGAGGAGGGGGAAGAGAAGTTAGAGAAAAAAGCCACCGGAGGAAAGG AAAAAACATCGGCCAACCTAGAAACGTTTCATTCGTCATTCCAAGAGAGAGAGAGAGAAGAAAAA [T/A]ACAACTTCATTCTTCTTCGCACGTTCATAAACATTCTACATA
X86400	118	A C	...	...	TCCTGCAAGAAGTTCTCAAGCCTTTCAAGTAAGTACAGCTTTGCATAAGAGTGAAA TTGGGCTAGCTTAAATGGATCCATAAACTTTCTTCTAATTTAAGTGAGA[A/C]TCTTTAAACACCT GTTAAATTTAATGTAGCAGTCTGAGAATCTAAAATTATGTACCACTCGTTTATTTGTTCATTCATCCA TCCCTTTCCCATGAATATTTCA
WI-8053	242	T A	...	...	GTGGCCACTACATGTTATAGAAACCATCATCTGTCACACAGCACAGTCTATGAATAAAAGGCTGAG TTATCACTAAGCAGGAGAAAAAGCATTAAAAAGTGTCCCATTAAAAGGGACTTTAATCAACCTAA TAAACTCTAATTCTGCTGACTTTTAAAGATCTAAGGTCATTTAATACATGCTGAAAAGGGTCACA ATTAATTCTTTGATCTTTTTACTCACTGTTAACTTATATATAA[T/A]TTCAGAAC
NI-6190	165	G A	...	...	TACACAATGAATTGCTTTTATTTCGGTATGCATCCACATTTCAGCATTTAGTGGTCCTGAACAGCAAG TGGAAAGACGCAGCAATTTGCCAGGAGGTCAAGCCACCAATTTCGGGGGATCTGCTGTGCACCGG GTTCCTTCTTAATCCCTGCTGAGGATCTTG[G/A]GAAGCAGCAGCACCAAAACCAAGGCATGCA CCGGATTCAAGGTCTCTTTGTTCCAGTTGTCAGATTCCAAACTAGACCCCA
NI-6275	148	G C	...	...	AACAGTCACCACCACCACCATGACAACTCGCCAGGCCAAGGCCTTGCTTCCCTCCCTCCTTTGCGTCCC ATGTGCCTAGTCAGCAAGGTCGGGGAGCACCGATGTTAGCTTCGCCCAAAGGGAGTATTACAGAGA GAGGCTTGGGAAA[G/C]GGAAGGAAAACCTGGACACAGGCTTTCAGCACTGAGAAATCACTTAAAACTG ATTTGCTTCAGTAACTGGTATGTCTGAA
NI-6421	41	G T	...	...	ACCAAGAGATCAGCTGTCTAAACAGCAGCTTTTTGATTGT[G/T]GGGCTTCCTGAAAGAAACCTTGC TGACAGCTTCTCACTGACCTGCAGGACGGAACCGTACCTGAGAGGGGATGGGGGCTCTCTCACAAAA GAATATTTGGGGCAGAACCCTGGAACTGGCCACCAGGGACATCCCAAATATCCCCTCCTCCTCCAGGG CTCACCCCGACATCCTCAGCCAAATGAAGGCTCTGAA
NI-6905	215	T A	...	...	GGGTGAGACGGGTTATTGTGCACATTACACAGCGTCACAGCGTCTGGGCTGCCAGCGGCCATGCTC CTGTGGTCGGGCGTTGCTCTCTACAAGGGGCGTTCACTTTCTTCACCACTATGTACAGTCAGTGCTCCAA GGTGATGGCTACAGTGCTCATCAGTGAGTCTGCATCAGTATTTTACATAAAATTACACGACTC ATACATGAAAAA[T/A]AGAGCCTAAGGGCCTGTATTTAATGAGAAAAAA
WI-9420	202	G A	...	...	AACTTGTTTACAAAATAGGCTTTGCAAACTTCATTACTGAATTGTAAAGTCAATGACTGTGTTGTTT TAAAATATGTACCAAGGAAAATAACAAATTGGATAATGATCATTTTCATGCTGTCAGGAGAGAACAGCAC AGAAATAAAGGATACTGCAAGGAAACCGGAAACCCATTGTGTACACTGTTCTTCACACAG [G/A]GCATTCTTTCTCACCTTAACTGCAGCTGTGCAAGATGCCTCAGTGTG

NI-9448	184	G	A	TGGGGCTGCTCTTTTAGACTTCATTCTAGAGCAGAGAGCACCTAGTGAGAGGAATACCTGGGAGAGAGAC TGCCTTGCCCATGGCTGGTTAAACCTACAGTGAGGGGACTGAAATCTCTTGGATGCCAGTCCAGATCCC TTTTTAAGAAAAATGGCCTTGTGGTTCCAAGGCTGAGAGCTGGCACCAC[G/A]CACTGGTTTCTAAA TCTCTGGCTTGGATTTATCCAAGCGCATGTTCCTAACGTGCCGGTGAGCAG
WI-9470	204	G	A	ATGTCAGAAGAGACACAGACAAGGAGTTTTCCCTTTAAATGCTAAACAAGTGCCACTAATCCACA GATCTGAAAAAGTACAGCTCTCCAGGTTGATAAATCAGATTCCAGGCTTTTCTTGTCAGTCCGCTTA TGAGATCACGAATATGATCTCCCTAAAGCCCCAGATTCCTACTAGAGCCGCTGGGGACACTGATGAC AA[G/A]GCAATCAACTCACTCATCTCCTCAAGCTCACCAGGGCTCACCTTCCCAAG
NI-1245b	201	G	T	GATGATTTCTGAAGTCCTCAGCAGCCCTGATTCTCAAGGCCTCAAGGAGAGTAGGTGTTAATGGCA TCCTAGGGCAATGGTAGGTGCCTGATGCAGATCTGCTGTGAGCCATGTGCTGGCATCACAGGGGTGGT TTATTAATTTCATTTATCATCTGGACAGCGCCCTTCTTATAAACGTACATCCTTGCCTCTTCTGAGAAA T[C]TAAGATCCCCAAGGTGGCTCCTGTATCCAGAAA
WI-1245a	85	T	C	GATGATTTCTGAAGTCCTCAGCAGCCCTGATTCTCAAGGCCTCAAGGAGAGTAGGTGTTAATGGCA TCCTAGGGCAATGGTAGG[T/C]GCCTGATGCAGATCTGCTGTGAGCCATGTGCTGGCATCACAGGGGT GGTTTATTAATTTCATTTATCATCTGGACAGCGCCCTTCTTATAAACGTACATCCTTGCCTCTTCTGAGGC GCTAAGATCCCCAAGGTGGCTCCTGTATCCAGAAA
WI-1031	149	G	A	TTCAGTGATAAGGACAGGTCTAGAACAAGCGTTCCCAACCCTGGCACCAATGACAGTTTGGACCAAA TAACTCTTTGTTTCAGGGGACTGTCCTACACATTGTGGGATGTTAGCAGCCTCCGTGGCTTCTACCCA CTAGATGCCAGCA[G/A]CACACAACCCCTCCCCAACAATCATGACAATGAAAATGTCTTTAGACATT GCCAAATATACCTTGTGGGACAAAATGGCCCCTGATTGAGAACCACTGGTT
WI-5385	110	G	A	AATGAGTCATTGTGGAGTTAGAGGAGGTTACTGAAAATGGTGACTCCAATGGTGGGATTTGAAGAGG GAAGTCTCGATAATTTTAACATATGGTTTCTTGCCAGGAATCG[G/A]CAATGCTAATCTATTGCTTAA TTCTTATCAACAGACTCTTTGAATCAATTTAGAGATACTCAGTGACCCCATGGCTCTAGAGTTCCTGAC CCCTGCTACGGGGAAACATTGAATGCA
WI-5403	199	T	G	ACCAAACCGTTGGCAAAGGCTCCCCAAGACTCACCACCCCAACTTGGTGCTTACCCTATGCCGGGTG GGATTGAAGAAATAACCATAAAATATAATTGCTACAATTTTCCAGTAGTTACCAGGCACCAGCCTAT TGGAAGAAATCATAAATGTAACCCTACAATGTATTGCTCTCTGGCTTGGTGCCAGGCATAGAGT[T/G]]GGGCCTACAACCCATTTATCATTGAACCCTACAGTTGGGGCT
WI-5801b	157	G	A	TGGTATTTTCCTTTTCCTTTTCCTAAAATGTTATGATTAATTAGTGTCTTTGTAGAATTGAAAAAATGTAAA TCAGAGAACAGAAGAAAATAAAGTATAGTTGAAACCTCTAACAATTTTGAGATTTTTAAGGCCTAG GGAAAGAAAGAGAGAGCCTGGGAA[G/A]AGGGAATGAGAAAGCACAACCAGAAAAAAAAGTGTGT GGCTTAAGGGGAAGCCAAGGAAAGTTAAGT

ID	Pos			Sequence
I-5801a	48	A	G	TGGTATTTTCCTTTCCTAAAATGTTATGATTAATTAGTGTCTTTGT[A/G]GAATTTGAAAAAATGT AAATCAGAGAACAGAAAGAAAATAAAGTATAGTTGAAACCTCAACAATTTGAATTTTAAGGCC TAGGGAAAGAAAGAGAGCCTGGGAAGAGGGAATGAGAAAGCACAACCAGAAAAAAGTGTGT GGCTTAAGGGGAGCCAAGGAAAGTTAAGT
I-5696	61	C	A	TTCTATTTAAATCCTGTGCCCCATTGCAAGACTGCATTCAGTCTGCATGAGCCTTAGTTTC[C/A]TAA AAGCCCCCTCACACCGAGGACAATGTTCAGAACTAAATGACTGCAGGTGAGCAATTCTCTGTATTA TACAAACTGGGACCAAAGATGACTTTATAATAGTGCAAGAGACAATCAGGCAGACTGGGAGGACC TTATAAATAGATTATAAGGCTGTGGTGAGTTTATTTAACTT
I-7461	153	C	T	TATTACTAGGTTCATAGAGCCCCGTTGTAATGATAAATAGCCAAATAGTTAAAGAGGCTGCAGGCCC AATTCTAAACGCTCCTCACTTCCCTTCGAACCCAGCCTCAGAGATGACACTTAGGCTGCACATTCCCTG TGGGCAGGGACTGGTCTC[C/T]GTTCCCGTTGGGTCCCGGAACCCAGTGTGGTGCCTGGCACAGAG GAGGGCCTGAGTAGCATGTGCTGCA
VI-9716	221	G	A	AGAAGACAGGAGCACTGGGATCAAGGACTGATAAACTCTGAGGCTTTAATGGTCCCTGTCTCTAAC GCTTTTGGTATACTTCTCTTTCTCTGAAGACCAACCCTTCAAACTCTCAGAACACAGGCAAGATGCAT ATTCGTAGTTTTCAGATGTGTACTTCCTACATTCTGGAAAACTAGATGAGTTAGGCTCTCTTCATCT CAATTGAAAATTCTAGAA[G/A]AAAACACCTAATTGGCTCATCTTGGATCA
I-9760	49	C	T	TTTTCGTTAAGTCTGTGAAGCCACACAGAAGTGATCTACTCTCTTTAC[C/T]AAGTGTTACTTTGCA TATATTTATGGGGATGATTCTATCCCTACTTAAGATTTCTCTTCTCTCAGGTTAAATATTCCATTTCCT TTGTTCAGGAGTTTCTTATTTGGCCTTCTTCTTCTAAACCCTTAACCATTCTGCTTATTCTCTGCTTGACA CATGCTATTTAATCAAGGTGACATT
VI-9855	31	A	C	GAAAACCTCGTTGGCTCAAAGGAAACTGTAG[A/C]AAATTCTTTTTTATTTCTTTTTTGTTTTTAACTC AAAGAGAGTGGAGTTTGCATTGACCTTGTGATGGCACGCTGCTCTTTGTTTGGTGTAAATCCTCTAGT GGGCACTTTGCAAAAGCAATTTAGAGCAAAGGTGGTGGCATGGCAAAGGTGTGTGGAGGTTGCTGAAAG TAGCAAATGGAAGAAAGGTTAATTGGA
VI-10312	41	A	G	AAGGCCCAGTGTGGGAAAAAGCAGACAAAACACTCCAAGAATAC[A/G]AGATATAAAACATCATCATCA GTAGAGATGGGATGGGACCTAGGAGGTCATGCTGATGAGGGCATGTCAGACCAAAAGACATTTGGGTCT TGAGGGTTGAATAGGAGTTTGTGTGGTGAGTTCTTGCCCAGTCCCATAGTAGGTGTTCCATAAATAAAC AGTGACTAAACTGAGGTAGAGTCACAGAAGAAAATTTCA
VI-11152	179	C	T	GATTCTTTGCGACATGCGACAGCAGATACGGCAAGGCATCTTGGGCATTGGAAGGAAAACGAGCCCTA ATTCATAGAAAACAGACTCTACAAAGGACACCAGTTAAAGGTCTCGCACCAGGGGACTGGGTGGCCAAAG TCAGTCAAGGCATAAAGGGGACAAAAGGCTTGTCA[C/T]CTGTCAGAAACATTGAA AACAGCCAGTACATGCCACTGATAGA

VI-1968	167	A	G	TGGTGAGGAGCTGTAAGGCTGAAAGAATAGTCTCTGCTCTGGTCTTCGTTGGAAATGGATGAGTCCT TTTACAAAATTTTCCTCTGCCATGGGTGTTATGTTTAGAATCATGGAGTTGGAAGACTTAGATTCA ATTTGGGGCTGTACAGTTACTGGAAGTTGT[A/G]TGAACTTGAGCAAGTGTCTTAATGTCTCTCA GCCTCAATGCCCTTCCCTGTAA
VI-4701	198	G	A	GGGTTCATTTAACAGCCTTCCCCACTGGGTCTCAGATTGCACGGAGATGTAAAAAATAGGAAGAGATAG AAAAATGGTGCCCACTATTGACTTGATAACACCTACAAAACAACATTAAACTCCTCCCCACTCTA CCCGCCAAGTCTACCTTTGGTTCTTTATTTCTGCTAATGACCATACTATTTCCCAATTAGA[G/A] CCATGTCATTTTCAGAAAAGCAGTATA
VI-4823	164	C	A	TTTATCTTTCCAAACCATGTGTGTTTCTTCACATACTTTAGTGTAATTTTAAATCATGTCATTTAATTA TGCACTTACTGTTGGCTACCAGACATTGCTTCCCAATTGTAAATTCCCTAACAACAGCAAGCATAACT GATGTGTCCATCTTTGTATTCCTAAAA[C/A]AAAAGAAAAGTGCTTTTGTGCATCTGCCCCTCTCTGT CTTCCTCTGTTTCACCTCCTGTATTCCCTATTCCCTATTCAGCATTCAATGATTA
VI-4860	72	A	G	AAAAAAACAACTTCATTTGACATTCTAAGAAGATAAAGAAAAAACAACGATCCACTGTGTGTTTGCTT GATTT[A/G]GGAGATAAAACCTGATCTCTAAGAAAAATTAAACCAAAGCAGTACACTAAAATAGCCT TTGTGTGTGGTTTTCAGGAAGAAAGCCAATCCAACTAAGTTGCTAAGAAAATAATGTTTCATATCA CTCTAACTTCCCACATAGAGCATTAATATAGCA
				TGAAAGGACCAGTTCGAATGCCTACCAAGGTAAAGTAAATCGGAGGGGCAGGAAGTAGGAGTTGCTT CCGGATAGTTGCATAAATTCAGGTTCTTAAGGAGTTCGGCTGCC[C/A]AAAATTGTTAACACTGATGATGC TGTCTACAAACGCACATAGAAAATCGGTGGTACCGGTTCCTAGTAAGTAGCTAATGTTTAGATA TGATTGTTGAATTATTGTTGCTGTGTTCTTGGTG
NI-9705	111	C	A	CAAATAATCTCTGCTTAGAAGTTGCTCTAGGGCCATGGATTCATGTAAGGGTGGGGCAGGGTGGGACTG AAGATCTGTTGGCAGGGCTCACAGAGACGGGGGTGAGGGGAGAGATCGTGGGTTCATGAGATCCCAT CTTGGGCAATACGGTTATCCCGTGGTCTTCATACGCCACAGA[A/G]TCCTCCAATTTCAGGGGCTCCC GTGGGATGGTGGAGCCAATGAAGACCAGGTAGAGTGATGCCACCTAGAGATG
NGR-A004Z48	177	A	G	GGGGATTCAATGTGTCTGTCTCATCCAATAAGCAC[T/G]CATGACCTCAGCCCCCATACTCTTTCTTCCC TATGTTCCCAGAGAGACAGAATAGACCTGGCCCCTTCCTTCTAGGGGATCACAATATTGGAAGGATGAG GACTCCAAACAGCCAGCTCCCATGCCAAATAGAACGAGTGCTGGGATCAATTCTATGGGAGCC TGGGGAGAGGGATCCTTTCTAGTTGA
J17579	34	T	G	GTGAGAGCGAGGCTGAGCCTACAGATGAACTCTTTCTTCTGGCCTGCTTTCGTTAACTGTGTATGTACATA TATATATTTTTAATTTGAT[T/G]AAAGCTGATTACTGTCAATAAACAGCTTCATGCCTTTGTAAGTT ATTTCTTGTTGTTGTTTGTTTGGGTATCCTGCCCAGTGTTGTTGTTGTAAATAAGAGATTTGGAGCACTCTGA GTTTACCCATTTGTAATAAAGTATATAATATTTTTTATGTTTTGTTTCTGA
WI-7747b	88	T	G	

Clone	Pos.	Alleles	Sequence
VI-7747a	44	T C	GTGAGAGGCGAGGCTGAGCCTACAGATGAACTCTTCTGGCCTGC[T/C]TTCGTTAACTGTGTATGTAC ATATATATATTTTAATTTGATTAAAGCTGATTACTGTCAATAAACAGCTTCATGCCTTTGTAAGTT ATTTCTTGTTTGTTTGTTTGGGTATCCTGCCCAGTGTTGTTGTAAATAAGAGATTTGGAGCACTCTGA
VI-7189	197	T C	GTTACCATTTGTAATAAAGTATATAATTTTTATGTTTTGTTTCTGA TCCAGAATTTCCTTCTTCAGCTCATTTGTCTCTCACAATTAAGGGAGTAGGTTAAGTGAAAGGT CACATACCATTATTTCCCCTTCAAACAAATAATATTTTACAGAAGCAGGAGCAAAATATGGCCTT CTTCTAAGAGATAATATTGTTCACTAAATGTGGTTATTTTATATTAAGCCTACAACATTTT[T/C]AG TTTGCAAAATAGAACTAATACTGGTGAAAATTTACCTAAAAACCTTGGTTATT
VI-7850	57	G A	AGCCCCAGCTGGACTCATGGATGTGCACCCTTTGCTCCCTGCTCTTCTGCCTCTGG[G/A]CTCATGTA TCTGCGCAGCTCTGGTACCCTCTGTGGGTGCCATCTCTGACACAGACTGCCTGCCTTGAAGCT GAGAAGGCACAGGGCAAGGAGCCAAGGACCACAGAGCCTCAGCCAGGGGGCTGTCTACTAGAGCC ATTGGTGATGAATGAAATCAGGG
VI-7907	69	G C	CTCTTCTCTTCATCCCATCACCCCCTAAATAGGTCAGGTGAGGCTGGGAAGAGGTGGGAGGAGG G[G/C]AGAAGTGAAGGAAGATAGGAAGGATATTACCTCTTCTGTTATTTTTTAAGAAACATTGTTT GGTGGCCAGCAATCTCCCTGTCCCTATCCACTGTTAGAGGCCTAATTTATATCTATAAATATTAAAA AGCAAGTCAAACTTGGATGTATCAAGGTAAAAATTATTGTCAAAGTTAAAT
VI-7919	242	T C	GAAGGCAGCTGGATCACTTCCCGCAGTCCTTGGGCCAGCGCTTGCTGTGGAACACGAGAGCTCCT CAGGGGCCTGCCACTCACCTTCTATTCTGTGTATGATGTATTGGTAAACACTGTCAAATAATAGAGAT GTGCCAGATTTAGATTTTCTTACCCTAATCTGTTTAATATTGTTAATTGTGTTAATCTTATTCCATTGAAAGTGTCA AGCCCATTCAGATAAGCTATAATCTGGTCTTTAAGGAA[T/C]AACTTT
VI-7928	101	T G	CTCCCTTCCTATGTCTCTCAGCAGCACGTTGGGGCACACTTGTCATCTTCTGACCGTTTGCTGCGGCTA TTCCCCTGCAGTGCAGATCGTCAAAATTCA[T/G]ACAAGAGGAAATTTCATGCAGAAAGCTGTA TGCAGGATGCTCACTGAGTGTTTGCACTTAAAACTGAAATTCAACTCTTTATATAGGATTTCTTTT CTATCTCCATCTCCTCATTAAAAAATACGTACATTCGAGGTAATGGTA
VI-7936	131	T A	TTTTGAGTCAAAGACTTAAAGGGCCCAATGAATTATTATATACATACTGCATCTTGGTTATTTCTGAA GGTAGCATTCTTTGGAGTTAAAAATGCACATATAGACACATACACCCAAACACTTACACCAAAC[T/A] ACTGAATGAAGAAGTATTTTGGTAACCAGGCCATTTTGGTGGGAATCCAAGATTGGTCTCCCATATG CAGAAATAGACAAAAGTATATTAAACAAAGTTTCAGATGATATTGTTGAA
VI-7944	99	T C	TACACGTTCCAGCCGGTTGCCCCACTCATCTGCGCGCTTTGCTTTGGTTGGGGGGCAGATTGGGTTGG AATGCTTTCCATCTCCAGGAGACTTTCATGT[T/C]AGCCCAAAGTACAGCCTGACCACCCTGGTGTG TGTAGCTAGTAAGATTACCCTGAGCTGCAGCTGAGCCTGAGCCAATGGGACAGTTACACTTGACAGA CAAAGATGGTGGAGATTGGCATGCCATTGAAACTAAGAGCTCTCAAGTCA

ID	Pos			Sequence
WI-7805	101	A	G	TTTCTAGGCTGTACAGTCTGTGATGCATGATTTTTTATAAATATTTCATACTCTTGTGAATTTGGATCTT TTTACTTGAGCATATATTTTAGAATATGTGT[A/G]TGTTAAAGGATCTCCACAATGTCTGCAGTGTG AAGGCAGGTTCATTGTGGAATAGTTAACAGTCAGGAAGGCTAAACTGGTCAGTATTAATGTGTAGC CCTACCAAAAATAGCCAGTAGTATCTGAAAATGAAAAATAAATGAAGTAT
WI-7416	137	G	T	GGCCAGGAGATTAGCAACAAGGATTCATTCTGTTACTTGCCCCTTTTTATCTTTCCCTCTTGCCC CAGTCCCTTCTCTCCAGCTTCATGTGAAGCTCTGCACAGACACTCAGTGTCCTTGGCAGTGCT [G/T]CTACTCCTCAGGTGCAGCATACATAACCAGTAAGAGACTAAAATCTGCAATATATAAAGAGCTC CTACAAATCAGTAACATGAAGAACACTCAAAAATTGGCAAATGTCATCAG
WI-140	252	C	T	ATTTGAAGAGATTTGGAGGGCTTTGCAGAGAGGAAAATAGATTTCAATTGGATCCCAAACTATAATGACA AGTTTTTAATTAGGTGTGATCAAGGCTTCTAAAAGTGAAATGCAAGTTGTTACCAGTAAAGTTTATA TCTTCCATTCAGCCCAGCTCATTTGCCAGAAAATTCAGGTGAGTGGATTGGCCAGACTATCTGGCAAG GATGAAAATTTAGTTTAAAAATGTGTCATTTGTCTGTATTGGCATTCCT[C/
WI-198	218	C	T	GAGGTCTTTCAGCAACATGGAGAGCCCTACTGCTTCAACCCCGAGTTCCCCGGATCAAGTGCTGGCACC CATGATGGAAACTCTTGCCATGGTTTTAGTACCCTGGACCAAGTAGTAACCACTTCCATCCTGACTTTAAAA TTCTAAACAGCCTTTGATGGGACAATCTCTGCTAAAGACTAACCACTTCCTTATCTTATCTTCAGCTA CCTGCTTCCCTTTC[C/T]GTTAACAAAGCATAGAAATATTCTGAACAACT
WI-205c	146	T	C	TTCATGTGGTCCCAAGACAGATTTAAAGAAGAAAATAAGCCTCATCTCCTAACTATGACTTGGTCGG AAGCCAAGAACCTACTTCAACATTTGACCCATAACCTTCTCTTGAGATGATGGGCTGACTTTTCAAT GCATGAGTTTGT[T/C]CCAAAGGCTTGATGGGAAATCTCAACATTTGTTACCTAAGAAAGAGGATGT ATCTTACTTTGTTAAAAAACTGCATATGCCTTTATTTTGTTTTAGTTCCC
WI-205b	146	T	C	TTCATGTGGTCCCAAGACAGATTTAAAGAAGAAAATAAGCCTCATCTCCTAACTATGACTTGGTCGG AAGCCAAGAACCTACTTCAACATTTGACCCATAACCTTCTCTTGAGATGATGGGCTGACTTTTCAAT GCATGAGTTTGT[T/C]CCAAAGGCTTGATGGGAAATCTCAACATTTGTTACCTAAGAAAGAGGATGT ATCTTACTTTGTTAAAAAACTGCATATGCCTTTATTTTGTTTTAGTTCCC
WI-234	165	G	C	GAAGACTGAGTTCCAGGAGGTTGCAGCCGTTTCTCTCGGGCCATATGGCTAATAAGGAGCTTGAGCA GGGATTCAAGCTGTTTGCAACCCAAGTNCTTCCAAGAGGTCTCAGCTACCTGCTCCATCTCCCCCT CTCCCCCACCACACACAAAATACAGAGATT[G/C]AATTGCAGGAGCCAGTTTCTAGGTGGGCTTTGAGC AATCATACACAGTAATCTCTTGGTGCTTAGTTTTCTCAAATGGGAAATGG
WI-276b	25	A	G	AGCTTTTGAAATCCAAAAACCACAT[A/G]CTTGACTCTCTTATCCTCCTTGTTGTAACATCTATCC CTGAGGCAGAAAAATACAGAACCACCCTGTGGCTGCCGAACGGAGGAAGGATGGGGGCGGGGAGACAT CGGTCAATGTATCAAGCATCTCCTGCCTGAAAGACCTCTCCTGAAAGACCTCTGAAAGCAGATGAGCTATTAGGAGC TCTGGCAAGGGCTTTGTCTTATCCTCCTTGCTCTATCCCTGATGACTGGGCAAA

Marker	Position	Allele	Sequence
WI-276	25	A G	AGCTTTTGAAATCCAAAAACCACAT[A/G]CTTGACTCTCTTATCCTCCTCTTGTTGTAAACATCTATCC CTGAGGCAGCAGAAAATACAGAACACCCTGGCTGCCTGAAACGGAGGAAGGATGGGGGCGGGGAGACAT CGGTCAATGTATCAAAGCATCTCTCTGCCTGAAAGACCTCTCCTGAAAGACATGAGCTATTAGGAGC TCTGGCAAGGGCTTTGTCTTATCCTCCTTGCTATCCTGATGACTGGGCAAA
WI-427	59	G A	TTTCCCAATCCACAGGTAAAACTAATATAAATGGATGTATAGAACTACTTCC[G/A]GTTT TTCCCTGGGGAAAATATTCACAAAACATTTGTGGTCTGCAATCAGGTTAAAGACATAGTGTGCCA TTTGTCATCAGACAGGTAGAGGCCTGACTCTGGCAGGATTAGCTACCACTAGCTGTGAGACTTTATGT ATTCATTTATTAGAGCCAGGGTCTTCTTGCTCTGTCGTCTGTCCCAGCTTCAGTGCAGT
WI-562c	106	T C	CTCTTCACTCCAACACTATATTGCTTACTTAATGGTTACAGATTAAGCCCAGAAAGGAAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATTTAA[T/C]AAATGGTCCTTTATTAAAAAAAA AAAGNTATCTAAAGAGAAAACCATAATAATCTCTCAGGTAATTATGGCCACAGCCAAAACCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-562b	106	T C	CTCTTCACTCCAACACTATATTGCTTACTTAATGGTTACAGATTAAGCCCAGAAAGGAAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATTTAA[T/C]AATAAATGGTCCTTTATTAAAAAAAA AAAGNTATCTAAAGAGAAAACCATAATAATCTCTCAGGTAATTATGGCCACAGCCAAAACCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-562	103	T C	CTCTTCACTCCAACACTATATTGCTTACTTAATGGTTACAGATTAAGCCCAGAAAGGAAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATTT[T/C]AATAAATGGTCCTTTATTAAAAAAAA AAAGNTATCTAAAGAGAAAACCATAATAATCTCTCAGGTAATTATGGCCACAGCCAAAACCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-597c	141	A G	GTGTAATTTGGTGGCTTTGCAACTTTCCCACAGTAACCTTTAGAATNTNAAAGGTGGAAGGTAAGG ATGAGGAAGAAGAGGGNGTAAGAAACAAAGATGTCTATGTTGAAGAAGTATCCTTAGGATATTCT GATACATG[A/G]TAATGACCCTCCAATTAATATACCTGGTACCTCATTACCAATGTGAGAATTATTAAC TTGATCTAATATTCTTCACAACTAATAATACCTGAGAGAAATAAGTCTATTTAAT
WI-597b	141	A G	GTGTAATTTGGTGGCTTTGCAACTTTCCCACAGTAACCTTTAGAATNTNAAAGGTGGAAGGTAAGG ATGAGGAAGAAGAGGGNGTAAGAAACAAAGATGTCTATGTTGAAGAAGTATCCTTAGGATATTCT GATACATG[A/G]TAATGACCCTCCAATTAATATACCTGGTACCTCATTACCAATGTGAGAATTATTAAC TTGATCTAATATTCTTCACAACTAATAATACCTGAGAGAAATAAGTCTATTTAAT
WI-597	136	A G	GTGTAATTTGGTGGCTTTGCAACTTTCCCACAGTAACCTTTAGAATNTNAAAGGTGGAAGGTAAGG ATGAGGAAGAAGAGGGNGTAAGAAACAAAGATGTCTATGTTGAAGAAGTATCCTTAGGATATTCT GAT[A/G]CATGATAATGACCCTCCAATTAATATACCTGGTACCTCATTACCAATGTGAGAATTATTAAC TTGATCTAATATTCTTCACAACTAATAATACCTGAGAGAAATAAGTCTATTTAAT

			Sequence
NI-611	66	G/C	TTCAAATTTAACACCATTGGGTATATTATATAATTTNGCTCTATCCATAGTTCTAACCCTCTCTCTCT[G/C]ACAGTGAGACACCTGCCTTCTATTGTCCTTGACGTATTAAGCTATTCGATCAGTCAGTACCATCTGGAGAACCTTCTCTTGTGTGGCCTTCCGCGTCCCTTCCTGCTGGGCTCCAATAC
NI-681b	156	A/G	TGAAGCCCCTCTCTCTATACCCAAGTGTCTTTATCTTAAAATGCTGTGGTGCAAGTATCTACCCCCTTAGGGATATTGTGAGAATTCAATAAGTTCATACAGGGGAAGCACTTTGTNCCTGGTATGTCATAAGCAATCCATAAATTGTTATAGCTATTA[A/G]TTATACTATGGCAACAGATTATAATGTCAGACCACCACGNATGTCCTTAAGATATGCAGCAAGCACAAATCTGTCATGGTT
NI-681	156	A/G	TGAAGCCCTCTCTATACCCAAGTGTCTTTATCTTAAAATGCTGTGGTGCAAGTATCTACCCCCTTAGGGATATTGTGAGAATTCAATAAGTTCATACAGGGGAAGCACTTTGTNCCTGGTATGTCATAAGCAATCCATAAATTGTTATAGCTATTA[A/G]TTATACTATGGCAACAGATTATAATGTCAGACCACCACGNATGTCCTTAAGATATGCAGCAAGCACAAATCTGTCATGGTT
WI-867b	119	G/A	AATCTTAACAGCCTTTAATTCTTTTGGAGCCTAAGATCAGTGCAACCCTCCAAGGCTCCCCAGTATCTGGCACATCTGGCACGTCTCTTTCCCTTTCATCTCC[G/A]TTTGTGTGTTTGGCAGTGCTATGGTTTGAATGTGTCCCCACAAAGCACACATTAGAAACTTA
WI-867	113	A/G	AATCTTAACAGCCTTTGATGCCAAAGCCACTTTCAGTCTTAATTCTTTTGGAGCCTAAGATCAGTGCAACCCTCCAAGGCTCCCCAGTATCTGGCACATCTGGCACGTCTCTTTCCCTTTCATCTCC[A/G]TTTCTCCGTTTGTGTTTGGCAGTGCTATGGTTTATCTTATGC
NI-867	119	G/A	AATCTTAACAGCCTTTGATGCCAAAGCCACTTTCAGTCTTAATTCTTTTGGAGCCTAAGATCAGTGCAACCCTCCAAGGCTCCCCAGTATCTGGCACATCTGGCACGTCTCTTTCCCTTTCATCTCC[G/A]TTTGTGTGTTTGGCAGTGCTATGGTTTATCTTATGCTCATCAGACCTGAGATTCAGCATGAAATCTACCAAAGGTACCACAAATGTAACCTTGTCCAAAACGAATCTCAGTTTCTGCATATGTAAAATGGAATGAAAGTTGTAATGACATTGTAAGTAAAGTTTGTAATGCACTGTTATGGCCTGAATGTGTACCCTAAAATTCATATGTTGAAGCCCTAACACCCAATATGNCTACATAA
VI-871b	123	C/G	TCATCAGACCTGAGATTCAGCATGAAATCTACCAAAGGTACCACAAATGTAACCTTGTCCAAAACGAATCTCAGTTTCTGCATATGTAAAATGGAATGAAAGTTGTAATGCACTGTTAATGCACTGTTATGGCCTGAATGTGTACCTG[C/G]AACTGTTTAAAATTCATATGTTGAAGCCCTAACACCCAATATGNCTACATAA
II-871	123	C/G	ATCTCAGTTTCTGCATATGTAAAATGGAATGAAAGTTGTAATGACATTGTAAGTAAAGTTTGTAATGCACTGTTATGGCCTGAATGTGTACCCTAAAATTCATATGTTGAAGCCCTAACACCCAATATGNCTACATAA

					Sequence
884	198	T	C	---	AGGTTCTGGACTTGATGCTGGGAAACAATGGGTNCTGGAGAATTCCTATTTGAGTNTTCACAGAT CAGTAGAGCCAAATGGGAAAGGTATCCTAGTCCATCCCTTTATTAGGAACTTTCCTGATCTATTGGGA ACTTCCTCCTAATAGATCAGGAAAATCCACCTCATTTAATCATGACAACNNAAAAGGAATA[T/C]G ATCCCGCATGCAACATTTATTCAGTGAAAACATGAAAATGAACATAAT
921b	205	G	A	---	CACTTCCCAAGGGCTCTGGGGGANGAGCGGTGGGGAACGGCTGCCGGGAAGCAGTCGACACTGACTGA TGCTTTGCTGCAGGGGCTCTGCTCTGAAGCCGGACACTGCCAGGTGCACACAGGACCAGTTATACTGG CAGTGATGCCTCTCACGCCTGCCCCCAAGAAAGTCTTNGCCAGGAAAAAGCACGATCCATCTAC TCT[G/A]GGGAGAGATCTGACAATTTAATCAGGAGGAAGAAATTCTTCCGAG
921	205	G	A	---	CACTTCCCAAGGGCTCTGGGGGANGAGCGGTGGGGACGGCTGCCGGGAAGCAGTTGCGACACTGACTGA TGCTTTGCTGCAGGGGCTCTGCTCTGAAGCCGGACACTGCCAGGTGCACACAGGACCAGTTATACTGG CAGTGATGCCTCTCACGCCTGCCCCCCAAGAAAGTCTTNGCCAGGAAAAAGCACGATCCATCTAC TCT[G/A]GGGAGAGATCTGACAATTTAATCAGGAGGAAGAAATTCTTCCGAG
945c	90	G	C	---	GGCTGGGATGAGAGGTCTACTTGTGGTACTGGGAGGTTTCACTGGCTTGTGCTAGAACTAGNAAAGNA GAAAGAGACAGNGATTGGCTAAC[G/C]CATGGCAGTAGTGGGCCCCAAGGCCTGAGTAATAAGAAA AAATCATTAGATAAATGTCTCATGACCAAACAAAGTTCAAACANTAGGTGCAGCACANNNGGGGTT TTCTCTGGTCATAGAATCTCTTAAAAGGGAATCATGACAGATTTCTTGGCTTTA
945b	90	G	C	---	GGCTGGGATGAGAGGTCTACTTGTGCTGGTACTGGGAGGTTTCACTGGCTTGTGCTAGAACTAGNAAAGNA GAAAGAGACAGNGATTGGCTAAC[G/C]CATGGCAGTAGTGGGCCCCAAGGCCTGAGTAATAAGAAA AAATCATTAGATAAATGTCTCATGACCAAACAAAGTTCAAACANTAGGTGCAGCACANNNGGGGTT TTCTCTGGTCATAGAATCTCTTAAAAGGGAATCATGACAGATTTCTTGGCTTTA
960b	167	C	T	---	TTGCTTCAAAGAAGTTCTTGCTCAGGAAGTTATTCATTCAGCAACCTAAAATTGTTTTGAGTACAT ATCAAGCACAGGGTTCTGAGCAATGTCTTAGGAAGAGCCATAAAGGTGAATAAAATGAGTGTTTCTACC CTGAGGAATTTATCAAAGATGTTAAGTTATCT[C/T]CTTAGAGGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
960a	155	G	A	---	TTGCTTCAAAGAAGTTCTTGCTCAGGAAGTTATTCATTCAGCAACCTAAAATTGTTTTGAGTACAT ATCAAGCACAGGGTTCTGAGCAATGTCTTAGGAAGAGCCATAAAGGTGAATAAAATGAGTGTTTCTACC CTGAGGAATTTATCAAAGAT[G/A]TTAAGTTATCTCCTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
1121	181	T	C	---	TCCCACTGAGTATGGCTTTCAGTAGTTTATTATTGATGTGCCTAGGTACATTTGTTTTATTGTTCTG CGAATTGTTGTATTACTTTGGGAGAAATGCTCAACTATAAATTGCTTCTGACCCTTTCTGTGTTC CTTCTTAAAGATACAAAATAAATGTAACATTAGACCTCTCACTA[T/C]GCTGTTTTACTCTCCCTCTG ATTTTTTTCCATTATTTTATTGCTCTGGCTTCATTTGTAAATNTG

ID	Pos			Sequence
VI-1147b	204	G	A	TTTGCCATTATTTGAAGATAAACCCACACCTTGGTGTCCAGGGTTTTCACAGGTATTAGTTGGTCAGTCACATAGGCATATAGTAGTACCTGTATGACTTCATTCCAGCCACCGCAAACTTCTCCTCTCCCTGCTGGCTCCTGAGCCAAAACAGGCATTTACCATAAATCACTTTGTTAGGATGAACTTATCTGGCCAAACTGATAC[G/A]GCATGACCCACCAGCCTCAGGTATATAAAAACACTCTCATCAGGCAGA
VI-1158b	147	C	T	GCATTCAGAGGGTTCGTTAATGACATTCACTGAGGCCCTGTCTATGTCAGGCCCTTGGTGTTGAAGACGCAATCAATCAACAAAATGAAAATACAATGTGTTCCTGAGTGTCTGATGTGTTGAAGATAAGTGCTGGGG[C/T]TCTGGGGTCAGGCTGCCTGGGTCCAAACTGCTTTGCTATGGCT
VI-1158a	124	C	G	GCATTCAGAGGGTTCGTTTAATGACATTCACTGAGGCCCTGTCTATGTCAGGCCCTTGGTGTTGAAGACGCAATCATGAACAAAATGAAAATACAATGTGGTCTCCTGAGTGTCTGAATG[C/G]GCCAGGTGGCTAAGTGCTGGGGTCTCTGGGGTCAGGCTGCCTGGGTCCAAACTGCTTTGCTATGGCT
VI-1304	124	T	C	AAGTTTACAGAAAAAAATACCAGAAAAGTGACTTCAAGANTCAGCTGAGATAGAAACATATGCCCATCATCTTCAANGTNCCCACAGACACTTATCCCCTAGACAGCCATTCTTTTTGAATGN[T/C]GNCANTAAAAATGATTTGAAATTGGGAATAAAGCCCTCCCTCCNTAATGATTTGACAGTGTTAGACCTTGCCTAG
VI-1305d	202	C	T	TTCTCAATTCCAATCTGTGTGTACTTTTATTTCTTCTTCCATTCTATGTTGGTAAATATAAAGATGATTGTGCAAAAGTATTAAATATCGTCTGATTATACCTNATGTCTNACAAAATNCACTGTTTCCTCACA/TAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
NI-1305c	46	C	T	TTCTCAATTCCAATCTGTGTGTTACTTTTATTTCTTCTTCCATT[C/T]ATGTTGGTAAATATAAAGACATCCACTGCTTTCANTAATTNACTCCACTNATGTCTNACAAAATNCACTGTTTCCTCACATGCAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
II-1305b	153	T	C	TTCTCAATTCCAATCTGTGTGTTACTTTTATTTCTTCTTCCATTCTATGTTGGTAAATATAAAGATGTCCACTGCTTTCANTAA[T/C]TNACTCCACTNATGTCTNACAAAATNACACTGTTTCCTCACATGCAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
I-1305	202	C	T	TTCTCAATTCCAATCTGTGTGTTACTTTTATTTCTTCTTCCATTCTATGTTGGTAAATATAAAGATGTCCACTGCTTTCANTAA[T/C]TNACTCCACTNATGTCTNACAAAATNACACTGTTTCCTCACA/TAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA

				Sequence
I-1306b	248	A	G	TTTCTGCATTGGAATAGTTGACTTCTATGAGNNNGCAATAATAAATGGACAATCTTGTNGNNNNTNG GGCTGGGGTGACTGTGCCTGGGTCATTTAGAAGCCATAGAAGTGAAAGTAGCCTGCAATAAAAGAGGA AAGTGAAGCTAATCTGAACCTAAGGGNGAGAAGTGGCCCCTNNTTTCTGATGGCTTTTCAGT CTGTGAGTAGTACACTCCTTGTGAAGGCCAGTTGAAATTTATCTTCCTA[A/G]GC
I-1306	240	A	G	TTTCTGCATTGGAATAGTTGACTTCTATGAGNNNGCAATAATAAATGGACAATCTTGTNGNNNNTNG GGCTGGGGTGACTGTGCCTGGGTCATTTAGAAGCCATAGAAGTGAAAGTAGCCTGCAATAAAAGAGGA AAGTGAAGCTAATCTGAACCTAAGGGNGAGAAGTGGCCCCTNNTTTCTGATGGCTTTTCAGT CTGTGAGTAGTACACTCCTTGTGAAGGCCAGTTGAAATTT[A/G][TCTTCCTAGC
I-1307b	118	T	C	GACAAGGCTGGTACTAGTTCCAAATCTATGTACACTTCCTCTCACTTCTCAAGTGGACA GATTTCTGCATTATACTGCTTGGGGGTTGGGGGAGCAGTGGTGTAGGCAA[T/C]GTGAGATTGTCTTT CCTACCCTCTTAAATGTATCTTTNCTAATTATNATGCTAAAACCGGGTACTGGTCATCACTGGTT TCTTTTTGGTGTTGTGTTGTTGCTGTGTTGTTTCTCCTGTAAAGNTGTTT
-1307	118	T	C	GACAAGGCTGGTACTAGTTCCAAATCTATGTACACTTCCTCTCACTTCTCAAGTGGACA GATTTCTGCATTATACTGCTTGGGGGTTGGGGGAGCAGTGGTGTAGGCAA[T/C]GTGAGATTGTCTTT CCTACCCTCTTAAATGTATCTTTNCTAATTATNATGCTAAAACCGGGTACTGGTCATCACTGGTT TCTTTTTGGTGTTGTGTTGTTGCTGTGTTGTTTCTCCTGTAAAGNTGTTT
-1325b	169	T	C	GAGAGATGGCCAAGAACAGAGAGGGAGAGAAGCAGAGAGAGCAACCNTCTGTGGTTTATCGCAGCAAGCN ATGTCTGTCTCCATACCCAGAAATGAGCATGTGCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCATTAGGCAACTACAACTACAATGTGCCTTGCTCC[T/C]ACCCTCAGAACTTCCTTGAGGGGCAGGC ATTATGATTCCCACTTACATCAGTGGAATTTGGACTTGGTGAAGTTAGGTT
-1325	165	C	T	GAGAGATGGCCAAGAACAAAGCAGAGAGGGAGAGAAGCAGAGAGAGCAACCNTCTGTGGTTTATCGCAGCAAGCN ATGTCTGTCTCCATACCCAGAAATGAGCATGTGCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCATTAGGCAACTACAACTACAATGTGCCTTGCTC[C/T]TCTTACCCTCAGAACTTCCTTGAGGGGCAGGC ATTATGATTCCCACTTACATCAGTGGAATTTGGACTTGGTGAAGTTAGGTT
-1327b	162	T	C	CTACGATAATTAGGTTTGGCAGTGAGGGTATTAAGCTGTGTAGTGCAAGAAGTCCTGTATTGTAAA ACACCAAGTGCGGTTAATGGAATGCGTATGTGTGAGTNCATATTCAGGACAGGCTGGGGANGACTC CAGCGACACTATGGAGCTGAGAGTCTGT[T/C]GAAGTTGGGTAGCTACCAGGCCTCCCCAAATGTAGT TCTTGNGCTGAAAGTCTCTCCTTACTGAAGAGGCAATGGTTCCATCTGAGT
1327	175	C	G	CTACGATAATTAGGTTTGGCAGTGAGGGTATTAAGCTGTGTAGTGCAAGAAGTCCTGTATTGTAAA ACACCAAGTGCGGTTAATGGAATGCGTATGTGTGAGTNCATATTCAGGACAGGCTGGGGANGACTC CAGCGACACTATGGAGCTGAGAGTCTGTGAAGTTGGGTAG[C/G]TACCAGGCCTCCCCAAATGTAGT TCTTGNGCTGAAAGTCTCTCCTTACTGAAGAGGCAATGGTTCCATCTCTAAG

WI-1341b	136	G A	---	TATCAGCATGATTGTGGCTGTTGGACACAAAGTCAATTTGTACTTTGTNTGCNNNTCCTTTCTNTTT ACCTGATCCACTATCTTCTCTCAAGATCANGTTCAAATTGGCTTNCTTTGTTNAATTATACCCAAGC [G/A]GGATTGTGATGGATCTGTTATTTCCTGTCGTGTTTCCCCAGCCCACTTGCACTTAGCAAGTGT GTTTCAGGATTGTCTCTGTTTCCCCGAGTCAACACCACTTGCACTTAGCAAGTGT
WI-1349e	192	G C	---	CTGACAAATGTCATATCTCACTCCTAAAAACCCACAGGTCATAGAATCAGTTAGCTACCCTCAATCCA GCAACCCCAGCTTGAAATGGATGCAGGGCAGGTGGTGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTGCTGAAATTCCATCTCTGA[G/C]TTCAAA ATAATTTGAGAAAATATGATAGAAATTGTGAAGTACTAGATTTCAGAAAATA
WI-1349d	264	C A	---	CTGACAAATGTCATATCTCACTCCTAAAAACCCACAGGTCATAGAATCAGTTAGCTACCCTCAATCCA GCAACCCCAGCTTGAAATGGATGCAGGGCAGGTGGTGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTGCTGAAATTCCATCTCTGAGTTCAAAATA ATTTGAGAAAATATGATAGAAATTGTGAAGTACTAGATTTCAGAAAATATGAT
WI-1349c	192	G C	---	CTGACAAATGTCATATCTCACTCCTAAAAACCCACAGGTCATAGAATCAGTTAGCTACCCTCAATCCA GCAACCCCAGCTTGAAATGGATGCAGGGCAGGTGGTGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTGCTGAAATTCCATCTCTGA[G/C]TTCAAA ATAATTTGAGAAAATATGATAGAAATTGTGAAGTACTAGATTTCAGAAAATA
WI-1349b	264	C A	---	CTGACAAATGTCATATCTCACTCCTAAAAACCCACAGGTCATAGAATCAGTTAGCTACCCTCAATCCA GCAACCCCAGCTTGAAATGGATGCAGGGCAGGTGGTGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTGCTGAAATTCCATCTCTGAGTTCAAAATA ATTTGAGAAAATATGATAGAAATTGTGAAGTACTAGATTTCAGAAAATATGAT
WI-1349	264	C A	---	CTGACAAATGTCATATCTCACTCCTAAAAACCCACAGGTCATAGAATCAGTTAGCTACCCTCAATCCA GCAACCCCAGCTTGAAATGGATGCAGGGCAGGTGGTGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTGCTGAAATTCCATCTCTGAGTTCAAAATA ATTTGAGAAAATATGATAGAAATTGTGAAGTACTAGATTTCAGAAAATATGAT
WI-1403b	57	C T	---	TGGTATTTGGAATGGGGTTCAGACTCCGGGTTCTGGCCTTTGGTAAGTTG[C/T]TTCCGAAT GCCACTTTATAAAGTTAGAGGTATTACCTTGGAGGGGGACGTAGAGTAAGCCATAAAATACGT AAAGTTTACATCAACATAATTCTTGCCCTGACATCATGCAATATGTCACATAGCTGTCCTCA TAATCCCCAAAGTGCCAAAAGGGTTGTATCTGATTTGT
WI-1403	58	T C	---	TGGTATTTGGAATGGGGTTCAGACTCCGGGTTCTGGCCTTTGACCTTTGGTAAGTTGC[T/C]TCCGAA TGCCACTTTATAAAGTTAGAGGTATTACCTTGGAGGGGGACGTAGAGTAAGCCATAAAATACG AAAGTTTACATCAACATAATTCTTGCCCTGACATCATGTCAATATGTCACATAGCTGTCCTC ATAATCCCCAAAGTGCCAAAAGGGTTGTATCTGATTTGT

ID	Pos	Allele	Sequence
II-1417c	31	C/T	CAGGCCGGAAGAGAGATTCACGTGGAGAGATGT[C/T]TTGGCCAGGGCGGGCAGAGATGTGAGCCCACGGG GGTGACAGCAGCATGCCTGCTGGCATTTGGAGGGCCCAGAAGGAATCCCAGTGGCCCTCTCAATGACTTG GGGTCCTCGACTTCGGAAGTTAAGGGGCTCGGCTTCAAAAGCTGGGTCCGGTTTGCTTTGTAGAAAAGTCGC AGGCGAGGCCCTTAGGTCCGTATTTAATGTTTGCTTTGTAGAAAAGTCGC
II-1417b	31	C/T	CAGGCCGGAAGAGAGATTCACGTGGAGAGATGT[C/T]TTGGCCAGGGCGGGCAGAGATGTGAGCCCACGGG GGTGACAGCAGCATGCCTGCTGGCATTTGGAGGGCCCAGAAGGAATCCCAGTGGCCCTCTCAATGACTTG GGGTCCTCGACTTCGGAAGTTAAGGGGCTCGGCTTCAAAAGCTGGGTCCGGTTTGCTTTGTAGAAAAGTCGC AGGCGAGGCCCTTAGGTCCGTATTTAATGTTTGCTTTGTAGAAAAGTCGC
II-1729	172	A	CCATGAGCAAACAGCATGTTTCTACTCTGTGATGTGTATGTTAGGGGGCATGTATATCTGTATTTCTT TTTTATTTCTCCAAAGAAATTTCATTATGCAAAACATTATCAGGCAATGCAATGTATATCTGTAATAAAGA TGTTGGGAGAACTGAAAAGAGAGCTTACATGCAAACCCAATAGCAAAACTCTCCACACATTTCCAGCA GATGTATGTGTCCTTCCGTGGTNACCTTCTCTCCCACCATCACCTGTTTTT
II-1732b	122	T/C	TGCCTTACTTCTTTGTTCATTCCCACCATTACCATTTTGTAAATTGGAACTTCTAGGAGGTTAGAAGGA TATGCTGATCAAAAAAGGGGACATATTCAAGGAGTNTCCCTGGGTCAACCCTT[T/C]ATTCAGTCT CTGCCACATGTCTAGTAACTGTGAGTGGTGCATCAGTCAGTATAATCCTGAGCCTCCCAAGGTACAGC CTTTCACTACTATTCATCATCATATTGGCTAAG
II-1732	114	C/T	TGCCTTACTTCTTTGTTCATTCCCACCATTACATTTTGTAAATTGGAACTTCTAGGAGGTTAGAAGGA TATGCTGATCAAAAAAGGGGACATATTCAAGGAGTNTCCCTGGGT[C/T]AACCCTTATTCAGTCT CTGCCACATGTCTAGTAACTGTGAGTGGTGCATCAGTCAGTATAATCCTGAGCCTCCCAAGGTACAGC CTTTCACTACTATTCATCATCATATTGGCTAAG
I-1750	97	A/G	GCGAATTTAATGACTCCAAAGGTAGTAATTCCTTTCCCCCAAAAAGGTTTAAAATCTGTGTTGGA CATAATGTTTGAATTTGCAGTTCACCTTGG[A/G]TTAAGGTGTGCTGTTTTTCTGGCAAAGAGTCAG CTACATTCACTTTATGATCCTGCCAGGGTTCTTCCA
-1780	31	A/G	GGTACACAAGAAATGCTTCTGGAAATCTAC[A/G]TAGCCGCCTTAACATTTTGGCTGAGTATTAATC TGTACATGTGTAATGTGAACCACCATGAAAGACAATTCCTAGGAAAAGTACAATTAC TGGGAAACTGTAGAACAACAATAATTCTCATAGTTACACATAGCTGGGAATCACTCATGTTCCCATCA ACTGAGAGACCTTGTTGAGTACAGAGGACATTCAAGAATAATCATAAAAAT
-1803c	77	A/G	CCACTCAGTAATAATAGTGTTGGGAGATAAGTAGTATATGGTAGGCACATAATAATATTTTCAGGCAGAA CCATTATGAT[A/G]AGT(A/G)TAGGGTAGAGCATCACACTTGGGAGGACGATATTCTGGAGTNAGATATCCTG GGTGCTAATTTCAAATATCTTCTACTAAAGCACATGACTTCTAGAAAATTACTTATTACTCTTGTCTCCTCAA GGAAATGGGAATACCTATAATACACAGTCTTATTGAGGAAATAACTGGAATCA

ID	Pos	Var	Sequence
VI-1803b	77	A G	CCACTCAGTAATAATAGTGTTGGGAGATAAGTATATGGTAGGCACATAATAATTATTTCAGGCAGAA CCATTATGAT[A/V/G]AGTAGGTAGAGCATCACACTGGGAGGACATATTCTGGAGTNAGATATCCTG GGTGCTAATTTCAAATATATCTACTACAGCATGAATCTCTATTACTAGCTATACTCTGTCCTCAA GGAAATGGGAATACCTATAATACAGTCTTATTGAGGAAATAACTGGAATCA
VI-1837b	112	C T	TTTACTTGGGATTTTTCATAGCTGATCATAATTTACCATTGATAATTCACTCTCTTTTCCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGAATAGACCCGTTTATAC[C/T]TCTGTCCCCAGTTTATTTTT AAGGTTTTTTCATTGCACCTGATGCCAAAACAAAACCTCAAAGACCTTGAGTGAATTTTGAGCT CGTGTAACAACTGGGAAGTCTGGGGAACGTTTAGCTTCTGCTGTGGCT
VI-1837	112	C T	TTTACTTGGGATTTTTCATAGCTGATCATAATTTACCATTGATAATTCACTCTCTTTTCCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGAATAGACCCGTTTATAC[C/T]TCTGTCCCCAGTTTATTTTT AAGGTTTTTTCATTGCACCTGATGCCAAAACAAAACCTCAAAGACCTTGAGTGAATTTTGAGCT CGTGTAACAACTGGGAAGTCTGGGGAACGTTTAGCTTCTGCTGTGGCT
VI-1840b	79	G T	TCACCTAGGGAGGTCGCTAAAAATGTAGCTTCATTAAGACACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCACT[G/T]GAGAATCTGAATATTCAGCACATACAAGTGTGACAACCACTGTTTAGTAT ATTTTATCTCCAGAGTGTTTGAATTTACTAAAAAGTTCCTAAAGAGCCATGAAGAATTATAAGACT ATCGCA
VI-1840	79	G T	TCACCTAGGGAGGTCGCTAAAAATGTAGCTTCATTAAGACACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCACT[G/T]GAGAATCTGAATATTCAGCACATACAAGTGTGACAACCACTGTTTAGTAT ATTTTATCTCCAGAGTGTTTGAATTTACTAAAAAGTTCCTAAAGAGCCATGAAGAATTATAAGACT ATCGCA
VI-1879b	110	C T	GGGCTCACTTCATCAGAGCACATATCACGTGATAGTCTGTTCCTTCTTTCATAACTTACTCCCCCG CACTGTAGGNTTCTTTGAGGTNAAGGACCTGCCNTTTTA[C/T]GTCTGCNAAATAAACTCCCAAAA AAGTGGTTAGTCCACAGGGTTTTAATAGTTCTTGTTGAATGAATTTCTGTGTGCGACCCGTGCCTTCT CAAGAAAAAAACATTGAAAAATCTCCACAGAGCCCTTACCCACT
VI-1879	110	C T	GGGCTCACTTCATCAGAGCACATATCACGTGATAGTCTGTTCCTTCTTTCATAACTTACTCCCCCG CACTGTAGGNTTCTTTGAGGTNAAGGACCTGCCNTTTTA[C/T]GTCTGCNAAATAAACTCCCAAAA AAGTGGTTAGTCCACAGGGTTTTAATAGTTCTTGTTGAATGAATTTCTGTGTGCGACCCGTGCCTTCT CAAGAAAAAAACATTGAAAAATCTCCACAGAGCCCTTACCCACT
VI-1900b	119	C T	TGTTCTCTGGTCCAGGCACCGGGCTAAGTCTTGTCTGCATAATGAATAATCAACTGGACAACCCNG CTNAGGTAGGNTACCTNGGCAATTAGCCCCATCTTACAGCTGCAAAAGAGG[C/T]GCTCTGAGAGGT AAAGTGCCCTGCCCCAACGCGCACAACTAGAGAGCAGCCAAACAGGTGTTGAACCCAGCTCTGCCT GACTTCAGATCTGTGTGCTTAACTGCCATGAGACAAACCACTTTTCTTTGCTCC

Il-1900	119	C	T	...	TGTTCTCTGGTCCAGGCACCGGCTAAGTCTTGTCTGCATAATGGAATAATCAACTGGACAACCCNG CTNAGGTAGGNTACCTNGGCAATTAGCCCCATCTTACAGCTGCAAAAGAGG[C/T]GCTTCTGAGAGGT AAAGTGCCCTGCCCCAAGCGCACAACTGCCATGCAAACAGGTGTTTGAACCCAGCTCTGCCT
Il-1943c	165	C	T	...	GACTTCAGATCTGTGTGCTTAACTGCCATGCCATGAGAACACCACTTTTCTTTTGCTCC ATTCCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGGACAGGATGCACAGCGT GTTGGGCTCAGGATCTCTGGGAGGTGGCACCTGTGACCTGGGCTAANCATGCTACTTTCAGAGTCAAGC AGCAAGCCAATGGGAAAGACCAGGC[C/T]CTCTGAANCTGGGTCCCACGTGGAGATAGTGAA TACAGGGCACCGNTGAGCATTCCAGATGACTCCAAAGCCCGGCTGGAGTAT
VI-1943b	165	C	T	...	ATTCCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGGACAGGATGCACAGCGT GTTGGGCTCAGGATCTCTGGGAGGTGGCACCTGTGACCTGGGCTAANCATGCTACTTTCAGAGTCAAGC AGCAAGCCAATGGGAAAGACCAGGC[C/T]CTCTGAANCTGGGTCCCACGTGGAGATAGTGAA TACAGGGCACCGNTGAGCATTCCAGATGACTCCAAAGCCCGGCTGGAGTAT
VI-1943	164	C	T	...	ATTCCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGGACAGGATGCACAGCGT GTTGGGCTCAGGATCTCTGGGAGGTGGCACCTGTGACCTGGGCTAANCATGCTACTTTCAGAGTCAAGC AGCAAGCCAATGGGAAAGACCAGC[C/T]CCTCTGAANCTGGGTCCCACGTGGAGATAGTGAA
NI-1960c	270	A	T	...	CCAGGTGAGGCTGAAAGAGGCAATTGCTGTTGGAGTGAGGGATTCTGGAGAAGCACCCT GCAGAGCTTCATTCTGTTTCAAAAGTGTGCCATGCANGGTCNTCTGGGTTGTGAGCTCATNGCTGAG GTTGCAATTAAATCCGTGGTGTCTGAAAACTTAAAAATGCACCTCCCAACTTT
NI-1960b	270	A	T	...	CCAGGTGAGGCTGAAAGAGGGAAGGAGGCAATTGCTGTTGGAGTGAGGGATTCTGGAGAAGCACCCT GCAGAGCTTCATTCTGTTTCAAAAGTGTGCCATGCANGGTCNTCTGGGTTGTGAGCTCATNGCTGAG GTTGCAATTAAATCATGAAAAATAGGTACTTCCCAAGCTCTGACTAGACCTTGGCA
VI-1977	203	T	C	...	CTGATGCCAAGTGCAGCTTAGAGTNAGGAATCCAGAGAAAGTNTTTGGATCTGGTAAGTAGGAGTCA TTCTGGGCATTTCTTCATAGAGTNTTGTTTTAGTCTCGTAATATACTGTTGCCCTAGGAAGGTTGTT /CTAACAATCAAACACTGGCTGAGGCTGTTGG
I-2012	102	T	C	...	AAATTCTAGAAGCCAGAAGTGCAGCTCAGTTTATAAAGTTGAAGTAAATGCATTGTAGTTTCATGT TTTCTCTTAATTCTGCACAAAACTAGCTAAAAATC[T/C]TTAAATC[T/C]TTAAATCAGTTACCAGAGGCAATACCT GGGTTAATGTAAGCACTCAAAAGTTATGTAGAGTAGCTGTCTGTCGAGTCACTTTTTCTACTCTCATT

				Sequence
I-2013	127	C	T	CTTTAGAGGTGGTCATTCGGTTCCCTTCTGGAAAGTGTTGTGTTTAAGAAAAATAGATGCAACG TTGCTAAGTACACCTAACCTAAACATTTAAACAGTTCCAGCAGATAAATGCTGATACTGACACT[C/T]CTCA CCAGAAAAAGAGAAATACCCATCATGAGGAAGAGAAATGACTTTTGTTCAGTTATGCTCCCGGGTCC CCTTTCACTGGAGGGGATATCTCAGCTTTCTGAGCCCTGGTTACTGCAATCC
II-2032c	166	G	A	ACCAGACATCCCATCAGGAGGTAGTCCTTGGCAAGCCAGCCCTGCCCTTCTGATTTCCCAAAAACC TCAATTTTTTCTTNACTTACTCATAATATTGCTAGAGTACAC[G/A]TGTGGGACCTCGTGTCTCAACCTAACC ACATCACCCAACTGGTTTCTAGATGTACAGTTAGGCTCACCTTCTGTAATTGCTTCTGTTTTCAAAGGG AGATCATTGGTTAGGCTCACCTTCTGTAATTGCTTCTGTTTTCAC
II-2032b	219	C	G	ACCAGACATCCCATCAGGAGGTAGTCCTTGGCAAGCCAGCCCTGCCCTTCTGATTTCCCAAAAACC TCAATTTTTTCTTNACTTACTCATAATATTGCTAGAGTACAC[C/G]TGTGGGACCTCGTGTCTCAACCTAACC ACATCACCCAACTGGTTTCTAGATGTACAGTTAGGCTCACCTTCTGTAATTGCTTCTGTTTTCACAGA
II-2032	219	C	G	ACCAGACATCCCATCAGGAGGTAGTCCTTGGCAAGCCAGCCCTGCCCTTCTGATTTCCCAAAAACC TCAATTTTTTCTTNACTTACTCATAATATTGCTAGAGTACAC[C/G]TGTGGGACCTCGTGTCTCAACCTAACC ACATCACCCAACTGGTTTCTAGATGTACAGTTAGGCTCACCTTCTGTAATTGCTTCTGTTTTCACAGA
I-2054b	188	C	T	CGTTTCTTCTACATCTTGGGGNACATAAAGANGAAGAAAGAGNAGCTGTCTTTTTGTGGTAGTTTGCT CAGAGCTGCCTAGAGCNAGGACNAGGACAGGTGACCTTTCAAAATACCTTACAGACTTAGGATTGGA TTTTCATGGTGGTTGGCACAGCCCAGGCTCAACAGAACTAATACCTGTGTTC[C/T]TTCTGCCTCCAC
I-2054	183	T	C	CGTTTCTTCTACATCTTGGGGNACATAAAGANGAAGAAAGAGNAGCTGTCTTTTTGTGGTAGTTTGCT CAGAGCTGCCTAGAGCNAGGACNAGGACAGGTGACCTTTCAAAATACCTTACAGACTTAGGATTGGA CAGCCCTATCTCTTAGGCTCAAGGAGAAATTTTACTGGATGGGCTGTCTT
2573d	129	T	C	TGGGATTAAAACCCTGTTTCTTCCTTCCCAGTTCAGTTGTGCCTTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAAAATAGCTCTTAAAAATGCACTTGCCGTTCACAAGGTGTTTCCGTGCTTT/C]TGA TATCATCTGATCTTCCCAACCAGGCTTATTTA[A/C]TGCCTAGGTAAGGGGTAAGCAAACAGAGGCTGTGT GAAGTGAAATGATGATTTGCTTGCACAAGGTCATATGGGCTTGGCGTTGGACGAG
2573c	165	A	C	TGGGATTAAAACCCTGTTTCTTCCTTCCCAGTTCAGTTGTGCCTTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAAAATAGCTCTTAAAAATGCACTTGCCGTTCACAAGGTGTTTCCGTGCTTT[A/C]TGA CATCTGATCTTCCCAACCAGGCTTATTTA[A/C]TGCCTAGGTAAGGGGTAAGCAAACAGAGGCTGTGT GAAGTGAAATGATGATTTGCTTGCACAAGGTCATATGGGCTTGGCGTTGGACGAG

				Sequence
VI-2573d	129	T	C	TGGGATTAAAACCCTGTTTCTTCCTCCCAGTCAGTGTGCCTTAATGTTTGTGTGCTAGAAATTAACA TTAACAGCAGTAAAAATAGCTCTTAAAATGCACTTGCCGTTCACAAGGTGTTTCCGTGCTT[T/C]TGA TATCATCTGATCTTCCCAACCAGGGCTTATTTATGCTAGGTAAGGGGTAAGCAAACAGAGGCTGTGT GAAGTGAAATGATTTGCTTGCACAAGGTCATATGGCTGGGCTTGGACGAG
VI-2573c	165	A	C	TGGGATTAAAACCCTGTTTCTTCCTCCCAGTTCAGTGTGCCTTAATGTTTGTGTGCTAGAAATTAACA TTAACAGCAGTAAAAATAGCTCTTAAAATGCACTTGCCGTTCCGTGCTTT/CGATAT CATCTGATCTTCCCAACCAGGGCTTATTT[A/C]TGCCTAGGTAAGGGGTAAGCAAACAGAGGCTGTG TGAAGTGAAATGATTTGCTTGCACAAGGTCATATGGCTGGGCTTGGACGAG
I-2573b	165	A	C	TGGGATTAAAACCCTGTTTCTTCCTCCCAGTTCAGTGTGCCTTAATGTTTGTGTGCTAGAAATTAACA TTAACAGCAGTAAAAATAGCTCTTAAAATGCACTTGCCGTTCACAAGGTGTTTCCGTGCTTT/CGATAT TATCATCTGATCTTCCCAACCAGGGCTTATTT[A/C]TGCCTAGGTAAGGGGTAAGCAAACAGAGGCTGTGT GAAGTGAAATGATTTGCTTGCACAAGGTCATATGGCTGGGCTTGGACGAG
I-2573a	129	T	C	GACTTCATGCTCATGAACAAGCATTGTCTTAATTACAGACATTAAGAACAAGCTTCC[A/G]CTC CCACTTCCCTCCCACTATCACCTCAACCTCTCATCCACTTTAAAGAGGTTCTTAGGTCCTCTGCAT ATCATGGAAGCCAACTACTCTATTAACGCTTTCCCAATGATGCAGCCCAGTTCTGCATACAGTTTGTA CAGAAATGCTATATTTATGGAAACAGCTGAAAAATGAAAATATCGATATAC
I-2868b	60	A	G	GACTTCATGCTCATGAACAAGCATTGTCTTAATTACAGACATTAAGAACAAGCTTCC[A/G]CTC CCACTTCCCTCCCACTATCACCTCAACCTCTCATCCACTTTAAAGAGGTTCTTAGGTCCTCTGCAT ATCATGGAAGCCAACTACTCTATTAACGCTTTCCCAATGATGAAACAGCTGAAAATGAAAATATCGATATAC
-2868	60	A	G	CATGCTGTAACCTCTGTGCTGCTGCTGTCTCATTGAGGAGACAAGATGAACATCAGGAAATTGTATAATCCTAGGC TTCAAGGAGCTTCTCATCTCATTGAGGAGACAAGATGAACATCAGGAAATGACTGGATAATGA[T/C] AGAAATGAATAGAGCCCCATTTAAATTATATCACAGCTTTATGTCCACTTCCTGTTCCTGCCATCAC TGGGCTTTTTACAAAGGAGGGCTT
2870b	131	T	C	CATGCTGTAACCTCTGTGCTGCTGTCTCATTGAGGAGACAAGATGAACATCAGGAAATTGTATAATCCTAGGC TTCAAGGAGCTTCTCATCTCATTGAGGAGACAAGATGAACATCAGGAAATGACTGGATAATGA[T/C] AGAAATGAATAGAGCCCCATTTAAATTATATCACAGCTTTATGTCCACTTCCTGTTCCTGCCATCAC TGGGCTTTTTACAAAGGAGGGCTT
2870	131	T	C	

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VI-2954c	49	T	A	TTAGCACACATATCTGTTGTGGGACTTAACTGAGACAAGGCATAAAAA[T/A]CAGCACCTGGGGCACAGAGGGGAGCTCTATGCATTNAATTCCTACCCCCTCTCATTCAATGAGTCCTTTGAGTCCTTGGAAAGACTCTATTCCCTGGCCATCCATTGCGACAAATAAGTCCAGAG
VI-2954b	41	A	G	TTAGCACACATATCTGTTGTGGGACTTAACTGAGACAAGGC[A/G]TAAAAAATCAGCACCTGGGGCACAGAGGGGAGCTCTATGCATTNAATTCCTACCCCCTCTCATTCAATGAGTCCTTTGAGTCCTTGGAAAGACTCTATTCCCTGGCCATCCATTGCGACAAATAAGTCCAGAG
VI-2954a	38	G	T	TTAGCACACATATCTGTTGTGGGACTTAACTGAGACAA[G/T]GCATAAAAAATCAGCACCTGGGGCACAGAGGGGAGCTCTATGCATTNAATTCCTACCCCCTCTCATTCAATGAGTCCTTTGAGTCCTTGGAAAGACTCTATTCCCTGGCCATCCATTGCGACAAATAAGTCCAGAG
VI-2971b	62	T	C	ATTACAAATCCTACCTAGCAACTGCTGACACTTCCCAGTTAGACTCACCAGCATTCTAAGA[T/C]GCTGCCAGCACCAATAAGCTTTCTTTCAAAACAATTTGTAACCTCCTCCTCCTTAATAAACCTAACAGTTCTTTAATGTTATTCTGAAAGAAAACCTTTTACTTAGGGATTTGTCT
I-2971	62	T	C	ATTACAAATCCTACCTAGCAACTGCTGACACTTCCCAGTTAGACTCACCAGCATTCTAAGA[T/C]GCTGCCAGCACCAATAAGCTTTCTTTCAAAACAATTTGTAACCTCCTCCTCCTTAATAAACCTAACAGTTCTTTAATGTTATTCTGAAAGAAAACCTTTTACTTAGGGATTTGTCT
2995d	133	A	T	TTCCTGGGAAAGAAAAGATGGGGGTTTTTNTTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC/TJAAATCTTTCTTTCTTGGTGTTTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAGAATGAGACAGAACTAGCAGAAAGTGTT
2995c	151	G	C	TTCCTGGGAAAGAAAAGATGGGGGTTTTTNTTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC/TJAAATCTTTCTTTCTTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAGAATGAGACAGAACTAGCAGAAAGTGTT
995d	133	A	T	TTCCTGGGAAAGAAAAGATGGGGGTTTTTNTTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC/TJAAATCTTTCTTTCTTGGTGTTTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAGAATGAGACAGAACTAGCAGAAAGTGTT

Label	Pos	Var	Sequence
VI-2995c	151	G/C	TTCCTGGGAAAGAAAGAGATGGGGGTTTTTNTTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGTT
VI-2995d	133	A/T	TTCCTGGGAAAGAAAGAGATGGGGGTTTTTNTTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTT[A /T]AAATCTTTCTTTCTGGTGTTTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAG GAATGAGACAGAACTAGCAGAAAGTGTT
VI-2995c	151	G/C	TTCCTGGGAAAGAAAGAGATGGGGGTTTTTNTTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGTT
I-2995b	151	G/C	TTCCTGGGAAAGAAAGAGATGGGGGTTTTTNTTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTT[A /T]AAATCTTTCTTTCTGGTGTTTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGTT
I-2995a	133	A/T	TTCCTGGGAAAGAAAGAGATGGGGGTTTTTNTTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTT[A /T]AAATCTTTCTTTCTGGTGTTTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGTT
I-3147	85	C/T	GTGGTGCAGTTCATCCTCTGGAGCTCCCTGTGAGATCAGAGCTGGAGCCAGTCTCCAGCTTGAGACCAC ATCTCACTTAGCTCCTT[C/T]CTGCCCATATCCTGTTTTCCTTACTCCTATCCTCCTGAGACTTCTTCCT GAATGAATTACATGCACTCAATCCCTGCCCTGCTCTCCAGTCTGCTTTNAGGGAACTTGACCTAAGACAGAA ATCTTAGTACCAAATACTTTGCAAGG
I-3234b	68	T/C	ATTCTGTAATGTTTTCACTGCTTCCAGTAAAATTCTTTATTGAGGTCCATGTCCATTACCTCTACTTA[T/C]GACAAGCAGAACAACAGAAAAGCCTCTGTTTGCAATCTGGCCTCTTATAAATACTTTCTG TATATTTTAAACAAGTACTGTAGAGTNATGAATCATTACATCCTTAATAAGCATATCAAAATTTTAC TCAGTAATTCAGAGAAAGGACAATGGAATGTACTTATTTNATATCTTAT
I-3234	68	T/C	ATTCTGTAATGTTTTCACTGCTTCCAGTAAAATTCTTTATTGAGGTCCATGTCCATTACCTCTACTTA[T/C]GACAAGCAGAACAACAGAAAAGCCTCTGTTTGCAATCTGGCCTCTTATAAATACTTTCTG TATATTTAAACAAGTACTGTAGAGTNATGAATCATTACATCCTTAATAAGCATATCAAAATTTTAC TCAGTAATTCAGAGAAAGGACAATGGAATGTACTTATTTNATATCTTAT

ID	Pos.	Alleles	Sequence
WI-3292b	106	G/A —	GTTTTGCTAGACTAGGAGTTTCAGCTTCATCCAAATCCCTTAAGGATANTTAGCTCTGCACTCATCCTCCCTGTCCCCGTCCCAAGCCTATGTTTCTCATTACTGGTATGCT[G/A]TGGTATTGGGATTGGGATTACTTGCCATGAATATTTCCATTGTTTCTCATTAATGTATTAATTAAGTAAAATATTATTNCCATGAGACACAATGGAAAAATGGAAAAACATTCATGGAAAAAAACCCATTTCAATC
WI-3292	106	G/A —	GTTTTGCTAGACTAGGAGTTTCAGCTTCATCCAAATCCCTTAAGGATANTTAGCTCTGCACTCATCCTCCCTGTCCCCGTCCCAAGCCTATGTTTCTCATTACTGGTATGCT[G/A]TGGTATTGGGATTGGGATTACTTGCCATGAATATTTCCATTGTTTCTCATTAATGTATTAATTAAGTAAAATATTATTNCCATGAGACACAATGGAAAAATGGAAAAACATTCATGGAAAAAAACCCATTTCAATC
WI-3355	19	G/C —	CCATGAACCATGGGCTACA[G/C]ATATTCCTAAACTTCAGAGTCCCTCCTTACTGGAGAGGGATCCACTTTTTAAATATGATTTCTTGAAGTGGCTGCATACTATTCCTTCCAAGCACTTAAAACTCATCAGAAAAAAAAATCATCAAAAAGTCGAAGTTAGTTTTTNATTACCTTCACCTTTTCAATGGAAAAACTTTATAAACTGTGGATCAATTTATTACTTTGGATCAGTTTAGATGACTTTNAGTTG
NI-3408	194	G/A —	CCATGAAGAATGAGTTCCTCCCCCCTCCCCCGGGTCACGTGTAATGGCATTGTAATGGCTGATGAATTCCTCCGCTCTAAGACACCCTTGAGAATTNACTCTGGNAGAAGCCACTGGGAAGTCGAAGGAGTGACTTCAAATCAGGATCTCTGGNAGAAGCCACTCNTACATTCAATGTGCCACCCTCGTGTGGGATCACTTCTCC[G/A]TGCCCC
I-3505b	131	G/A —	TAACTTATGCCTCATCTGGCTTACTGCTTAGTTCCATTGTCATCAGTGCACTTAAAAATTATTTTGAAAAATTGCCATTTTAATATCTTTGGAACTTCCTAACACATTACCTATTTTTNAACCAAAC[G/A]AGGTGATTCCTTATGGGAAAATATCTTTAATATATTTGGGAAAATATACAGCAAGAAAAANANANGGAAAAAATGTTGATGATACCTGTTTAATTGGGAAATATGTTTGCATAT
-3505	131	G/A —	TAACTTATGCCTCATCTGGCTTACTGCTTAGTTCCATTGTCCATTGTCATCAGTGCACTTAAAAATTATTTTGAAAAATTGCCATTTTAATATCTTTGGAACTTCCTAACACATTACCTATTTTTNAACCAAAC[G/A]AGGTGATTCCTTATGGGAAAATATCTTTAATATATTTGGGAAAATATACAGCAAGAAAAANANANGGAAAAAATGTTGATGATACCTGTTTAATTGGGAAATATGTTTGCATAT
3564b	177	C/T —	GCTAGTAAGGTTCCACCTAAATGGTTCCAAGTCAGGAGAGTCACTAAATGTTTTGAGAAATAAAAGTGAAAATCAATGTGTCTTCCCAGTGTATTCACGTGTAACGTTAACATGTCATGTCTGTT[C/T]AACAAGTGTTTGTTGGTGTCATC
3564	177	C/T —	GCTAGTAAGGTTCCACCTAAATGGTTCCAAGTCAGGAGAGTCACTAAATGTTTTGAGAAATAAAAGTGAAAATCAATGTGTCTTCCCAGTGTATTCACGTGTAACGTTAACATGTCATGTCTGTT[C/T]AACAAGTGTTTGTTGGTGTCATC

VI-3649	64	A	G	AATGTCCATGCTGTGACTGACCTGTCTCAACACCTTCCTTAGTGTATTCCTTAGTGTGGAAGAATTCAC[A/G]AGACCAGTTTGCCTTCACTTAGTAGGGCCAATGATGTAGAGACTTTTAGGTGCTACCACAAGGGTACCTGCACAGCCACATCAGTATGTCACAGTAGTTGCAAAGGACCTGTCTAGACTCCTTCTGCCTGCCTTGGTCTTCCTGTTTTACCCATATTAATGACATGACTCAGAGCCTTTA
II-3674b	133	G	C	ACAGTACACATGGCCCCATTATGGAAACAATCATCTGACTTATGTACCTGAGAAGTTCCCTCTCTAAATTTAACTACCAGGCGGAGTGCTTTTATAGTAATTAAATATGTTTATTTAGAAAATAACAAAT[G/C]AAGAAAAAATGATAGTCAAGTTGTAGACACTATTTAAAATTGTAACTTGGTCAAATGATTGTTAATTCTTAATTAATTGTGTTTATGTTTTNATTACTGCCAATCACAGCCAAG
I-3674	133	G	C	ACAGTACACATGGCCCCATTATGGAAACAATCATCTGACTTATGTTACCTGAGAAGTTCCCTCTCTAAATTTAACTACCAGGCGGAGTGCTTTTATAGTAATTAAATATGTTTATTTAGAAAATAACAAAAT[G/C]AAGAAAAAATGATAGTCAAGTTGTAGACACTATTTAAAATTGTAACTTGGTCAAATGATTGTTAATTCTTAATTAATTGTGTTTATGTTTTNATTACTGCCAATCACAGCCAAG
-3682	137	G	A	CAATATAGACCAAATGACTGCCACAAAGAGAAATTAGTGGATCTACATTTAGAAACCACCATGTTTTTATTGGCTCTCTCTCTCTCTTTTAAGTGCTCTCCAACCAATTCACTTTATTCTTTTCAAT[G/A]AGCATTTGTCCAATTTAAAGTCAATGAAAAATAATGTACATTTTCAACAAGTATACATTAAGCCCTGCAAAGTGCTTATATGCTAT
3854b	194	G	A	GGTATGTGTTGAGGTCAGCTAATGGTCACTGTGGTTGGAGTGAATCTAAATGGATTTTTGCCCTTGGACAAAGACCAAGGACAACCTGTAGGACTTCTGCATGGTCTACCTCACTTAGGCTTCTTGATTAATAACTCTGGTTCAGGAAGGCAAGGGCAGTTATGACCACTTACAACTGGTTATAACAGAGTCAGAGCCAGTTAAATGGCCTGTCCCACTCCACAGAAATGGTTATAACAGAGTCAGAGCCA
3854	194	G	A	GGTATGTGTTGAGGTCAGCTAATGGTCACTGTGGTTGGAGTGAATCTAAATGGATTTTTGCCCTTGGACAAAGACCAAGGACAACCTGTAGGACTTCTGCATGGTCTACCTCACTTAGGCTTCTTGATTAATAACTCGTTAAATGGCCTGTCCCACTCCACAGAAATGGTTATAACAGAGTCAGAGCCAGTTAAATGGCCTGTCCCACTCCACAGAAATGGTTATAACAGAGTCAGAGCCA
1039	210	G	A	AGCCAGCCACATCCATGTTGAGTCCATTAACAAGAGAACTCTGATTACATTGTATGTTTGTGGTTACACTACAGAATCCAAGATGACCTCCCCATCCTCCAAGGTCAACTAATTAACACCTTAATTCTTGCAATCTTTGTCATTACCAATAACATATTCATGG[G/A]TTCTGGGGATAAGGGGTAGACATTTTATGGGAGGCATTA
110b	130	T	C	GAAAAATGATGTTTTTGATTCCCTTCCTATCTTCAGATTATTGGAGTGTCATTAGAAAACTGATAGTAACCTTTTATTTGATGAAAACTCTGTCTATAATAAACCTTCCTTCCTGCTTATTTGCC[T/C]ACAGTTTAGGTAATAAAAGATGCCCAAGAATTCAGTACACAAGTATTCAAGTAGCAACCATGGGGTAGGGACAAGTNCAGAAAAAGGGAGGGAGGTNGGGGGGTTTTCTGGGAAGA

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I-4110	130	T	C	---	GAAAAATGATGTTTTGATTTCCCTTCCTATCTTCAGATTATTGGAGTGTCATTAGAAAAACTGATAGT AACCTTTATTGATGAAACTCTGTCTATAATTAAACCTTCCTGTCTCTCTATTTGCC[T/C]CACA GTTAGGTAAATAAAAGATGCCCAAGAATTCAGTATTCAAGTACAGTAAAAAGTAGCAACCATGGG GTAGGACAAGTNCAGAAAAAGGGAGGAGGTNGGGGGGTTTCTGGGAAGA
I-4119b	168	G	A	---	ACCTCTCTATGCCTGAAAGCCCTGAGTGTCCAGCAAGGCTTGGGTGGGAAAAGTAAATAG AATGGAAGGATAAATAAAGGTAACTACGGGGAAGAACAGAACAGAGAAGAGAGGGGTT AGAGGAAGGAATCAGTTGTGTGCCATTCAAAGTTAA[G/A]CAAGGTACCAAATTTGTTTTCTTCA TGAGACCGTCTGCATTCTTCTTTTGTTTTTAAGGGCTCTGTTGATCATCATCTTCA
I-4119	168	G	A	---	ACCTCTCTATGCCTGAAAGCCCTCATGAGTGTCCAGCAAGGCTTGGGTGGGAAAAGTAATAAATAG AATGGAAGGATAAATAAAGGTAACTACGGGGAAGAACAGAACAGAGAAGAGAGGGGTT AGAGGAAGGAATCAGTTGTGTGCCATTCAAAGTTAA[G/A]CAAGGTACCAAATTTGTTTTCTTCA TGAGACCGTCTGCATTCTTCTTTTGTTTTTAAGGGCTCTGTTGATCATCATCTTCA
I-4123b	51	T	G	---	CAAAGTCAGATTTTGATTATTCAGGATAACAATTTGAAAATAGAAAAGTG[T/G]TTTAAACTATTT CAAATAAACAATAACATGACAAAAACATGATGAAAATTCTTCGTTACATAATTGTATAGAATTAGTGGGG TTCTTCCATGACATTGGCTTGTTCTTCTCTCAACAGTGGGTGGTTCCTATGCTTTCTC AGGCACAAACAGTGAAGAAACCTTAGCAACATTCTGCTGTGTG
I-4123	51	T	G	---	CAAAGTCAGATTTGATTATTCAGGATAACAATTTGAAAATAGAAAAGTG[T/G]TTTAAACTATTT CAAATAAACAATAACATGACAAAAACATGATGAAAATTCTTCGTTACATAATTGTATAGAATTAGTGGGG TTCTTCCATGACATTGGCTTGTTCTTCTCTCAACAGTGGGTGGTTCCTATGCTTTCTC AGGCACAAACAGTGAAGAAACCTTAGCAACATTCTGCTGTGTG
-4149b	145	G	C	---	TTGTACATGTTCATTCATCCCCTCCCCATTCTTTCTGTCTTATAAAGAACCTCGCTTCTCTCCAAGT CTTACTTCTCCACCTGAGCCACACAGATCTCTTATTCCATCAAGCTTTCTCAGCATCTTCTATATACT GTGCTGT[G/C]CCTTGTGAAGAAGCCAGAGCCAGACCGAGCATACCAACATGATCTTTGCTTGAACTGTAGT AGGAGAGACAGAACAGAGATGTGCGGGTCCCCATGATATAAGGTAATTG
-4149a	137	T	C	---	TTGTACATGTTCATTCATCCCCTCCCCATTCTTTCTGTCTTATAAAGAACCTCGCTTCTCTCCAAGT CTTACTTCTCCACCTGAGCCACACAGATCTCTTATTCCATCAAGCTTTCTCAGCATCTTCTATATAC[T/C]GTGTGCCTTGTGAAGAAGCCAGAGCAGCCAGACCGAGCATACCAACATGATCTTTGCTTGAACTGTAGT TAGGAGAGACAGAACAGAGATGTGCGGGGTCCCCATGATATAAGGTAG
4182	188	G	A	---	TAACACTTTTCATTTGGTTTCCTATTACTGCAGTAAAGGACCATCCATTATTACAATTCCCTC AGTTCTATGCTTTAGAGTNCTATTATAGGACTACTGTAAAATTCAGAGGAATTACTCCTTGGAGTA GGGGAATGAGTTAAATAATCTACCACATGCCAATTGCAGGGACTGTGGTTAA[G/A]ATGTCCTCTCT TGCCCCCTTCCCAAGTTCTTAAATTCCTAG

VI-4230	93	T	AGAGACGTTGAATGGGACATCTTTCTATTCGATTTAGTTTAACATTTGATAAGAAATTGATGAAA GTTGTCACATTCCAGATTTATCTTTATAGCAGCAGAAGTCTGGCAAATAATAACAGCACACTGACT TTTCCATGGTAAAAGAAGTTAGAGAAAAACAGCCTATTTTCTTAAGTGTTAAATGTAATTCTGAAT ACATTTAAATGGAGGAGAATGAATAGTGACCTTGAAATTTATGG
NI-4241	118	C T	GAAAATTCCATTGAAGTTTGACCTGATCTCATTAATACTTTNCTTGTAGTGGTGTATTT CATTTTGACAACAGAACGAAATTCCACTTAAAATTAAATTCTC[C/T]AAGTATCTATGAT TTAGCACTGTTAGCACCAGAAACTGTGAAATTATCTCCTAGATATTCTTCAGAATCTAGGATGGAAG AA
NI-4271b	151	A	CAGGGCTTTTGGGAAGATCAGTTAAAAGCAGAANCTGGACCTAAAAAGACTAAGCACATTTCAGCAT CAACAAAAGGTGACATGTTACCCATGAAGGTCCCTGGAGGATTAAAGATCAAATAAGAGCCTCAGG GGACTGAATCCAACGGGGAATATTAGAGTNCTACAGGGAGCCCCAACCCTCCCCCTTTGTCTCAGG CTCTTAGAAGGTCCAGTCAGGGGC
NI-4271	151	A	CAGGGCTTTTGGGAAGATCAGTTAAAAGCAGAANCTGGACCTAAAAAGACTAAGCACATTTCAGCAT CAACAAAAGGTGACATGTTACCCATGAAGGTCCCTGGAGGATTAAAGATCAAATAAGAGCCTCAGG GGACTGAATCCAACGGGGAATATTAGAGTNCTACAGGGAGCCCCAACCCTCCCCCTTTGTCTCAGG CTCTTAGAAGGTCCAGTCAGGGGC
WI-4389b	156	G A	AATCGAAACATTGATTTTTTGTAAAGGAACCACATTATTTATGATATTGTGCCCAGTTTAGCATAT GAAATTTGAAAGGGATGAACCTGGAGGAAGAGAGAATAGAAAGGATATTATTGCATAACCTTTGGA AGGTAAGATGTGAACCTATACA[G/A]TNGCAAGGAAAGTAGAAATGGAACAGACATGATTGACTTA AGAGGTATTGTGAGGAACTGGAAGCGGTAA
NI-4389	156	G A	AATCGAAACATTGATTTTTTGTAAAGGAACCACATTATTTATGATATTGTGCCCAGTTTAGCATAT GAAATTTGAAAGGGATGAACCTGGAGGAAGAGAGAATAGAAAGGATATTATTGCATAACCTTTGGA AGGTAAGATGTGAACCTATACA[G/A]TNGCAAGGAAAGTAGAAATGGAACAGACATGATTGACTTA AGAGGTATTGTGAGGAACTGGAAGCGGTAA
WI-4488	31	A G	GATGACAATTATTGTGTATTGGCATTTAAA[A/G]GTACCATTCCATTTCTTCTGGCTTTCGTGTGTT TGTTGTTGAGAGTCAGGGGTTAGTGTATTCTCCTTTCTCAGTTCTTCTCAGTAGGAAGGAAGACTGATC CTAAACAACCTAATTACCCATGCCAAAGTACGTCCAAACTGATCTTTAAAGAACATAAATCAAATTG TATTATCCTATGCTTAAAATGCTCAG
WI-4491	145	G C	ACCATCAATGTATCACCTTCTAAAATTTATTAGATGATTAACTGGCTCTGTTAAAAAATAAAAACCT GTCTTGGACATTGAAAATAAACATTACTATTGGTCATTTCTGCTACTTACAAAGGTACTGCACTA AACAAGTTAAG[G/C]GTTTTTGGAGGGGAAAAATCATAAAAATTCATAAAAATTTCTACCACTGTCA TTTCTTGTCCCATAAAATAAAATTTTACATGCCT

ID	Pos			Sequence
VI-4584	144	A	G	TTGGTTGGCATTTAGCCTCATAAACAACTATTTACAATCATAATTGTTACTCTTATTTACAAACAAG AAAAATGAGGCTTAACATCACACTTCTGCTTAGTCGCAGAGCCAAGATTTGAACCCAGGAATCCATT CACCGGTAC[A/G]TGCTACCTGGGTAAAAAATGTTAATTAAAATCTATGGCATTAGATTTCAAAGA GTCCTAATGTGGTTTGAAAATAGGTGTCTTAATTGTTTATCAGTATGC
VI-4639	185	C	T	TTTCTGCATTTGAATGTGTATGGTCAGACTTCAGAGAACCCAGGAATCTCATTTATTCAGTACAATA TGGTGGCCAGGTGCTCCAGGCCCTATTATCAGAGAGAGATCTCAGTTTAACTTTCCAATTCCACCATTAC TGACCATATGACTTGGGGAACATTATCTCACCTATCTGAGTCTGTATCC[C/T]CATCTTTAAATTGTA AATTTTAAGGACACCTATCCATCATAGTAATATTGTGAGGATAAAATGAAATAA
VI-5327	63	A		AAATGAATCCGCTTAGAGCAGCAAATACCAGTAAGGGCTGGTGCAGGATGGTGGTGGCTGAGAGA[A/--]GATTACTTCATAAAAGCATATTAATTTTATAAAATGAGAAATTAACTAGATAATTAAATGTGAAT TGAGTTTGAAGGTTGCATGAGAGTAGGGAGGGAGGTAGTTCTACTTATAGGGTTTATATAAGTNTGCT TCAATAGAATGGCTCTTCGGATGACAATGATGAACTGTTCTAAGCAGACAG
NI-5390	87	C	T	GCTTTTGAGAATGAAAAGGGGAGCCTGGACCATTGCAGGGCTTCTCATCTCTGATTATTTGTGTAT TTATTGTTCACTTATT[C/T]GTCGTCTCCCTTCTGGTATGCTTGTGTCATGAACAA[A]GAATTC CCCAGTGCCTGCCCGATTCGTGCCTCCTAGAGGTGTCCAGAAAAAAGTTCGGTGAATAGAATTG ACGAATGGGTTCAGAGTTCAGAAACCTGTGAATCTATGGAAGACAAACGAAT
NI-5390	87	C	T	CCTTGCCTGCTTTATGCATAATGAGAATAGAGTTGACTCTCCTGTCAAGAAATCAATTATTAAGCAGT GCAAACATTATTTAATT[G/A]AAAGAAACTTGTTTCTGAAACTTGTACTCTTGTAGTNAAATTG AATCTTTCCTTCTCAGCAGTTCCATGGTCGTGAATCCACCCCATCTCTTTCACCAGTAGCAAGATT GCTACTTATATGGAAGGGTTTTAGAGTTCATAACAA
NI-5404b	87	G	A	CCTTGCCTGCTTTATGCATAATGAGAATAGAGTTGACTCTCCTGTCAAGAAATCAATTATT[G/A]AAAGAAACTTGTTTCTGAAACTTGTACTCTTGTAGTNAAATTG GCAAACATTATTTAATT[G/A]AAAGAAACTTGTTTCTGAAACTTGTACTCTTGTAGTNAAATTG AATCTTTCCTTCTCAGCAGTTCCATGGTCGTGAATCCACCCCATCTCTTTCACCAGTAGCAAGATT GCTACTTATATGGAAGGGTTTTAGAGTTCATAACAA
WI-5404	87	G	A	TAGGAAAGGGGGATGGTGATGGCCTCTGAGACATTTAAATCTAAATCTATTCTTCACCACTCACACTGCCGCCA TATCTCCTC[A/C]CCAACACCTCTGTTTTCTGACAGCCAAGTTTCCATCAGTTGATATGGGACTATTT GTTGCAAAACAATTGTTAAAAGATTTGGCTGACTTTGGCTGAATTGCTACAACTCCAAAAGANTC GAGATACACCATGAATTTATTTTCATTTCA
WI-5545b	77	A	C	TAGGAAAGGGGGATGGTGATGGCCTCTGAGACATTTAAATCTAAATCTATTCTTCACCACTCACACTGCCGCCA TATCTCCTC[A/C]CCAACACCTCTGTTTTCTGACAGCCAAGTTTCCATCAGTTGATATGGGACTATTT GTTGCAAAACAATTGTTAAAAGATTGGCTGACTTGGCTGAATTGCTACAACTCCAAAAGANTC GAGATACACCATGAATTTATTTTCATTTCA
WI-5545	77	A	C	

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WI-5860b	134	A	G	ACTCAAGTTTGGGGGATAAAATCAGAAGTTTCTATGTACAACTTAAATTTTGCTAAGATTTTTATTGTTTCTTTTTATATAAATTATGGATTTGTTTTTACTTCCCTAACCAACCTTCTAACTGAGGAACTAC[A/G]TTATACTGGAATCATCATGTGAAGACATTCTAAAGGGTACCCAGGTGCACATAGTTTAAGGGAATCAATTTCCAAATCATCAACTTCTGTAT
WI-5860	134	A	G	ACTCAAGTTTGGGGGATAAAATCAGAAGTTTCTATGTACAACTTAAATTTTGCTAAGATTTTTATTGTTTCTTTTTATATAAATTATGGATTTGTTTTTACTTCCCTAACCAACCTTCTAACTGAGGAACTAC[A/G]TTATACTGGAATCATGTGAAGACATTCTAAAGGGTACCCAGGTGCACATAGTTTAAGGGAATCAATTTCCAAATCATCAACTTCTGTAT
WI-6106	208	C	G	GCAAACAACCTATTATACCTGATTCCAACCCAGGTCTACTAACATTAATCAACCCTAACCACAATACTATATATTGTCCGTTCTGTTCTGAATTATTTCATTTAGAATCTGATGAGATTAGCATGGGATAAGTGCAGTGCAGAGATAGTAAACACTGCTCTCTTTTGCTTCCAGGAGTCTCAATGTGAAGTATAATTCTTACAGAGTAATT[C/G]ATAGTAGGTCACCACACAAAGTCTATATTGTATGTGAAGGAAAG
WI-6109d	129	T	C	AAGATAGACAAACATATGCCAGACCAACAAAAACACAGACCTGTCATATTTCTGAGAGAAATGTACATTGAGTCTTCCTTCTCTGGGACTATAAGGAGATCAGGTGGAATAAAACGAAGGAAAAAAACCTAAAACCCTATATTTNCTGTCTGTGCATACTTTAAAATGTATAATGTGGGAGAAGGAATTTTGATGGNAAAATTATCCCCTGAAAATTTTATACCA
WI-6109c	147	T	C	AAGATAGACAAACATATGCCAGACCAACAAAAACACAGACCTGTCATATTTCTGAGAGAAATGTACATTGAGTCTTCCTTCTCTGGGACTATAAGGAGATCAGGTGGAATAAAACGAAGGAAAAAAACCTAAACCCTATATTTNCTGT[T/C]C[T/C]TGTGCATACTTTAAAATGTATAATGTGGGAGAAGGAATTTTGATGTGNAAAATTATCCCCTGAAAATTTTATACCA
WI-6109b	147	T	C	AAGATAGACAAACATATGCCAGACCAACAAAAACACAGACCTGTCATATTTCTGAGAGAAATGTACATTGAGTCTTCCTTCTCTGGGACTATAAGGAGATCAGGTGGAATAAAACGAAGGAAAAAAACCTAAAACCCTATATTNCTGT[T/C]C[T/C]TGTGCATACTTTAAAATGTATAATGTGGGAGAAGGAATTTTGATGTGNAAAATTATCCCCTGAAAATTTTATACCA
WI-6109a	129	T	C	AAGATAGACAAACATATGCCAGACCAACAAAAACACAGACCTGTCATATTTCTGAGAGAAATGTACATTGAGTCTTCCTTCTCTGGGACTGTTGTGCAATATCCCCAGTCGCCTTAGACAATGCCTCCCATACAAACCCTATATTTNCTGTGTGCTTGTGTGCATAATGTGGGAGAAGGAATTTTGATGTGNAAAATTATCCCCTGAAAATTTTATACCA
WI-6112	96	T	C	AATGCCTATCACCTTCCATCATGCTGCATAACTGATTGATTCATAATGCTTATTGTTTAGCCACCTGTCTTCCAACACACATGCTGTTTGTTCAATGATCCCAGTGGTATTTGACTAAAACATACTTGTTAAAATCAATAAATTAATCAACTTGTTAAAATTAATCAACTTGGCATATGCAGGGAAC

				Sequence
VI-6244	103	T	C	TAATTGCACAACTTACATATCAGGGTTTCTGATTGAAGGAAGAGAATATTCCTTTCTTTAGTGATT GCTTAATATTAATTCATATAAGTCAACATCTCTT[T/C]GCTCCTTATAAATGTGTTAGAAGAAGG AAATTGAGTGTTGGGAATTAAGCAACCAGGAGACATTTTATATACTCCTACAGTGGGGGAAGACTT CCTATTTCTTCCCAAGGATGGATACATTCTAC
VI-6268	124	C	T	CTGGCCTTATAATCCAGTTAGGATTAATCTTACCCCAACTTAATAGACTTCCAGACAGTTGCAGTT GTCTACAAGATTCCTCCTAGTAGGGCTTTGGGTGTTGGCACCGTTGGCTCATTC[C/T]ACTCTCCCT GGGTCTTATTGACTTCAGGGAGCCTAGAGAGACTGGACAAAACCTGCTTCTTTGCAGAAAGAGTCG GGGTTCCAAGAGTTCGTTACGATTTTTA
NI-6336b	234	C	T	AGGGTGCCATTTAATCCATTCAAATTTGGAAGCTACATCTTCAAGGGTCTGAGAGAGCTCACTCCCCC ATATATTCCCCCTTTACATGTTTTCTTATAAGACATACAGTTTAATCAATTAAACAAACTAAACAGCTT ATATACTGGCAATATATTACAGATGGGTTTATGTCAGAGTAATAGATCACATGAAATGGACCATGTG GTACCCCAGTGCATTATGTCTTGGGTAGAGCC[C/T]TGAGGACACTGACAGT
WI-6336	234	C	T	AGGGTGCCATTTAATCCATTCAAATTTGGAAGCTACATCTTCAAGGGTCTGAGAGAGCTCACTCCCCC ATATATTCCCCCTTTACATGTTTTCTTATAAGACATACAGTTTAATCAATTAAACAAACTAAACAGCTT ATATACTGGCAATATATTACAGATGGGTTTATGTCAGAGTAATAGATCACATGAAATGGACCATGTG GTACCCCAGTGCATTATGTCTTGGGTAGAGCC[C/T]TGAGGACACTGACAGT
WI-6381	92	C	A	TTGGATACAAAAATTCAGTTACACAATCAGTAGCATTCAAAATTAGTTATGAGTATTTATACAATTA CAAAAATGGNTTCATGTTTAACAA[C/A]GTATTTAAAAGCTCAAACATTTTAAAACAGGCACAAT ATTCTAAANGGCATATGCATTCACCATGGCCTTTGAATGTCCTCCCAACTTCACAATCAAAATC TACAGANGCGGGCAAAAGATCAGAGTTCAG
WI-6436	198	C	G	GGTTGAGGCATTGGGAAAGGCAGAAATTGAGGCAGTAGAAAATGGACATTTTAGGAAAGAGAAGT TCAGAGGCAAAGTCATGACAGAACAGGAAATACAAGGCTTAGGAAGAACAGTAGTCTCTGTGGTTGAA ATTTTGGTGTCATAATAAGAAGTTAGACTTGGTGTGTAGTTGTAGTAGTAGGCGTT[C/ G]ATTGGGTATTCCACAGACAAGGTGATGTTCTAAGAATTGATATTTATTGT
WI-6449	186	C	T	GAGGCCTCTTGCTTTCCTCAGTCAAGGCGTATCCAGGGTTGATATCTAGCCTATATGCCATATGT GTATGGCTAGTGTTTGTCTGATTGGTTGGTGCTCACACTGCCCAGATTGTTAAATATTTGAAAATC GTATCTGGTTCTATCATCTGCATTCTCGATCTTATGTCTGCTCTATT[C/T]ATCCCTATTCTCTGA TCTTATGTCTCAGACCTGAAGTTCCTCTAATTTTCTGTGGTGTATTTATA
WI-6449	186	C	T	GAGGCCTCTTGCTTTCCTCAGTCAAGGCGTATCCAGGGTTGATATCTAGCCTATATGCCATATGT GTATGGCTAGTGTTTGTCTGATTGGTTGGTGCTCACACTGCCCAGATTGTTAAATATTTGAAAATC GTATCTGGTTCTATCATCTGCATTCTCGATCTTATGTCTGCTCTATT[C/T]ATCCCTATTCTCTGA TCTTATGTCTCAGACCTGAAGTTCCTCTAATTTTCTGTGGTGTATTTATA

NI-6463	72	T	C	---	GCTGGAGAGAAAGACCTCCAAAAGAGAAGAAACTAAATCAGAGTCTCTTGAGCAAGAGGAATTGAAA AGAACA[T/C]TGAAAAAAATTAAAGTAGAACTCAAAGAGCCAAAAGTCCCAATTGTGTCCATTA TAAGAAATATTTGAATGGAAATCTTAAGAATGATTTTATTGATCAGTTAAATGTTCTTCCTCTCCTC CAGTCCCATTTATATGACATTCCGCATGCTG
NI-6474b	76	C	T	---	AAGCAGTAAATCTTCCATCATGCCATGGATGCCAGTGGGTAAATGTTATAGAAACTTCAGAGGANAC AGAGGCAAA[C/T]GTTGGTTATAGCAGTCAGTCAACGACATCATCAATGAAGACATGACTTGCTTAGAGCC AAGAAAAAGTAGGATTTTGAAAGGCACAGAGAAAAGGGGTGTACTAGAGGAGAACTATGTAAGCAG AGGTATAGAGGGAACTAAAGTATAAAAGAGTGAGCCATAACTTAGGGTACCATAA
NI-6474	76	C	T	---	AAGCAGTAAATCTTCCATCATGCCATGGATGCCAGTGGGTAAATGTTATAGAAACTTCAGAGGANAC AGAGGCAAA[C/T]GTTGGTTATAGCAGTCAGTCAACGACATCATCAATGAAGACATGACTTGCTTAGAGCC AAGAAAAAGTAGGATTTTGAAAGGCACAGAGAAAAGGGGTGTACTAGAGGAGAACTATGTAAGCAG AGGTATAGAGGGAACTAAAGTATAAAAGAGTGAGCCATAACTTAGGGTACCATAA
WI-6478b	175	T	A	---	GAACTCAATTAACTTGCAACACTGAGAAAATCGGATTTGGAGATCTGCAAAGCTGAGGTTGAGATT TTGGACCTTGGTGATCCAAATGGGAATGCCACGCTTCGAGGCCTGTCTATATGCTTTATTTTGTGA CACTGTCTATTTACCCTCCCCCAATAGTGGAGAATCAGAG[T/A]GCTCCTTGTCAGTGTTGCTACAGA GAAGATATACAGGATGGAAGGACAGCTCCTCGTAGGACCTAGACACAACTG
WI-6478	175	T	A	---	CACATTTTGAATGCAACTGAGAAANTGGTTTTNTAGGCCTACCTTTTATTTAAGAGTACATCTGGCTC CAATGTTACCCCAAACATGCAAAACATAAGGCAACAATTCTGATCATTTTATAGGNTCCCAAGCCCA TTAGCAATATCTTA[G/A]TCAAATTTTAAAAAGAGAACAGGAAATAAGGAAGGCCTAACAGAGGAG TTAAATAATTGTGCAAAACTTATCAGTTCTTC
WI-6559	149	G	A	---	TTCTTTATTGGTCCTACCAATGTGACTCTTTACCCAGCCCACTGTTCCTATGC[G/A]CACTGGCTTTG TAGGCATTCACATCTCATATGTCTGTGTCCTGAAAATCTCAATTAATTTCTCCTNCCTATTCCTTTTCCAT GCTCTGCCTCATTNCTCAGAAATTGAAGGCATTTGATTATNATTTTTTGTTTGGGTCTGTGTAAAG GTTCCTTGGCAGGAGAACATGCATATGACTTTAAAATAAAGACCAACA
WI-6564b	54	G	A	---	TTCTTTATTGGTCCTACCAATGTGACTCTTTACCCAGCCCACTGTTCCTATGC[G/A]CACTGGCTTTG TAGGCATTCACATCATATGTCTGTGTCCTGAAAATCTCAATTAATTCTCCTNCCTATTCCTTTTCCAT GCTCTGCCTCATTNCTCAGAAATTGAAGGCATTTGATTATNATTTTTTGTTTGGGTCTGTGTAAAG GTTCCTTGGCAGGAGAACATGCATATGACTTTAAAATAAAGACCAACA
WI-6564	54	G	A	---	TTCTTTATTGGTCCTACCAATGTGACTCTTTACCCAGCCCACTGTTCCTATGC[G/A]CACTGGCTTTG TAGGCATTCACATCATATGTCTGTGTCCTGAAAATCTCAATTAATTCTCCTNCCTATTCCTTTTCCAT GCTCTGCCTCATTNCTCAGAAATTGAAGGCATTTGATTATNATTTTTTGTTTGGGTCTGTGTAAAG GTTCCTTGGCAGGAGAACATGCATATGACTTTAAAATAAAGACCAACA

ID	Position	Allele 1	Allele 2	Sequence
VI-6608b	46	C	-	CTAATCACAGTAGCACTGAACATGGCTCTAGTGAGTGGGCCTCAGT[C/-]AGTTCAGGCAGCTAAAGGGAGGGGGGATTCCTCCTAGTCCTCTCCCTAGAGCTAAATATGCATCTGGGAAAAATTAGGCTCTGGAGCACAGAGGTATTTTCTAGAGGAAAAAGAACTGAACTCCCAGCACTAGGTAAAACTGCAAAAGAAAGAAACACCTGTGCCCAGCGCACTAGCTACAAGGCCACCAGAAAAGGAA AGC
VI-6608	46	C	-	CTAATCACAGTAGCACTGAACATGGCTCTAGTGAGTGGGCCTCAGT[C/-]AGTTCAGGCAGCTAAAGGGAGGGGGGATTCCTCCTAGTCCTCTCCCTAGAGCTAAATATGCATCTGGGAAAAATTAGGCTCTGGAGCACAGAGGTATTTTCTAGAGGAAAAAGAACTGAACTCCCAGCACTAGGTAAAACTGCAAAAGAAAGAAACACCTGTGCCCAGCGCACTAGCTACAAGGCCACCAGAAAAGGAA AGC
VI-6666	68	C	A	GTTAGACAGTATCCAGCAAAAAGGTTATTTTATACCTCTACTTTTCCAAAACGAGGAAACCTCCCCA[C/A]AAATCCCATCAACACACAGTCATGCTGGAAGGCATTCGTGTTCTTACTCTGTTCATGTAAATGTTTGGGGTGACTCATTCCGCCCTCTCTTTCTCAAGTTCCAGGCTTCTTGGGTAGACCAAAACTAATACACAATGTTAGAGCACACAAGAGA
VI-6670b	120	A	G	AGATTAACATAATTATACTGGGGCCATTGTAGGGTTNGGGAGGAGTGTTTTTCTATCTGCAGCCAAACAGAAATACTGTAGTACAGCAAAACCGTCTCAACAGTAAGCACACAATGAAC[A/G]TTGTTAGCCAGCATTGCCATTCAGGCGCCGAGTCAGGGTTTGTGGGCCAGGTTTGTGGGCAGGTTTGTGGGGAATTCTGAAAAAAAAAGAAATACAGAATTGTAACACAGACACAGAATCTTAGAAGGGAT
VI-6670	120	A	G	AGATTAACATAATTATACTGGGGCCATTGTAGGGTTNGGGAGGAGTGTTTTTCTATCTGCAGCCAAACAGAAATACTGTAGTACAGCAAAACCGTCTCAACAGTAAGCACACAATGAAC[A/G]TTGTTAGCCAGCATTGCCATTCAGGCGCCGGAGTCAGGGTTTGTGGGCCAGGAAGTTTAGACAATTGGGGAATTCTGAAAAAAAAAGAAATACAGAATTGTAACACAGACACAGAATCTTAGAAGGGAT
VI-6704c	33	T	C	TTTGAAAATAAATTCATGCACCAATGTTTAAC[T/C]CACATATATCATACAGTGCAGGATTTATGAACATACATAAAATCAAAATCATACCATATAAAGTTTACAAATAAGTTTTCATGACACACGGNCACTATTGCTCTTTAAATATGGTTGTACATGTCATCATTAATCGATTCATTGTTCTTCCACATGGTTATTTCAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG
VI-6704b	33	T	C	TTTGAAAATAAATTCATGCACCAATGTTTAAC[T/C]CACATATATCATACAGTGCAGGATTTATGAACATACATAAAATCAAAATCATACCATATAAAGTTTACAAATAAGTTTTCATGACACACGGNCACTATTGCTCTTTAAATATGGTTGTACATGTCATCATTAATCGATTCATTGTTCTTCCACATGGTTATTTCAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG
VI-6704	28	T	C	TTTGAAAATAAATTCATGCACCAATGTT[T/C]TAACTCACATATATCATACAGTGCAGGATTTATGAACATACATAAAATCAAAATCATACCATATAAAGTTTACAAATAAGTTTTCATGACACACGGNCACTATTGCTCTTTAAATATGGTTGTACATGTCATCATTAATCGATTCATTGTTCTTCCACATGGTTATTTCAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG

WI-6710	106	G	A	CCATGGACAGTTTAATTAGGAAGCTTCGACTTGTTAGAATAAACAGAGGAGAGTCCCAGTTATCTACCT ATTCCTTAAAACACATTTGTGTCAGGCTGGAATGATTCCC[G/A]TAGTAAAACTCAACATCCACACCT GCATAAACATCGCCTCCCAAGTGACTATTTATTACTGAGTCGACACAGGATGTCACCAGTGAGCCTC ATCTCCAGTCCAATGGAGGAGTTGACTTAGACCTTCCTTGGACAGGAAGGGTC
WI-6766b	148	G	C	AAAACAAATGGTGCATTGCATAATATTTGTGGTCACAGTATAAAACAATACAATTAGTTCATATAAC ATTGGATATGGACAAAAATACACANGATCCTTTGTCTACGGAAAATNCTGCAGATCCTTATGT GCCACACTTAAAAN[G/C]AAAGTCAACGTTTCTCTTCTAGGGNTCTGCACACATATTTATCACTGA GAATTTGGTCAAACAGTGGAGGNGAACTTACCCAAATCCCAGTTCCCTTCTTC
WI-6766	148	G	C	AAAACAAATGGTGCATTGCATAATATTTGTGGTCACAGTATAAAACAATACAATTAGTTCATATAAC ATTGGATATGGACAAAAATACACANGATCCTTTCTTGTCTACGGAAAATNCTGCAGATCCTTATGT GCCACACTTAAAAN[G/C]AAAGTCAACGTTTCTCTTCTAGGGNTCTGCACACATATTTATCACTGA GAATTTGGTCAAACAGTGGAGGNGAACTTACCCAAATCCCAGTTCCCTTCTTC
WI-6787b	97	A	G	ACAGATAAAAGTCTTTATTCCCGTGTATGTTACATAAGAAAGTTCTTTACAGACTTTTTTTATACA ATACTTGTGCAGCAATGTTCAAATTTCAC[A/G]TTTTTACTGCATAAGATATCTTCATGTACAACTGT ATGCTTTGTCTTCTTGGGAAGGACGGTTAAAGACCGTTAAAGAGTAAATTCAGGT GAGTGCAATAGGGCAGAGTAGANTACTCACAGGAAAAAGAGTAAATTCAGGT
WI-6793	105	C	G	GAACCCACCAGGTCCTGTGTATTTTATTAAGGAGCATTACATTATGATAGCAAGTTCAACACATTCA TCAACAAGGCGGTCTTCAAATCAGTCAACCCCC[C/G]GAGTTAGAAGTAGAGTCATGAGGAA GAGCTGCTTGGCTGTGTAGGAAGTAGGGTTAATGCCCCTCTAATCCCCGGAAAGGGGCCAGACTGAAGCCA GAGCCAGANTCCTGGCAANTCCTCATCACAGGTAAAAAGGCAAC
WI-6810b	37	T	C	CACAATAATAAAATCACTCCCTACCTTGAAAACTTTA[T/C]AGAAGCATTTTAATTTTACAACACA AAGCTCAAACGNACCTACACAATAAGTCTAGTGTTACGNGCCAAGGGATAAGGCTGAACAATA AATTAACCCTTAAAAATGTCTATGNACAAGTACAACAATTTCTTTTGAGTTCTGCAGAGCAATGACC ACTAAGNAATATTTTAAAGGCTGAACAGAATCCAGCGCAATGAAGTTAAT
WI-6810	37	T	C	CACAATAATAAAATCACTCCCTACCTTGAAAACTTTA[T/C]AGAAGCATTTTAATTTTACAACACA AAGCTCAAACGNACCTACACAATAAGTCTAGTGTTACGNGCCAAGGGATAAGGCTGAACAATA AATTAACCCTTAAAAATGTCTATGNACAAGTACAACAATTTCTTTTGAGTTCTGCAGAGCAATGACC ACTAAGNAATATTTTAAAGGCTGAACAGAATCCAGCGCAATGAAGTTAAT
WI-6817b	145	C	A	GCATGATTAAACCAGTGCAGAAAAAATACCAAGTACATTGGGTGAACGATGAGCTAGCTGTTCTAGTA TTTGCTTTTTGTAATCCAGTTGTATGGGATACCCTGTCGTGCTCTACTNGCCTCCAAAGGCATTCAGGGGATCATCA GCAGGGTAAC[C/A]TGTGGATACCCTGTGTCGTGCTCTACTNGCCTCCAAAGGCATTCAGGGGATCATCA AAGATGTTGGACACCTTGTTCAAATCTTGGTTCAGGTGCGGCCTGTGCAG

ID	Pos.	Alleles		Sequence
WI-6817	145	C A	...	GCATGATTAAACCAGTGCAGAAAAATACCAAGTACATTGGGTGAACGATGAGCTAGCTGTTCTAGTA TTTGCTTTTGTAATCCAGTTAAGACCATCAGCCATCATACAACATCACTAACTCAACAATGTAGCT GCAGGGTAAC[C/A]TGTGGATACCCTGTGTCTCACTNGCCTCCAAAGGCATTCAGGGATCATCA AAGATGTTGGACACCTTGTGTTCAAATCTTGGTTCAGGTGCGGCCTGTGCAG
WI-6819b	221	C		GATGGAAAGCCATTTATTTTCTCTAAATTTAAAATAGAAGACTTTAATGGAAAACATTTAGTAC CATCATCATGTCACCCTGAATGCCAGCAATACCTGACTTTACACACGCAGGAAGCCTAGTAAAGCCC CGTCAGTAGTACACAATTTCTCTATGGTCCTTCAACAGTTTGCATATACAAAATTTTCTGCTATTTG CTTTAGCAAACAGCAATAACTTTTGTGTTCCTATATGACACCTAATATCCAG
WI-6819a	175	G T		GATGGAAAGCCATTTATTTTCTCTAAATTTAAAATAGAAGACTTTAATGGAAAACATTTAGTAC CATCATGTCACCCTGAATGCCAGCAATACCTGACTTTACACACGCAGGAAGCCTAGTAAAGCCC CGTCAGTAGTACACAATTTCTCTATGGTCCTTCAACAGTTT[G/T]CATATACAAAATTTTCTGCTATT TTGCTTTAGCAAACAGCAATAACTTTTGTGTTCCTATATGACACCTAATAT
WI-6826b	154	A G		GCAAAAAGCTTATTGGCTCCAACAAATTATCCCTTTAAAACTCCTCTCTTCTTCTGGTCTCAGTG GAACAACACATTTGAATTTCAGATTTGCAGTTTATAGCATTTTTCCCTAAGAACCATATAAATAC ATGCAAAACCTTGTACAT[A/G]GAGCTAAATATCAAAATGCAAATATAGATTGGGTGCACTGT TAAGCTGAATTGCAAATTATGGCAACACACTGGACTGGGTATACGTTG
WI-6826	154	A G		GCAAAAAGCTTATTGGCTCCAACAAATTATCCCTTTAAAACTCCTCTCTTCTTCTGGTCTCAGTG GAACAACACATTTGAATTTCAGATTTGCAGTTTATAGCATTTTTCCCTAAGAACCATATAAATAC ATGCAAAACCTTGTACAT[A/G]GAGCTAAATATCAAAATGCAAATATAGATTGGGTGCACTGT TAAGCTGAATTGCAAATTATGGCAACACACTGGACTGGGTATACGTTG
WI-6857a	122	T C		AGTGCAAACTATTTTGAACAAAGTAAACTATGAGTCACAGCATTCAGCAAGACCATCAGACACGGA AGAGTGAACAATATTCACTAAGTAAAATACAGCAGATGAGATGTCTCTCACATGTA[T/C]ATTAAT TATTCATGCTTTTCAATAGTCTCTTAGTCAACTTCAGTGTAATTCCACAAATATAGCAGCTCA AACACAAATGCAGGAGCACAATGGCAAAGTTGGCAACTGTTTGGGCTAATT
WI-6865	153	G A		TTATAGAATACTTATGGGGCATACGNGTAAATGAACTGTCAACCTTAAAATCTAAACAAACAGCTTG TTTGTGGTTCGTCGTCCTGAAATCCTCCCGCTCACAAAACGCCAGCTACTNGGTTTTCTAAAGACGTA ATTTTGCAGGCAAACTTC[G/A]TAGAGCCAAACTTCTTTGCGCTGTTAGAGAACTGAGCTCATTAA
WI-6909	73	C T		ATTGAAAACTGGTTAGCAACAGATAAATTACAATAGAGCCTGGATATAAAAATGAGAGAAGAATGC AGACTTA[C/T]AAGCTTATAGAGAAAAGTCAAAAGGAGCAAGTTTTGAAATCAGATTTTATGATAC GGAAAAAAATTTCCTTTTTGCCAACAGGATTATTTCGAATAATAAATCTGCCAGTGCCAATCAG AAACACCATTTCCAACAATATTTGCCTATTTTATACACATATC

ID	Pos			Sequence
WI-6910b	163	G	T	CACTCAAAACCCTTATTCATTGATTTACAAACTGTACAAATATTTACAAAGTTTAGGCATTAATCCCATATTGACATGAATGCTGTGGAGAGTCTAAAAATAAATATGTGGCACATAGCTTAATATACACATCATGGCTCTTTACACTTAGCCATTACCAATA[G/T]TGAGATGTAATGGAGAATTTAATGTGGTAGAAAAGTCAGAGTGGCTGACCAGTCCCGACCTTCCATGTGAATGACTCTTCCTTGGC
WI-6915	144	A		GCTTGTTTTTTGTTTGTTTTTTAAGTGACACCTTGGCCTTGTGTGGCATTCTTCACTTATCTTACCCAAAAGTGCCTTTGGGCCCAGCCACTGACTTAAAACCCAGAAATGTGGTTTAAACAATGTGGTCGTGGTGAATTCAGGTGATTTNATTTCTATTTGGTAGTATTTTCAGATTTCCCACAAGAACATGTATTGTCTTTGTAAATTTGAAAAAAAATCAACACAGGATAGTAAAGATAT
WI-6928b	175	T	C	CAATCAAAAAGTTCCAAGTTTCAAAGCTGGGATGAAAAGCCAGGTCTTCTGACTTGCACTCTGTCACACTGGAITTNCCTCTGATCCAGCTGCAGCCTCCCATAAGAAGTTCACTCTTAATTCATGTCCCATGCTTTGTCTTGGTCCCGTGAGGAAAGGGGGTCAGCTAAAGG[T/C]AACTGTTCTATAAGGATGGGTAGGTATCCTGGCAAGATATTCCTCTGAAATAGTAAACGTGACCTTAGAAGTTA
WI-6928	175	T	C	CAATCAAAAAGTTCCAAGTTTCAAAGCTGGGATGAAAAGCCAGGTCTTCTGACTGCACTCTGTCACACTGGATTTNCCTCTGATCCAGCTGCAGCCTCCCATAAGAAGTTCACTCTTAATTCATGTCCCATGCTTTGTCTTGGTCCCGTGAGGAAAGGGGGTCAGCTAAAGG[T/C]AACTGTTCTATAAGGATGGGTAGGTATCCTGGCAAGATATTCCTCTGAAATAGTAAACGTGACCTTAGAAGTTA
WI-6955b	79	G	A	TTTTTATGAAACATTTCAGATTCCCTCATATCACAGCACATCAATAAGCAGTATGTACATAGACTGACTTTTATAGTAC[G/A]NGTCATGTCCCAAATTCCCAAATTACCAAANTACAAGTAGCCGNTAATTAAACTATAGGTAGTATATTAANCAAAAATGNGTTTTTNGCAATTATGTGAAATAAGGCTTTAACCAAAGC
WI-6955	79	G	A	TTTTTATGAAACATTTCAGATTCCCTCATATCACAGCACATCAATAAGCAGTATGTACATAGACTGACTTTTATAGTAC[G/A]NGTCATGTCCCAAATTCCCAAATTACCAAANTACAAGTAGCCGNTAATTAAACTATAGGTAGTATATTAANCAAAAATGNGTTTTTNGCAATTATGTGAAATAAGGCTTTAACCAAAGC
WI-6957	47	C	G	AAACTAAAAACCCTTATTGTCTCCAAGTGTGTGGCAAATAGAAAAT[C/G]TTTCAATTACATTAGGAAATCGGGTGGATAACGGAGTAGTTATTCCACTTAGTAGTTATTCCAGTCAAATAATCACAAAAACAAATTCAGATTGCTTGGATCTTGGTCATTTATGGCTTGAAGAACTGGATTTGAAAAACCACTTTAGGCTAAATAAATGTATATGAATAATGCATTTTTGGTCATTTATGTATCTAGAAAATCATGC
WI-6996c	242	G	T	ACTTCTAGTGCCTCTGTTACCCACCACTCTAATGCCTCTGGTCGCCGCACTCTGATGTCCGTAGGCCTTAAATCTGCCTGGCGGTCCCCTCCCCTGTCTTCAGCACCCAGTCCTTAGGCAGGAGAGGAGGGGGCCCCTGTCTGCTCCTCAGGACCCCTGTCCTGACTCTCTCCTGATGGTGGGCCCCTGTCTTCTTCTTCCG[G/T]GTCGGATC

WI-6996b	242	G T	ACTTCTAGTGCCTCTGTTACCACCACCTCTCCTGGTCGCGCCACTTCTGATGTGTCCGTAGGCCT TAAATCTGCCTGGCGTCCCCTCCCTCCTGTCTTCAGCACCTCAGTCCCCTGCTCCTGCTCCTGACT CAGGAGAGAGGAGGGGGCTCAGCCCCTGCTGCTGGACCCAGTCCCCTGCTCCTCTCAGGACCCCTGTCCTGACT CTCTCCTGATGGTGGGCCCCTGTGTGCTCTTCTTCCG[G/T]GTCGGATC
WI-6996	228	T G	ACTTCTAGTGCCTCTGTTACCACCACCTCTCCTGTGTCGCGCCCACTTCTGATGTGTCCGTAGGCCT TAAATCTGCCTGGCGTCCCCTCCCTCCTGTCTTCAGCACCACCTCAGTCCCCTGCTCCTGCTCCTGACT CAGGAGAGAGGAGGGGGCTCAGCCCCTGCTGCTGGACCCAGTCCCCTGCTCCTCTCAGGACCCCTGTCCTGACT CTCTCCTGATGGTGGGCCCCTGT[GT/G]GTCTTCTTCCGGTCGGATC
WI-7021b	112	G A	TGGGGAGGACAGGGAGATGCTGCAGTTCCAAAAGAGAAGGTTCTTCCAGAGTCATCTACCTGAGTC CTGAAGCTCCCTGTCCTGAAAGCCACAGACAATATGGTCCCAAATT[G/A]CCGACTGCACCTTCTGTG CTTCAGCTCTTCTTGACATCAAGGCTCTTCCGTTCCACATCCACAGCCAATCCAATTAATCAAACC ACTGTTATTAACAGATAATAGCAACTTGGGAAATGCTTATGTTACAGGTTA
WI-7021	108	A G	TGGGGAGGACAGGGAGATGCTGCAGTTCCAAAAGAGAAGGTTCTTCCAGAGTCATCTACCTGAGTC CTGAAGCTCCCTGTCCTGAAAGCCACAGACAATATGGTCC[A/G]AATGCCCGACTGCACCTTCTGTG CTTCAGCTCTTCTTGACATCAAGGCTCTTCCGTTCCACATCCACAGCCAATCCAATTAATCAAACC ACTGTTATTAACAGATAATAGCAACTTGGGAAATGCTTATGTTACAGGTTA
WI-7056c	118	C T	GGCAGTAGGACCACCAGTGTGGGGTTCTGCTGGGACCTTGGAGAGCCTGCATCCCAGGATGCGGGTGG CCCTGCGAGCCTCCTCCACCTCACCTTGTGTGTTCCAAGTTCCAAACAGTTGGTGA[C/T]GGTTGGGGAGCCTCT GGGGGCTGTTGAAGTCACCTTGTGTGTTCCAAGTTCCAAACAACAGAAAGTCATTCCTTCTTTTTAAA ATGGTGCTTAAGTTCCAGCAGATGCCACATAAGGGGTTTGCCATTTGATA
WI-7056b	118	C T	GGCAGTAGGACCACCAGTGTGGGGTTCTGCTGGGACCTTGGAGAGCCTGCATCCCAGGATGCGGGTGG CCCTGCGAGCCTCCTCCACCTCACCTTGTGTGTTCCAAGTTCCAAACAACAGAAAGTCATTCCTTCTTTTTAAA ATGGTGCTTAAGTTCCAGCAGATGCCACATAAGGGGTTTGCCATTTGATA
WI-7091b	153	A C	AATTCGCTGAAAAAGGAACTACCTATCCTTACATTCACCTACTAATGTCTCTTCTTCTAACATCTTAGAG GTCCATGGAGAAGGCATATGGAGAACATGTTTATACTGCTCTATAAATAGTATTCCAATCACTGTG CTTAATTAAATAGCATT[A/C]TCTTATCATTTATCGGTTCTATATAAGAATGCTAT ACATATATTATTTCATTGGTCTTCTTTTTATCTGGTTCTATATGAATGCTAT
WI-7091	153	A C	AATTCGCTGAAAAAGGAACTACCTATCCTTACATTCACCTACTAATGTCTCTTCTTCTAACATCTTAGAG GTCCATGGAGAAGGCATATGGAGAACATGTTTATACTGCTCTATAAATAGTATTCCAATCACTGTG CTTAATTAAATAGCATT[A/C]TCTTATCATTTATCAGCCTTTATGTATTTCATGTATTTCCAAGTAAAATATTA ACATATATTATTTCATTGGTCTTCTTTTTATCTGGTTCTATATGAATGCTAT

NI-7136	58	T	C	TGTGAAGCCACATTTCCAACATGAGCCTCATGAAGCCAACTAAGTGTTATTGAACTGT[T/C]AATTC TCTCAATAACTCAGTGTAGCACTTTAAAGTCTGAAAGACCAACAGCAACATGAAAGAGCATATCAATGTG GTGGAGAAAGGGAAGGGGTTGGCTTTTAATTATTTTCTTCATCTTTATAACAAGAAAGNNNNNN NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGTAGCTTCTATATATG
NI-7146c	210	A	G	GGGACGCCTGTTGTTTGGCTCAATTTGGGTTGTTGGTCACATGGAGCTCTTCCATTTCGTTTAGCTG AATAATGAGTTGTTCCTAGAGGAGACAGCAGCCTGTCTCTCCTGTTGCCCCCAAAGCCCATGCCCTGCCG TGGTGGCAGCTGGGGCTGTGGATGGGAGGGGTCCCAACATGGATGTGTTGCCCCTCCTCCCGCATGCC AACGC[A/G]GTTCATGTCATGTACAAGGCCCCTCTGCAACTGGAGAGAAAATTA
NI-7146b	210	A	G	GGGACGCCTGTTGTTTGGCTCAATTTGGGTTGTTGGTCACATGGAGCTCTTCCATTTCGTTTAGCTG AATAATGAGTTGTTCCTAGAGGAGACAGCAGCCTGTCTCTCCTGTTGCCCCCAAAGCCCATGCCCTGCCG TGGTGGCAGCTGGGGCTGTGGATGGGAGGGGTCCCAACATGGATGTGTTGCCCCCTCCTCCCGCATGCC AACGC[A/G]GTTCATGTCATGTACAAGGCCCCTCTGCAACTGGAGAGAAAATTA
NI-7146	202	G	A	GGGACGCCTGTTGTTTGGCTCAATTTGGGTTGTTGGTCACATGGAGCTCTTCCATTTCGTTTAGCTG AATAATGAGTTGTTCCTAGAGGAGACAGCAGCCTGTCTCTCCTGTTGCCCCCAAAGCCCATGCCCTGCCG TGGTGGCAGCTGGGGCTGTGGATGGGAGGGGTCCCAACATGGATGTGTTGCCCCCTCCTCCCGCAT[G/A]CCAACGCAGTTCATGTCATGTACAAGGCCCCTCTGCAACTGGAGAGAAAATTA
NI-7153	161	A	T	ATATTACAACTTGCTTTTAGCTGATCTCCATCCTCAAATGACTCTTTTTCTTTATATGTTAACATA TATAAAATGGCAACTGATAGTCAATTTTGATTTTATTCAGGAACTATCTGAAATCTGCTCAGAGCCT ATGTGCATAGATAGAAACNNNNNNNN[A/T]AAAAAAGTTATTTAACAGTAATCTATTTACTAATTAT AGTACCTATCTTAAAGTATACATTTACACATGTAAATGGTATGTT
NI-7155	156	T	G	TAGAATAGATGCGGTCATATCTTCTTGGCTTCTTCCAGCCCTCATGGTTGGCATCACATAT GCCTGCATGCCATTAACACCAGCTGGCCCTACCCCTATAATGATCCTGTGTCCTAAATTAATATACAC CAGTGGTTCCTCCTCCTGT[T/G]TAAAGACTAATGCTCAGATGCTGTTTACGGATATTTATATTCTAG TCTCACTCTCTGTCCCACCCTTCTCTTCTCTCTCCCAACTCCAG
NI-7169b	161	A	G	AGCTCCACCAGATGCAGATTTGTGTTTCTTGTTTCTTGTTATCACTGTCACACAGCTTATAAACATGTAT GCTTTTTCAGAATACAGTTGTCTAGCCAAGCCATCAAGTGTCTGAAATTCAATATTGGTTTATGCAAAT ACAGCAAAACTTTATTTAAGTAGAT[A/G]GGAGAATATGTTTAAAATATTAGGAATCCTAGACCATA TTTTCAAGTCATCTTAGCAGCTAGGATTCTCAAATGGAAGTGTTATATA
WI-7175b	194	C	T	CTCCTAGACTAGTGCTTTACCTTTATTAATGAACTGTGACAGGAAGCCCAAGGCAGTGTTCCTCACCA ATAACTTCAGAGAAGTCAGTTGGAGAAAATGAAGAAAAAAGGCTGGCTGAAAATCACTATAACCATC AGTTACTGGTTCAGTTGACAAAATATAATGGTTTACTGCTGTCATTGTCATGTGCCTA[C/T]AGAT AATTTATTTGTATTTTGAATAAAAAACATTTGTACATTCCTGATACTGGG

II-7175	194	C T	CTCCTAGACTAGTGCTTACCTTATTAATGAACTGTGACAGGAAGCCCAAGGCAGTGTTCCTCACCA ATAACTTACTGGTTCAGTTGACAAAGTCAGTTGGAGAAAATGAGAGAAAAGGCTGGCTGAAAATCACTATAACCATC AGTTACTGGTTCAGTTGACAAAATATATAAAAAACATTGTACATTCCTGCCTA[C/T]AGAT AATTTATTTGTATTTTGAATAAAAAACATTGTACATTCCTGATACTGGG
II-7178b	273	G A	TGTATCAGGTCAGGGACTTGGACAGGAGTCAGTGTCTGGCTTTTCCTCTGAGCCCAGCTGCCTGGAG AGGGTCTCGCTGTCACTGGCTGGCTCTAGGGGAACAGACCAGTGAAAAGCATAACACCA ATCCCAGGGCTGGCTCTGCACTAAGAGAAAATTGCACTAAATGAATCTCGTTCCCAAAGAACTACCC CCTTTTCAGCTGAGCCCTGGGGACTGTTCCAAAGCCAGTGAAATGTGAAGGAA
VI-7178	273	G A	TGTATCAGGTCAGGGACTTGGACAGGAGTCAGTGTCTGGCTTTTCCTCTGAGCCCAGCTGCCTGGAG AGGGTCTCGCTGTCACTGGCTGGCTCTAGGGGAACAGACCAGTGAACCCCAGAAAAGCATAACACCA ATCCCAGGGCTGGCTCTGCACTAAGAGAAAATTGCACTAAATGAATCTCGTTCCCAAAGAACTACCC CCTTTTCAGCTGAGCCCTGGGGACTGTTCCAAAGCCAGTGAAATGTGAAGGAA
VI-7182b	116	A C	GCATATTTGGCAGCTATTGCTTCGAAACCCAGCTGGTCACCAAAAGCTTGATATACAGAGAAGAAG AAGGCTCAAGAATTATTCACCAGTTCCTCTGCAACCCACTCTGAGCCTA[A/C]TCTCTCCTATTT TACTTGAGGCTGCCAATTACCAGCCCCACGTTTCAGCTCAAGAGATGCCTTAAGATAATTATGTGAGG CCACTTGGTAGCAAGAATGGCAGCTATTTCCTGAGCCTAGTACCCCAATT
			GCATATTTGGCAGCTTATTGCTTCGAAACCCAGCTGGTCACCAAAAGCTTGATATACAGAGAAGAAG AAGGCTCAAGAATTATTCACCAGTTCCTCTGCAACCCA[C/A]TCTGAGCCTATCTCTCCTCCTATTT TACTTGAGGCTGCCAATTACCAGCCCCACGTTTCAGCTCAAGAGATGCCTTAAGATAATTATGTGAGG CCACTTGGTAGCAAGAATGGCAGCTATTTCCTGAGCCTAGTACCCCAATT
VI-7182	106	C A	ATAATTGCTTGTGTTTCTAGCCTGGCAAGATATTTTCATAAAAGAGGATAACAATGCTGATTACTAC CTTTTAAAATATTTAGATAAATGCACAGCACCACACATCCTAAGCATTAGTGATGGGTAGC TGATGTCAGCTTCATGTGGATTTTAAGCACTCTAGAAACAATGAAGCTTCTTGGCATATTTAAGGAG CTCCCAAAATGTGTTACCTATTATAAATTGTAACTCAGCAAGTAGAAGACCATT
VI-7191b	273	T A	CCCAGTGGTGAACAGAACCTCCAAATTTGAGTTGCACCCTTCCCTGTGGCCTTATGAGCTCAGCCTC GCTTTGAGGTACCCACCGTCCTGTCCTCAGCTATGAGC[T/C]GGGGCCTGACTAGGAAAAGT TGGGAGTTAAGGAGGAAAATTAGCATTCCTTAATGTTTTGTTTGGTGCTCTGAATTTCTTCTTTATTAT AGTCCTATAGTTTTACTCCTCAGTTCCTCACCATCATCTTGTCTAA
VI-7199c	112	T C	CCCAGTGGTGAACAGAACCTCCCAAATTTGAGTTGCACCCTTCCCTGTGGCCTTATGAGCTCAGCCTC GCTTTGAGGTACCCACCGTCCTGTCCTCAGCTATGAGC[T/C]GGGGCCTGACTAGGAAAAGT TGGGAGTTAAGGAGGAAAATTAGCATTCCTTAATGTTTTGTTTGGTGCTCTGAATTTCTTCTTTATTAT AGTCCTATAGTTTTACTCCTCAGTTCCTCACCATCATCTTGTCTAA
VI-7199b	112	T C	

			Sequence
WI-7216c	237	T C	TGACACTAACACTCTAATTCAAGCGAATGTTGGAACACCATGACCTCCTCTGTGTGTCCTTTCTCCCCAAGGACAAAAATGTAGAAAGATGTGAGATAACTTACTCAAGATTCCCCTCCACTAAAATACGTATGTTTAAAAACCCTTCCTGCTATACATAGGAAAAGACACACAGTTTGTTT[T/C]CTTGTAATCACTT
WI-7216b	237	T C	TGACACTAACACTCTAATTCAAGCGAATGTTGGAACACCATGACCTCCTCTGTGTGTCCTTTCTCCCCAAGGACAAAAATGTAGAAAGATGTGAGATAACTTACTCAACACATCCCCTCCAGAAAAATACGTATGTTTAAAAACCCTTCCTGCTATACATAGGAAAAGACACACAGTTTGTTT[T/C]CTTGTAATCACTT
WI-7220b	147	A T	AGGATGATGCTCCAAAGGGGACCTTGAACCTATTCACCATTATTGTCTCTTTAAGCTGGCAAACCCATCATTAAATAGCACATAAAATAGCAATCATATGGGATAAGTAGTACAGCTTCAGTAATCAATGGGCAGTGGCACTAGAA[A/T]AATCTTGAGCACAGTGAATGACCTATCCTGCAAACATCTAATGGATCTCTAAAGGGTAACAAACCCTATAAATTCTGGCTTACTGCACATATTTAGTGTGTTT
WI-7220	140	A T	AGGATGATGCTCCAAAGGGGACCTTGAACCTATTCACCATTATTGTCTCTTTAAGCTGGCAAACCCATCATTAAATAGCACATAAAATAGCAATCATATGGGATAAGTAGTACAGCTTCAGTAATCAATGGGCAGTGGC[A/T]CTAGAAAAATCTTGAGCACAGTGAATGACCTATCCTGCAAACATCTAATGGATCTCTAAAGGGTAACAAACCCTATAAATTCTGGCTTACTGCACATATTTAGTGTGTTT
WI-7226	232	C	GATCGAATTTTCAGATGATTCGGAAATTTCATTCAGGTATTGTAATAGTGACATATATATGTATATACATATCACCTCCTATTCTCTTAATTTTGTTAAAATGTCAGTAAGTCTTTTTGATCATTCCCTTTCCATATAGGAAACATAATTTGAAGTGGCCAGATGAGTTTATCATGTCAGTGAAAAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTT
WI-7228b	254	G A	ATAGCTTCCAGATTACAAAGGCCAAGGGTAATAGAAATGCATACCAGTAATTGGCTCCAATTCATAATATGTTCACCAGGAGATTACAATTTTTGCTCTTCTTGTCTTTGTAATCTATTAGTTGATTTAATTACTTTCTGAATAACGGAAGGGATCAGAAGATATCTTTGTGCCTAGATTGCAAAATCTCCAATCCACACATATTGTTTTAAAATAAGAAATGTTATCCAACTATTAAGATATCTCAATGT
WI-7228a	163	G A	ATAGCTTCCAGATTACAAAGGCCAAGGGTAATAGAAATGCATACCAGTAATTGGCTCCAATTCATAATATGTTCACCAGGAGATTACAATTTTTGCTCTTCTTGTCTTTGTAATCTATTAGTTGATTTAATTACTTTCTGAATAACGGAAGGGATCAGAA[G/A]ATATCTTTGTGCCTAGATTGCAAAATCTCCAATCCACACATATTGTTTAAAATAAGAAATGTTATCCAACTATTAAGATATCTCAA
WI-7233c	213	C T	CGATCGTACTGCCAGTAGCATTGTCTGTGTCCGGTCTGTTTGTACATTCCATTTCAATTGTTACAGATGTGAACTTTATTCCTTGTCACTAATTATATTTAAAATTAATTTCTAGGAAGTCAAAAAAATATAATAAAGGGTTGAGCCCTCTACTTTCTTCTTGCCACCTTTTTGTGGCAATATTAAAGTGAACTGCTAATAGTGTAAGTA[C/T]GTGCACAAAACCACTGCCAGATAACCAGAGGGCCTG

VI-7233b	213	C T	CGATCGTACTGCCAGTAGCATTGTCTGTCTGTCCGGTCTTGTTGTACATTCCATTTCAATTTCAATTGTTACA GATGTGAACTTATTCCTTGTCACTAATTATTTAAAATTATTCTAGGAAGTCAAAAAATATAA TAAAGGGTTGAGCCCTCTACTTTCTTCTGCCACCTTTTGTGCAATATTAAAGTGAACTGCTAATA GTGTAAGTA[C/T]GTGCACAAAACCACTGCCAGATAACCAGAGAGGGCCTG
VI-7233	211	T C	CGATCGTACTGCCAGTAGCATTGTCTGTCTGTCCGGTCTTGTTGTACATTCCATTTCAATTTCAATTGTTACA GATGTGAACTTATTCCTTGTCACTAATTATTTAAAATTATTCTAGGAAGTCAAAAAATATAA TAAAGGGTTGAGCCCTCTACTTTCTTCTGCCACCTTTTGTGCAATATTAAAGTGAACTGCTAATA GTGTAAG[T/C]ACGTGCACAAAACCACTGCCAGATAACCAGAGAGGGCCTG
NI-7238	128	T C	GCGTCTACAGACAGCTCACCATTTTGTCCTGTATCTGTAAACACTTTTTGTTCTTAGTCTTTTTCTTG TAAAATTGATGTTCTTTAAAATCGTTAATGTATAACAGGGCTTATGTTTTTCAGTTTGTTT[T/C]CCGTT CTGTTTAAACAGAAAATAAAAGGAGTGTAAGCTCCTTTCTCATTCAAAGTTGCTACCAGTGTAT GCAGTAATTAGAACAAAGAAGAAACATTCAGTAGAACATTTTATTGCCTA
NI-7252f	520	T C	CCACCAGGATCCCAGCCCAAGCGGCCCCTCCCGCCCACTCGCAGCAGACGCCGGGGACAGAG GCCTGCCCGGCGCGCGCAGCGCCCCCTGGGCTGGGCCCCCTGGTCTCTGGTCCG GACACTCCTAGAGAACGCAGCCCTAGAGCCTGGGTTTCTAGCAAGTCAGTACTCCTCCTCCA CTCCTCTCCTGGAGGATGCAGGTGGAACTCAGTCATTAGACTCCTCTCCA
NI-7252e	552	T C	CCACCAGGATCCCAGCCCAAGCGGCCCCTCCCGCCCACTCGCAGCAGACGCCGGGGACAGAG GCCTGCCCGGCGCGCGCAGCGCCCCCTGGGCTGGGCCCCCTGGTCTCTGGTCCG GACACTCCTAGAGAACGCAGCCCTAGAGCCTGGGTTTCTAGCAAGTCAGTACTCCTCCTCCA CTCCTCTCCTGGAGGATGCAGGTGGAACTCAGTCATTAGACTCCTCTCCA
NI-7252d	540	T C	CCACCAGGATCCCAGCCCAAGCGGCCCCTCCCGCCCACTCGCAGCAGACGCGGGGACAGAG GCCTGCCCGGCGCGCGCAGCGCCCCCTGGTCTCTGGTCCG GACACTCCTAGAGAACGCAGCCCTAGAGCCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACTCAGTCATTAGACTCCTCTCCA
WI-7252c	552	T C	CCACCAGGATCCCAGCCCAAGCGGCCCCTCCCGCCCACTCGCAGCAGACGCGGGGACAGAG GCCTGCCCGGCGCGCGCAGCGCCCCCTGGTCTCTGGTCCG GACACTCCTAGAGAACGCAGCCCTAGAGCCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACTCAGTCATTAGACTCCTCTCCA
WI-7252b	540	T C	CCACCAGGATCCCAGCCCAAGCGGCCCCTCCCGCCCACTCGCAGCAGACGCGGGGACAGAG GCCTGCCCGGCGCGCGCAGCGCCCCCTGGTCTCTGGTCCG GACACTCCTAGAGAACGCAGCCCTAGAGCCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACTCAGTCATTAGACTCCTCTCCA

WI-7252a	520	T	C	CCACCAGGATCCCAGCCCAGGGCCCCTCCCGCCCCTTCCCACTCGCAGCAGAGCGGGGACGCGGGGACAGAG GCCTGCCCGGGGCCGGGGCCGGGGCCTGGCCTCGGCCTGCGGGGCTGCGGGGCCCCTGGTCTCTGGTCCG GACACTCCTAGAGAACGCAGCCCTAGAGCCGTTCTCAGCAAGTGAGAGAGGATGGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACTCAGTCATTAGACTCCTCCTCCA
WI-7265m	252	T	A	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAAGGCATGCTATGTGTTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTCACCCATTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTGTTTATATTATGTAAAATATAACGATCTCTT AAAAATACCACCAGTTTGTATTTTTCTT[T/A]AAGGAGTAAAGATTTGCCTTT/
WI-7265l	231	T	A	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAAGGCATGCTATGTGTTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTCACCCATTCTGTGGTTCATTGTAGTT GTTTAAGGAAACCAAGCATATAGATGCATTAGTGATTTGTTTATATTATGTAAAATATAACGATCTCTT AAAAATACCACCAGTTTGTATTTTTCTT[T/A]AAGGAGTAAAGATTTGCCT
WI-7265k	121	T	G	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAAGGCATGCTATGTGTTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTCACCCATTCTGT[T/G]GGTTCATTGTA GTTTAAGGAAACCAAGCATATAGATGCATTAGTGATTTGT[T/A]TATATTATGTAAAATATAACGATCT CTTAAAAATACCACCAGTTTGTATTTTTCTTTCTTTAAGGAGTAAAGATTTGCCT
WI-7265j	174	T	A	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAAGGCATGCTATGTGTTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTCACCCATTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTGTTTATATTATGTAAAATATAACGATCTCTT AAAAATACCACCAGTTTGTATTTTTCTT[T/C]CTTAAGGAGTAAAGATTTGCCT
WI-7265i	227	T	C	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAAGGCATGCTATGTGTTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTCACCCATTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTGTTTATATTATGTAAAATATAACGATCTCTT AAAAATACCACCAGTTTGTATTTTT[T/C]CTTAAGGAGTAAAGATTTGCCT
WI-7265h	80	T	A	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAAGGCATGCTATGTGTTACGTGTTT TTTCCAGTATGT[T/A]ATTTGCCACCAAAAAGTCATTTCACCCATTCTGTGGTTCATTGTA GTTTAAGGAAACCAAGCATATAGATGCATTAGTGATTTGTTTATATTATGTAAAATATAACGATCT CTTAAAAATACCACCAGTTTGTATTTTTCTTTAAGGAGTAAAGATTTGCCT
WI-7265g	170	T	G	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAAGGCATGCTATGTGTTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTCACCCATTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTG[T/G]TGTTTATATTATGTAAAATATAACGATCT CTTAAAAATACCACCAGTTTGTATTTTTCTTTCTTTAAGGAGTAAAGATTTGCCT

NI-7265f	231	T	A	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAAGGCATGCTATGTGTTACGTGTTT TTTCCAGTAGTGTTTATTTGCCACCAAAAAGTAAATGCATTTCACCCATTCTGTGGTTCATTGTGAGTT TAAGGAAAACCAAGCATATAGATGCATTTGTATTTTTCTTT[T/A]AAGGGAGTAAAGATTTGCCT AAAAATACCACCAGTTTGTATTTTTCTTT[T/A]AAGGGAGTAAAGATTTGCCT
NI-7265e	227	T	C	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAAGGCATGCTATGTGTTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTCACCCATTCTGTGGTTCATTGTGAGTT TAAGGAAAACCAAGCATATAGATGCATTAGTGCATTTTGTTTTATATTATGTAAAATATAACGATCTCTT AAAAATACCACCAGTTTGTATTTTT[T/C]CTTAAGGGAGTAAAGATTTGCCT
WI-7265d	174	T	A	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAAGGCATGCTATGTGTTACGTGTTT TTTCCAGTATGTGTTTATTTGCCACCAAAAAGTAAATGCATTTCACCCATTCTGTGGTTCATTGTGAGTT TAAGGAAAACCAAGCATATAGATGCATTAGTGCATT[T/G]TGTTTATATTATGTAAAATATAACGATCT CTTAAAAATACCACCAGTTTGTATTTTTCTTTAAGGGAGTAAAGATTTGCCT
WI-7265c	170	T	G	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAAGGCATGCTATGTGTTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTCACCCATTCTGTGGTTCATTGTA GTTTAAGGAAAACCAAGCATATAGATGCATTAGTGCATTTTGTTTATATTATGTAAAATATAACGATCT CTTAAAAATACCACCAGTTTGTATTTTTCTTTAAGGGAGTAAAGATTTGCCT
WI-7265b	121	T	G	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAAGGCATGCTATGTGTTACGTGTTT TTTCCAGTATGT[T/A]TATTTGCCACCAAAAAGTAAATGCATTTCACCCATTCTGTGGTTCATTGTA GTTTAAGGAAAACCAAGCATATAGATGCATTAGTGCATTTGTTTATATTATGTAAAATATAACGATCT CTTAAAAATACCACCAGTTTGTATTTTTCTTTAAGGGAGTAAAGATTTGCCT
WI-7265a	80	T	A	---	GATCACCCCAGCCACAAGCCCTTCGAGGGCCCTATACCATGGCCCACCTTGGAGCAGAGAGCCAAGC ATCTTCCCTGGGAAGTCTTTCTGGCCAAGTCTCGGCCCTGCCAGTCTCCCATGGAAGGCCA CCCCATGGTCTGATGGGCATGAAGCATCTCAGACTC[C/A]TTGGCAAAAACGGAGTCCGCAGGCCGCAG GTGTTGTGAAGACCACTCGTTCTGTGGTTGGGGTCCTGCCT
WI-7281b	183	C	---		GATCACCCCAGCCACAAGCCCTTCGAGGGCCCTATACCATGGCCCACCTTGGAGCAGAGAGCCAAGC ATCTTCCCTGGGAAGTCTTTCTGGCCAAGTCTCGGCCCTGCCAGTCTCCCATGGAAGGCCA CCCCATGGTCTGATGGGCATGAAGCATCTCAGACTC[C/A]TTGGCAAAAACGGAGTCCGCAGGCCGCAG
WI-7281	171	C	A	---	CAGGTGTTGTGAAGACCACTCGTTCTGTGGTTGGGGTCCTGCAAGAAGGCCT

I-7282b	159	G	C	---	TGTCACCTGGCACATTCATTTTCTCAGTTGAAGAAGAGAAAATTTGAAAAATGTCCTTATGCTTTTAGA GTTGCAACTTAAGTATATTTGGTAGGTGGTGAGTGTTCCACTCAAAATGTGTCAACTTNNNNNNNNNT AGGCCCTTTCATAAAACCAAACT[G/C]TAGCAAGATGCAAATGCATGGCAAATCTGTCGGTCTCCA GTTGGTTATCTGAATAGTGTCACCAATTCCACCAAGACACAGTGCTGAGATTGG
I-7292	92	T	C	---	CTTGATTACTTCCACTGAGGTGGGGAGCATCTCCAGTGCTCCCCAATTATATCTCCCCCACTCCACTAC TCTCTTCCTCCCACTTCATTTTCCT[T/C]TTGTCCTTCTTCTCTCAATTCAGTGTTTTGGAGGCCTGACTTG GGGACAACGTATTATTGATATTATTGTCTGTTTTCCTTCTTCCCAATAGAAGAATAAGTCATGGAGCC TGAAGGGTGCCTAGTTGACTTACTGACAAAAGGCTCTAGTTGGGCTGA
I-7301f	133	A	G	---	AACTATGGCAGTGGTCCTGGTTATAGTAGTAGAGAGCGGGTATGGTGGTGGACCAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTGTTGGAGGATATGGTGGTTACAATGAAGGAGGAAATTTTG[A/G]CGGTAGTAACTATGGTGGTGGTGGGAAACTATAATGATTTTGGAAATTACAGTGGACAACAGCA ATCAAATTATGGACACATGAAACATGAAAGCTCGGGCAG
I-7301e	94	T	G	---	AACTATGGCAGTGGTCCTGGTTATATAGTAGTAGAGAGCGGGTATGGTGGTGGACCAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTG[T/G]TGGAGGATATGGTGGTTACAATTACAGTGGACAACAGCAA TGACGGTAGTAACTATGGTGGTGGTGGGAAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAA TCAAATTATGGACACATGAAAGGGGGCAGTTTTGGTGGAAGAAGCTCGGGCAG
I-7301d	138	A	G	---	AACTATGGCAGTGGTCCTGGTTATAGTAGTAGAGAGCGGGTATGGTGGCGGTGTTGGAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTGTTGGAGGATATGGTGGTTACAATGAAGGAGGAAATTTTGA CGGT[A/G]GTAACTATGGTGGTGGTGGGAAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAA TCAAATTATGGACACATGAAAGGGGGCAGTTTTGGTGGAAGAAGCTCGGGCAG
I-7301c	211	A	C	---	AACTATGGCAGTGGTCCTGGTTATAGTAGTAGAGAGCGGGTATGGTGGCGGTGTTGGAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTTGA CGGTAGTAACTATGGTGGTGGTGGGAAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAATCA AATTATGGAC[A/C]CATGAAAGGGGGCAGTTTTGGTGGAAGAAGCTCGGGCAG
I-7301b	182	C	T	---	AACTATGGCAGTGGTCCTGGTTATAGTAGTAGAGAGCGGGTATGGTGGTGGACCAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTGA CGGTAGTAACTATGGTGGTGGTGGGAAACTATAATGATTTTGGAAATTA[C/T]AGTGGACAACAGCAA TCAAATTATGGACACATGAAAGGGGGCAGTTTTGGTGGAAGAAGCTCGGGCAG
I-7301	88	G	T	---	AACTATGGCAGTGGTCCTGGTTATAGTAGTAGAGAGCGGGTATGGTGGTGGACCAGGATATGGAA ACCAAGGTGGTGGATATGGTG[G/T]CGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTT TGACGGTAGTAACTATGGTGGTGGTGGGAAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAA TCAAATTATGGACACATGAAAGGGGGCAGTTTTGGTGGAAGAAGCTCGGGCAG

VI-7301	205	A C	AACTATGGCAGTGGTCCTGGTTATAGTAGTAGAGAGGCGGGGTATGGTGGTGGTGTGGGACCAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTTGA CGGTAGTAACTATGGTGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAATCA AATT[A/C]TGGACACATGAAGATGAGGGGCCAGTTTGGTGTGGGAAGAAGCTCGGGCAG
NI-7314c	49	G A	CTCTCCTTTTTCTTCAGATCTGCTCCTGGGTTTAATTGGGAGGTCA[G/A]TTGTTCTACCTCACTG AGAGGGAACAGAAGGATATTGCTTCCTTTGCAGCAGTGTAATAAAGTCAATTAAAAACTTCCCAGG ATTTCTTTGGACCCAGGAAACAGCCAGGGGTCCTTCGTCTGTGCACTATGAACGCTTCTTTCCCAGGA CAGAAAATGTGTAGTCTACCTTTATTTTTTATTAACAAAACTTGTTTTT
NI-7314b	49	G A	CTCTCCTTTTTCTTCAGATCTGCTCCTGGGTTTAATTGGGAGGTCA[G/A]TTGTTCTACCTCACTG AGAGGGAACAGAAGGATATTGCTTCCTTTGCAGCAGTGTAATAAAGTCAATTAAAAACTTCCCAGG ATTTCTTTGGACCCAGGAAACAGCCAGGGGTCCTTCGTCTGTGCACTATGAACGCTTCTTTCCCAGGA CAGAAAATGTGTAGTCTACCTTTATTTTTTATTAACAAAACTTGTTTTT
WI-7314	36	A G	CTCTCCTTTTTCTTCAGATCTGCTCCTGGGTTTA[A/G]TTGGGAGGTCAGTTGTTCTACCTCACTG AGAGGGAACAGAAGGATATTGCTTCCTTTGCAGCAGTGTAATAAAGTCAATTAAAAACTTCCCAGG ATTTCTTTGGACCCAGGAAACAGCCATGGGTCCTTCGTCTGTGCACTATGAACGCTTCTTTCCCAGGA CAGAAAATGTGTAGTCTACCTTTATTTTTTATTAACAAAACTTGTTTTT
WI-7321b	199	C T	ACTCAGGGAAGGGGATGCCCCATTAAAGTGACAAAAGGGTGGGGTGTGGGCACCATGGCATGAGGAAG AAACAAGGTCCCTGAGCAGGCACAGTCCTGACGGTCAAGGGACTGCTTTGGCATCCAGGGCCTCCA GTCACCTCACTGCCCATACATTAGAAATGAGACAATCAAAGNNNNNNNNNNAGGGTGGCACCACCATC[C /]TGTTTGCTGGGGTGTGGGCAGCCACATCCAAGACTGGAGCAGCAGGCTGGCCA
WI-7321	199	C T	ACTCAGGGAAGGGGATGCCCCATTAAAGTGACAAAAGGGTGGGGTGTGGGCACCATGGCATGAGGAAG AAACAAGGTCCCTGAGCAGGCACAGTCCTGACGGTCAAGGGACTGCTTTGGCATCCAGGGCCTCCA GTCACCTCACTGCCCATACATTAGAAATGAGACAATCAAAGNNNNNNNNNNAGGGTGGCACCACCATC[C /]TGTTTGCTGGGGTGTGGGCAGCCACATCCAAGACTGGAGCAGCAGGCTGGCCA
WI-7336b	248	A C	AGACATTCTCGCTTCCCTGAAAGACTGAAGAAAGTGTAGTGCATGGGACCCACGAAACTGCCCTGGC TCCAGTGAAACTTGGGCACATGCCAATGAAGTCCTCAGCTACTATAGGTCCAGAAGTCCTTATGTTAAGCCCTGGCAG GCAGGTGGTTTTTAAAATTCTGAATTTGGGGATTTCAAAAGATAATATTTTACATACACTGTATGT TATAGAACTTCATGGATCAGATCTGGGGCAGCAACCTATAAATCA[A/C]CA
WI-7338c	221	A G	CTCTTCTCAGCACATTGATGGGCAACTAGAATTACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTCACATGCCAATGACTACTAGGTGCAAAGAATATTGGCAAAAGGTGCTTTACCTTGAGC CATTATTTGTGTCAGAGAACAAAACAGAATCAATATATAAATTCAAAGACTATCTGCAGCTA GTGTGTTTCTTCTTTACACAC[A/G]TATACACACAGACATCAGAAAATTCTGTT

VI-7338b	125	A C	CTCTTTCTCAGCACATTGATGGGCAACTAGAATTACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAAGAATATTGGCAAAAGGTGCTTT[A/C]CCTTG AGCCATTATTTGTGTCAGAGAACAAAAGAACACAGATCAATATATAAATTCAAAGACTATCTGCAG CTAGTGTGTTCTTCTTCTTACACACATATACACACAGACATCAGAAAATTCTGTT
VI-7338	125	A C	CTCTTTCTCAGCACATTGATGGGCAACTAGAATTACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAAGAATATTGGCAAAAGGTGCTTT[A/C]CCTTG AGCCATTATTTGTGTCAGAGAACAAAAGAACACAGATCAATATATAAATTCAAAGACTATCTGCAG CTAGTGTGTTCTTCTTCTTACACACATATACACACAGACATCAGAAAATTCTGTT
VI-7338	221	A G	CTCTTTCTCAGCACATTGATGGGCAACTAGAATTACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAAGAATATTGGCAAAAGGTGCTTTACCTTGAGC CATTATTTGTGTCAGAGAACAAAAGAACACAGATCAATATATAAATTCAAAGACTATCTGCAGCTA GTGTGTTCTTCTTCTTACACAC[A/G]TATACACACAGACATCAGAAAATTCTGTT
NI-7384c	146	T A	CCTATGTCAATGAAATGCTAGGGGGCCAGGGAAACAAAATTTAAAATAATAAAATTCACCATAG CAATACAGAATAACTTAAAATACCATTAAATACATTGTATTCATTGTGAACAGGTATTCTTCA CAGATCTCATTT[T/A]AAAATTCTTAATGATTATTTTATTACTTACTGTGTTTAAAGGGATGTTA TTTTAAAGCATATACCATACACTTAAGAAATTTGAGCAGAATTTAAAAAAGAA
NI-7384b	146	T A	CCTATGTCAATGAAATGCTAGGGGGCCAGGGAAACAAAATTTAAAATAATAAAATTCACCATAG CAATACAGAATAACTTAAAATACCATTAAATACATTGTATTCATTGTGAACAGGTATTCTTCA CAGATCTCATTT[T/A]AAAATTCTTAATGATTATTTTATTACTTACTGTGTTTAAAGGGATGTTA TTTTAAAGCATATACCATACACTTAAGAAATTTGAGCAGAATTTAAAAAAGAA
WI-7384	145	T A	CCTATGTCAATGAAATGCTAGGGGGCCAGGGAAACAAAATTTAAAATAATAAAATTCACCATAG CAATACAGAATAACTTAAAATACCATTAAATAAATGATTATTTTATTACTTACTGTGTTTTCTTCA CAGATCTCATTTTAATGATTCTTAATGATTATTTTATTACTTACTGTGTTTAAAGGGGATGTTA TTTTAAAGCATATACCATACACTTAAGAAATTTGAGCAGAATTTAAAAAAGAA
WI-7388c	106	A T	TGAAATCCTGGGTCTCTTGGCCTGTCCTGTAGCTGGTTTATTTTACTTTGCCCCTCCCCACTTTTT TGAGATCCCATCCTTTATCAAGAAGTCTGAAGCGACT[A/T]TAAAGGTTTTGAATTCAGATTTAAAA ACCAACTTATAAAGCATTGCAACAAGGTTACCTCTATTTGCCACAAGCGTCTCGGGATTGTGTTTGA CTTGTGTCTGTCGTCCAAGAACTTTTCCCCCAAGATGTGTATAGTTATTGG
WI-7388b	106	A T	TGAAATCCTGGGTCTCTTGGCCTGTCCTGTAGCTGGTTTATTTTTACTTTGCCCCTCCCCACTTTTTT TGAGATCCCATCCTTTATCAAGAAGTCTGAAGCGACT[A/T]TAAAGGTTTTGAATTCAGATTTAAAA ACCAACTTATAAAGCATTGCAACAAGGTTACCTCTATTTGCCACAAGCGTCTCGGGATTGTGTTTGA CTTGTGTCTGTCGTCCAAGAACTTTTCCCCCAAGATGTGTATAGTTATTGG

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NI-7388	94	T	A	TGAAATCCTCGGGTCTCTTGGCCTGTCCTGTAGCTGGTTTATTTTTACTTTGCCCCTCCCCACTTTTTT TGAGATCCATCCTTTATCAAGAAG[T/A]CTGAAGCGACTACTAAAAGGTTTTGAATTCAGATTTAAAA ACCAACTTATAAAGCATTGCAACAAGGTTACCTCTATTTGCCACAAGGCGTCTCGGGATTGTGTTTGA CTTGTGTCTGTCCAAGAACTTTCCCCCAAAGATGTGTATAGTTATTGG
NI-7438	64	A	G	TTAGATTTTAATTGGCAACCAGCAACTCCACTGCCACCATTCCACTGCCGAGATCTNCTATTCCTGG[A/G] GTTGATATGACAAGGAAACCCTATTGGAACCAAGTCTTCACATTGTNCCATGTGCAGACAGGCTCCT TGTCTGTAGGTGTAGTAGCATGTACACTGTACTGTTCACTGTAACATAGTTGTNCTGGTATTTGTTA TTGGAAATGAATATCGCTTCCACTGACTTTACCA
NI-7454b	152	T	C	CCATGATCCCCTCCTTGCCAAATGGAGGAAGCCTGTGGATGGTACCAACAACAAGCCCCAAACC CAGTACAAACTGAGAAATGAGAGAACCCTGATAGCACTGTCTGAATTGCCAGGAGCCTCCAAGGCTAA TCCTACCCCCTGGATTCTT[T/C]TGTTGTTAAGTTATTCTAGCCACCACAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAAATCCCATTTGTCTACTTCTCAAATGTTTTTGACA
WI-7454	152	T	C	CCATGATCCCCTCCTTGCCAAATGGAGGAAGCCTGTGGATGGTACCAACAACAAGCCCCAAACC CAGTACAAACTGAGAAATGAGAGAACCCTGATAGCACTGTCTGAATTGCCAGGAGCCTCCAAGGCTAA TCCTACCCCCTGGATTCTT[T/C]TGTTGTTAAGTTATTCTAGCCACCACAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAAATCCCATTTGTCTACTTCTCAAATGTTTTTGACA
WI-7464c	177	G	C	AATTTGAAAAATCTGAAAAAAAGTGCATAAGCAGAGAAATGACACTTATTCCAAATAAATAAATTGT CCATTTTTCACTCAGTCCATCTCAACCATGTACAATGCACTAAATTACTATTTATAATTCCTATGTA CAACAGAGCCACAGCCACAGAGGGTGGGCATAAGCAGTTGCCA[G/C]CCAGAAGAGCTTCACTCAT GAAAGAAAAGCCCTACAAATAGGCCCAGGAGAAGCAACGTTCACCAACAATTAT
WI-7464b	168	C	A	AATTTGAAAAATCTGAAAAAAAGTGCATAAGCAGAGAAATGACACTTATTCCAAATAAATAAATTGT CCATTTTTCACTCAGTCCATCTCAACCATGTACAATG[C/A]ACTAAATTACTATTTATAATTCCTATGTA CAACAGAGCCACAGCCACAGAGGGTGGGCATAAG[C/A]AGTTGCCAGCCAGAAGAGCTTCACTCAT GAAAGAAAAGCCCTACAAATAGGCCCAGGAGAAGCAACGTTCACCAACAATTAT
WI-7464a	103	C	A	AATTTGAAAAATCTGAAAAAAAGTGCATAAGCAGAGAAATGACACTTATTCCAAATAAATAAATTGT CCATTTTTCACTCAGTCCATCTCAACCATGTACAATG[C/A]ACTAAATTACTATTTATAATTCCTAT GTACAACAGAGCCACAGCCACAGAGGGTGGGCATAAGCAGTTGCCAGCCAGAAGAGCTTCACTCAT GAAAGAAAAGCCCTACAAATAGGCCCAGGAGAAGCAACGTTCACCAACAATTAT
WI-7499b	134	T	G	CAATTCTCAATCCAACCTAGTCTGTNTGCCTAAACCATTCCAGACAAACTTCCACTTCGAAGGTTTA AATGCATAAGTCAGATAGCAATCCTTCATTTAGCAATCAGTGAGGCAATACACTGGCCACTCACGTTCTT /G]TATAGTCCTCTTCATTAGCAATCAGTGAGGCAATACACTGGCCATCATGATCCCTTTTTTAGGA ACTCTGTACAAAATTCCCTTGAAAATATAAATTTGGAAATGAGTGATGA

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WI-7499a	33	A G	CAATTCTCAATCCAACCTAGTCTGTNTGCCTAA[A/G]CCATTCCAGACAAACTTCCACTTCGAAGGTT TTAAATGCATAAGTCAGATAGCAATCCTTCAGTTGCCCCAGAGGCACATCACGTTCTTGAATGCTTC ATTATAGTCCTCTTCATTTAGCAATCAGTGAGGCAATACACTGGCATCATCATGATCCCTTTTTTAGGAA CTCTGTACAAATTCCCTTTGAAATATAAATTTGGAAATGAGTGATGA
WI-7506b	118	A C	TGGGAATAGTAAGAGAGAAAGATGGGAAAGGTGACCAAAAACAATATAGAGGCAGAGGCCAAGTGAAT GCATCCCAGCAGCAGACCACTTNAAAGTCCTGTGGTGCTGCTAGC[A/C]GGAGAGTTGAG TGCCCACAGGTAAGAATGAGTGAAGAGGAAAAAATCATGATGTCAGTAATTACTATGTCA GAAGAAAATATTTAAAATATTGGACCACTCTTGTTCTACCATCCCTACCCACT
WI-7506	118	A C	TGGGAATAGTAAGAGAAAGATGGGAAAGGTGACCAAAAACAATATAGAGGCAGAGGCCAAGTGAAT GCATCCCAGCAGCAGACCACTTNAAAAGTAGTCCTGGTGCTGCTAGC[A/C]GGAGAGTTGAG TGCCCACAGGTAAGAATGAGTGAAGAGGAAAAAATCATGATGTCAGTAATTACTATGTCA GAAGAAAATATTTAAAATATTGGACCACTCTTGTTCTACCATCCCTACCCACT
WI-7534b	143	C T	TGTGAATTCTTAGCTCTGGAAGGTGTTATGCCTTTGCGGGTTTCTTGATGTGTTCGCAGTGTCACCCA AGAGTCAGAACTGTACACATCCCAAATTTGGTGGCCGTGGAACACATTCCCGGTGATAGAATTGCT AAATTGT[C/T]GTGAAATAGGTTAGAATTTCTTAAATTATGGTTTCTTATTCGTGAAAATTCGG AGAGTGCTGCTAAAATTGGATTGGTGTGATCTTTTTGGTAGTTGTAATTT
WI-7534	135	T C	TGTGAATTCTTAGCTCTGGAAGGTGTTATGCCTTTGCGGGTTTCTTGATGTGTTCGCAGTGTCACCCA AGAGTCAGAACTGTACACATCCCAAATTTGGTGGCCGTGGAACACATTCCCGGTGATAGAATTGC[T /C]AAATTGTCGTGAAATAGGTTAGAATTTCTTAAATTATGGTTTCTTATTCGTGAAAATTCGG AGAGTGCTGCTAAAATTGGATTGGTGTGATCTTTTTGGTAGTTGTAATTT
WI-7543b	162	G A	GGGAAAGAATAAAATTAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGGAGACTTTGAAGACC AGTCCTGTTTGCAGGGGAAGCCCCACTTGCTCTT[G/A]GGAAGAACAGCCAGCTTGCAGTGACGACAGCTTGAGTGGTT TAGAATTGCATGCCCTCAGATTATTTTCCTCTGGCTCCTTGGATGTTAGTCAGTTA CTCTGCAGCCCTCAGATTATTTTCCTCTGGCTCCTTGGATGTTAGTCAGTTA
WI-7543	162	G A	GGGAAAGAATAAAATTAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGGAGACTTTGAAGACC AGTCCTGTTTGCAGGGGAAGCCCCACTTGCTCTT[G/A]GGAAGAAGTCTAAGAGTAGGTGTGACTTGAAC TAGAATTGCATGCTTCCTCCTTGTCTT[G/A]GGAAGAACAGCCAGCTTGCAGTGACGACAGCTTGAGTGGGTT CTCTGCAGCCCTCAGATTATTTTCCTCTGGCTCCTTGGATGTTAGTCAGTTA
WI-7555c	60	T C	GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCCTCAAAATTTGTAGAGG[T/C]CTA AAAAGAAAGTGGTATGTTGTGTGATGAAGTCCTGCATTCCTGTAAAGCCACTGGGGTC ATAAGAAGGGAAGTAAAAATGAAGTCTGACTAGAAATTCTATTGCAGAGGCCAAGTACATTTAGT ATGGCATTGAGTTGTGATATAGTTTCATTTGATGTGCATTTGAATTCAG

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NI-7555b	60	T	C	GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCCTCAAAATTTGTAGAGGG[T/C]TCTA AAAAGAAAGTGGTATGTTGTGATGATCAGCACTAAGTCCTGCATTCCTGTTAAAGCCACTGGGTC ATAAGAAGGGAAGTAAAAAATGAAGTCTGACTAGAAATTCTATTGCAGAAGTACATTTAGT ATGGCATTGAGTTGTGATATAGTTTTCATTTGATGTGCATTTGAATTTCAG
NI-7555	60	T	C	GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCTCAAAATTTGTAGAGGG[T/C]TCTA AAAAGAAAGTGGTATGTTGTGTGATGATCAGCACTAAGTCCTGCATTCCTGTTAAAGCCACTGGGTC ATAAGAAAGGGAAGTAAAAAATGAAGTCTGACTAGAAATTCTATTGCAGAAGTACATTTAGT ATGGCATTGAGTTGTGATATAGTTTTCATTTGATGTGCATTTGAATTTCAG
WI-7567b	290	G	T	TGAGCCATCACTAGAAGAAAAAGCCCATTTCAACTGCTTTGAAAACTTGCCTGGGGTCTGAGCATGAT GGGAATAGGGAGACACAGGGTAGGGAAAGGGCGCCTACTCTTCAGGGTCTAAAGATCAAGTGGGCCTTGG ATCGCTAAGCTGGCTCTGTTGATGCTATTATGCAAGTTAGGGTCTATGTATTTAGGATGCGCCTAC TCTTCAGGGTCTAAAGATCAAGTGGGCCTTGGATCGCTAAGCTGGCTCTGTTT
WI-7569b	63	T	C	AATGTATCCCCTTTCGGTCCAACAACAGGAAACCTGACTGGGGCAGTGGGCAGTGAAGGAAGGGATGGCA[T/C] AGCGTTATGTGTAAAAAACAAGTATCTGTATGACAACCCGGATCGTTTGCAAGTAACTGAATCCAT TGCGACATTGTGAAGGCTTAAATGAGTTTAGATGGGAAATAGCGTTGTTATCGCCTTGGGTTTAAATT ATTTGATGAGTTCCACTTGTATCATCATGGCCTAGTCCACCGGAGGAGAGGAGTTTG
WI-7574c	216	A	G	GCCACAGCAGAATGGAGCGGGTGTGAGGAAGGTCCCTTTCCTCTGTTTGTGTTGCCAAGGCCAAAC TCCCACTCTCTGCCCCCCTTAATCCCCTTTACAGTGAGTCCACTACCCTCAAGGAGAATGAGTTGGACAGTTCTTG TACCACTTACATTTAGGCTGGGGCAAGCAGCCCTGACCTAAGGGACCACGTTACTCATCCCGTTA ATAGCCCAGGGC[A/G]TCTGCTGGGCTGGGCTGAGCCTGGGGCTGGGGCTGGGCTGAGCCTGGGCTGGGGCTGGGCTGAGCCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGC
WI-7574b	216	A	G	GCCACAGCAGAATGGAGCGGGTGTGAGGAAGGTCCCTTTCCTCTGTTTGTGTTGCCAAGGCCAAAC TCCCACTCTCTGCCCCCCTTAATCCCCTTTACAGTGAGTCCACTACCCTCAAGGAGAATGAGTTGGACAGTTCTTG TACCACTTACATTTAGGCTGGGGCAAGCAGCCCTGACCTAAGGGACCACGTTACTCATCCCGTTA ATAGCCCAGGGC[A/G]TCTGCTGGGCTGGGCTGAGCCTGGGGCTGGGGCTGGGC
WI-7574	216	A	G	GCCACAGCAGAATGGAGCGGGTGTGAGGAAGGTCCCTTTCCTCTGTTTTGTGTTTGCCAAGGCCAAAC TCCCACTCTCTGCCCCCCTTAATCCCCTTTACAGTGAGTCCACTACCCTCAAGGAGAATGAGTTGGACAGTTCTTG TACCACTTACATTTAGGCTGGGGCAAGCAGCCCTGACCTAAGGGACCACGTTACTCATCCCGTTA ATAGCCCAGGGC[A/G]TCTGCTGGGCTGGGCTGAGCCTGGGGCTGGGGCTGGGC
WI-7576c	168	A	T	AATGATGATAATGATGATGACGACGACAACGATGATGCTTGTAACAAGAAAAACATAAGAGAGC CTTGGTTCATCAGTGTTAAAAATTTTGAAAAGGCGGTACTAGTTCAGACACTTTGGAAGTTTGTGT TCTGTTTGTTAAAACTGGCATCTGACACAAAAAA[A/T]GTTGAAGGCCTTATTCTACATTTCACCTAC TTTGTAAGTGAGAGAGAGACAAGAAGCAAGACAACGATCAAANNNNNNNNAAAGAAAAAATAAAC

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VI-7576b	168	A	T	AATGATGATGATAATGATGATGACGACGACAACGATGATGCTTGTGTAACAAGAAAAACATAAGAGAGC CTTGGTTCATCAGTGTTAAAAAATTTTGAAAAGGCGGTACTCAGTAGTTCAGACACTTTGGAAGTTTGTGT TCTGTTTGTTAAAACTGGCATCTGACACAAAAA[A/T]GTTGAAGGCCTTATTCTACATTTCACCTAC TTTGTAAGTGAGAGACAAGAAGCAAANNNNNNNNNAAAGAAAAATAAAC
VI-7577q	77	T	C	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCAACATAAGTGTTTGCTTTCCTTAA AAATATGCA[T/C]CAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCATTTGGTTACACGTAGGAAAGAAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACACTACATGACACTCTTCTGAATTGACTGTATTTC
VI-7577p	50	G	C	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCAACATAAGTGTTTGCTTTCCTTAA AAATATGCATCAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAATAA AGAAGTTCATTTGGTTACACG[G/A]TAGGAAAGAAGCATCAAAGTGGAGATATGTTAACT ATTGTATAATGTGGCCTGTTATACACTACATGACACTCTTCTGAATTGACTGTATTTC
NI-7577o	157	G	A	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCAACAT[A/G]AGTGTTTGCTTTCCTT TAAAAATATGCATCAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCATTTGGTTACACGTAGGAAAGAAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACACTACATGACACTCTTCTGAATTGACTGTATTTC
NI-7577n	48	A	G	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCAACATAAGTGTTTGCTTTCCTTAA AAATATGCATCAAATC[G/A]TCTCTCATTACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCATTTGGTTACACGTAGGAAAGAAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACACTACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577m	84	G	A	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCAACATAAGTGTTTGCTTTCCTTAA AAATATGCATCAAATC[G/A]TCTCTCATTACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCATTTGGTTACACGTAGGAAAGAAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACACTACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577l	93	T	C	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCAACATAAGTGTTTGCTTTCCTTAA AAATATGCATCAAATCGTCTCTCATT[T/C]ACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCATTTGGTTACACGTAGGAAAGAAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACACTACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577k	154	C	A	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCAACATAAGTGTTTGCTTTCCTTAA AAATATGCATCAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAATAA AGAAGTTCATTTGGTTTA[C/A]ACGTAGGAAAGAAGCATCAAAGTGGAGATATGTTAACT ATTGTATAATGTGGCCTGTTATACACTACATGACACTCTTCTGAATTGACTGTATTTC

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VI-7577j	117	A	G	AACCATGTTCCCTTCTCTTAGCACCACCAAATAATCAAAACCCAACATAAGTGTTGCTTCCTTTAA AAATATGCATCAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTA[A/G]ACAGTAGGAGTTAAT AAAGAAGTTCATTTGGTTACACGTAGGAAAGAAGCATCAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
VI-7577i	77	T	C	AACCATGTTCCCTTCTCTTAGCACCACCAAATAATCAAAACCCAACATAAGTGTTGCTTCCTTTAA AAATATGCA[T/C]CAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCATTTGGTTACACGTAGGAAAGAAGCATCAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
NI-7577h	50	G	C	AACCATGTTCCCTTCTCTTAGCACCACCAAATAATCAAAACCCAACATAAGTGTTGCTTCCTTTAA AAATATGCATCAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAATAA AGAAGTTCATTTGGTTACAC[G/A]TAGGAAAGAGAAGCATCAAGTCAAAGTGGAGATATGTTAACT ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577g	157	G	A	AACCATGTTCCCTTCTCTTAGCACCACCAAATAATCAAAACCCAACATAAGTGTTGCTTCCTTTAA AAATATGCATCAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAATAA AGAAGTTCATTTGGTTACAC[G/A]TAGGAAAGAGAAGCATCAAGTCAAAGTGGAGATATGTTAACT ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
NI-7577f	48	A	G	AACCATGTTCCCTTCTCTTAGCACCACCAAATAATCAAAACCCAACATAAGTGTTGCTTCCTTTAA TAAAAATATGCATCATCAAATCAAATC[A/G]AGTGTTTGCTTCCTT CTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCATTTGGTTACACGTAGGAAAGAAGCATCAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577e	84	G	A	AACCATGTTCCCTTCTCTTAGCACCACCAAATAATCAAAACCCAACATAAGTGTTGCTTCCTTTAA AAATATGCATCAAATC[G/A]TCTCTCATTACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCATTTGGTTACACGTAGGAAAGAAGCATCAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577d	93	T	C	AACCATGTTCCCTTCTCTTAGCACCACCAAATAATCAAAACCCAACATAAGTGTTGCTTCCTTTAA AAATATGCATCAAATCGTCTCTCAT[T/C]ACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCATTTGGTTACACGTAGGAAAGAAGCATCAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577c	154	C	A	AACCATGTTCCCTTCTCTTAGCACCACCAAATAATCAAAACCCAACATAAGTGTTGCTTCCTTTAA AAATATGCATCAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAATAA AGAAGTTCATTTGGTTA[C/A]ACGTAGGAAAGAGAAGCATCAAGTCAAAGTGGAGATATGTTAACT ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC

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II-7577b	117	A G	AACCATGTTCCCTCTTCTTAGCACCACCACAAATAATCAAAACCCACATAAGTGTTTGCTTTCCTTTAA AAATATGCATCAAATCGTCTCTCATTACTTTTCTCTGAGGGTTTAGTA[A/G]ACAGTAGGAGTTAAT AAAGAAGTTCATTTTGGTTTACACGTAGGAAGAAGAGAAGAGCATCAAAGTGGAGATATGTTAACTAT TGTATAAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
VI-7577	107	G A	AACCATGTTCCCTCTTCTTAGCACCACCACAAATAATCAAAACCCACATAAGTGTTTGCTTTCCTTTAA AAATATGCATCAAATCGTCTCTCATTACTTTTCTCTGAG[G/A]GTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCATTTTGGTTTACACGTAGGAAGAAGAGAAGAAGCATCAAAGTGGAGATATGTTAACTAT TGTATAAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
VI-7619q	106	C G	ACAAGGCGACTTGAAGAGGACGCAGGCTTCCAGAGGACAAACCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGGGTCATCCCCTCCCTAACGACACT[C/G]TCGTGTGCTGGGGGTCTAATTAC ATGGCAGGAAGAATGGGGGCCTCTAAGGGGAGTGTGGGGTCTGTCTCTCCCTTTTTCCATCTTTTTCCT CTCTCGCTTTCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
NI-7619p	150	T C	ACAAGGCGACTTGAAGAGGACGCAGGCTTCCAGAGGACAAACCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGGGTCATCCCCTCCCTAACGACACTCTCTGCTGGGGGTCTAATTACATGG CAGGAAGAATGGGGGCC[T/C]CTAAGGGGAGTGTGGGGTCTGTCTCTCCCTTTTTCCATCTTTTTCCTC TCTCGCTTTCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
VI-7619o	228	A G	ACAAGGCGACTTGAAGAGGACGCAGGCTTCCAGAGGACAAACCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGGGTCATCCCCTCCCTAACGACACTCTCTGCTGGGGGTCTAATTACATGG CAGGAAGAATGGGGGCCTCTAAGGGGAGTGTGGGGTCTGTCTCTCCCTTTTTCCATCTTTTTCCTCT CGCTTTCTTCTTCTTACACAGAAACATT[A/G]CACATACCGAGAAACCTATTTC
NI-7619n	237	G C	ACAAGGCGACTTGAAGAGGACGCAGGCTTCCAGAGGACAAACCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGGGTCATCCCCTCCCTAACGACACTCTCTGCTGGGGGTCTAATTACATGG CAGGAAGAATGGGGGCCTCTAAGGGGAGTGTGGGGTCTGTCTCTCCCTTTTTCCATCTTTTTCCTCTCT CGCTTTCTTCTTCTTACACAGAAACATACACATACC[G/C]AGAAACCTATTTC
NI-7619m	99	C T	ACAAGGCGACTTGAAGAGGACGCAGGCTTCCAGAGGACAAACCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGGGTCATCCCCTCCCTAA[C/T]GAGACTCTCGTGTGCTGGGGGTCTAATTACA TGGCAGGAAGAATGGGGGCCTCTAAGGGGAGTGTGGGGTCTGTCTCTCCCTTTTTCCATCTTTTTCCTC TCTCGCTTTCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619l	189	T A	ACAAGGCGACTTGAAGAGGACGCAGGCTTCCAGAGGACAAACCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGGGTCATCCCCTCCCTAACGACACTCTCTGCTGGGGGTCTAATTACATGG CAGGAAGAATGGGGGCCTCTAAGGGGAGTGTGGGGTCTGTCTCTCCCTTTTTCCA[T/A]CTTTTTCCTC TCTCGCTTTCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC

			Sequence
WI-7619k	90	C/G	ACAAGGCGACTTGAAGAGGACGCAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGGTCATCC[C/G]CTCCCTAACGAGACTCTCTGTGTGCTGGGGGTGCTAATTAC ATGGCAGGAAGAATGGGGCCTCTAAGGGGAGTGTGGGCCTCTGTCTCTCCCTTTTTCCATCTTTTTCCT CTCTCGCTTTCTTTCTTACACAGAAACATACAGGAAACCTATTTC
WI-7619j	206	T/G	ACAAGGCGACTTGAAGAGGACGCAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGTGCTGGGGGTGCTAATTACATGG CAGGAAGAATGGGGCCTCTAAGGGGAGTGTGGGTCTCTGTCTCTCCCTTTTTCCATCTTTTTCCTCTCT CGC[T/G]TTCTTTCTTACACAGAAACATACAGGAAACCTATTTC
WI-7619i	106	C/G	ACAAGGCGACTTGAAGAGGACGCAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGGTCATCCCTCCCTAACGAGACT[C/G]TCTGTGCTGTCTCTCCCTTTTTCCATCTTTTTCCT ATGGCAGGAAGAATGGGGCCTCTAAGGGGAGTGTGGGCCTCTGTCTCTCCCTTTTTCCATCTTTTTCCT CTCTCGCTTTCTTTCTTACACAGAAACATACAGGAAACCTATTTC
WI-7619h	150	T/C	ACAAGGCGACTTGAAGAGGACGCAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGTGGGGGTGCTAATTACATGG CAGGAAGAATGGGGCCT[T/C]CTAAGGGGAGTGTGGGTCTCTGTCTCTCCCTTTTTCCATCTTTTTCCTCT TCTCGCTTTCTTTCTTACACAGAAACATACACGAGAAACCTATTTC
WI-7619g	228	A/G	ACAAGGCGACTTGAAGAGGACGCAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGTGGGGGTGCTAATTACATGG CAGGAAGAATGGGGCCTCTAAGGGGAGTGTGGGTCTCTGTCTCTCCCTTTTTCCATCTTTTTCCTCT CGCTTTCTTTCTTACACAGAAACAT[A/G]CACATACCGAGAAACCTATTTC
WI-7619f	237	G/C	ACAAGGCGACTTGAAGAGGACGCAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGTGGGGGTGCTAATTACATGG CAGGAAGAATGGGGCCTCTAAGGGGAGTGTGGGTCTCTGTCTCTCCCTTTTTCCATCTTTTTCCTCT CGCTTTCTTTCTTACACAGAAACATACAGGAAAC[G/C]AGAAACCTATTTC
WI-7619e	99	C/T	ACAAGGCGACTTGAAGAGGACGCAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGGTCATCCCTCCCTAACGAGAC[C/T]TCTGTGCTGTGGGGGTGCTAATTACA TGGCAGGAAGAATGGGGCCTCTAAGGGGAGTGTGGGTCTCTGTCTCTCCCTTTTTCCATCTTTTTCCTC TCTCGCTTTCTTTCTTACACAGAAACATACAGGAAACCTATTTC
WI-7619d	189	T/A	ACAAGGCGACTTGAAGAGGACGCAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGTGGGGGTGCTAATTACATGG CAGGAAGAATGGGGCCTCTAAGGGGAGTGTGGGTCTCTGTCTCTCCCTTTTTCCA[T/A]CTTTTTCCTC TCTCGCTTTCTTTCTTACACAGAAACATACAGGAAACCTATTTC

				Sequence
WI-7619c	90	C	G	ACAAGGCGACTTGAAGAGGACGCAGGCTTCCAGAGGACAAAACCCAATACAGGAGGAAGCACAAGAC AGAGAAGGGCCAATGGGGTCATCC[C/G]CTCCCTAACGAGACTCTCTGTGCTGTGCTAATTAC ATGGCAAGAATGGGGGCCTCTAAGGGAGTGTGGGGTCTGTCTCTCCCATTTTTCCATCTTTTTCCT CTCTCGCCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619b	208	T	G	ACAAGGCGACTTGAAGAGGACGCAGGCTTCCAGAGGACAAAACCCAATACAGGAGGAAGCACAAGAC AGAGAAGGGCCAATGGGGTCATCATCCCCTAACGAGACTCTCTGTGCTGTCTCTCCCATTTTTCCATCTTTTTCCTCT CAGGAAGAAATGGGGGCCTCTAAGGGGAGTGTGGGGTCTGTCTCTCCCATTTTCCATCTTTTTCCTC CGC[T/G]TTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619	189	T	A	ACAAGGCGACTTGAAGAGGACGCAGGCTTCCAGAGGACAAAACCCAATACAGGAGGAAGCACAAGAC AGAGAAGGGCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGTGCTGTCTCTCCCATTTTTCCTC CAGGAAGAAATGGGGGCCTCTAAGGGGAGTGTGGGGTCTGTCTCTCCCATTTTCCATCTTTTTCCTC TCTCGCCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7626d	105	A	G	CCTTTGTATGTGGAAGTATACCTGGCTTTTAAAATATATGTATTTAAAACAAAAAGCAACAGTAA TCTATGTGTTTCTGTAACAAATTGGGATCTGTCTTGGC[A/G]TTAAACCACATCATGGACCAAATGTG CCATACTAATGATGAGCATTTAGCACAATTTAGTACACTATGTTCCTTTGACTGTTCAGT CTAACAGTTTGCCTGCTGTGTATTTATAGTAACCATTTTCCTTTGACTGTTCA
WI-7626c	155	C	T	CCTTTGTATGTGGAAGTATACCTGGCTTTTAAAATATATGTATTTAAAAACAAAAAGCAACAGTAA TCTATGTGTTTCTGTAACAAATTGGGATCTGTCTTGGCATTAAACCACATCATGGACCAAATGTGCCA TACTAATGATGAGCATTTAGCACAATTTAGTACACTATGTTCTTAGGTCAGT CTAACAGTTTGCCTGCTGTGTATTTATAGTAACCATTTTCCTTTGACTGTTCA
WI-7626b	281	T	A	CCTTTGTATGTGGAAGTATACCTGGCTTT[T/A]TTAAAATATATGTATTTAAAAACAAAAAGCAACAG TAATCTATGTGTTTCTGTAACAAATTGGGATCTGTCTTGGCATTAAACCACATCATGGACCAAATGTG CCATACTAATGATGAGCATTTAGCACAATTTAGTACACTATGTTCTTAGGTCAGT CTAACAGTTTGCCTGCTGTGTATTTATAGTAACCATTTTCCTTTGACTGTTCA
WI-7626	144	T	C	CCTTTGTATGTGGAAGTATACCTGGCTTTTAAAATATATGTATTTAAAAACAAAAAGCAACAGTAA TCTATGTGTTTCTGTAACAAATTGGGATCTGTCTTGGCATTAAACCACATCATGGACCAAATGTGCCA TACTAATGAT[T/C]GAGCATTTAGCACAATTTAGTACACTATGTTCCTTTGGACTGTTCA CTAACAGTTTGCCTGCTGTGTATTTATAGTAACCATTTTCCTTTGGACTGTTCA
WI-7689c	134	A	G	TCCCATAACCGCTGATTCTCAGGGTCTCTGCTGCGCCCCACCCAGAATGGGGAAAGCAACACAGGTGGGC TTCCCAGTGCCTGCTGCCCCAGAGGCCCCCTTAGGAGGCGCCACCCAGACTGTGATACAAATTGCAACAAAJA /G]TAAGGGCAGAGTCACACTGGGGCACTGTTGATACAAATTGGAATTCAGAGAGAGCTTAAT GATAATATTGTGGTGCCACAAATAAAATGGATTTATTTAGAAATTTCATATGAC

ID	Position	Allele 1	Allele 2	Sequence
WI-7689b	134	A	G	TCCCATAAACGGCTGATTCTCAGGGTCTCTGCTGCGCGCCCACCCAGATGGGGGAAAGCACAGGTGGGC TTCCCAGTGGCTGGCTGCTGCCCAGGCCCAGGACGCCCAGCAAAAAGGTTGTTCCTAAA[A /G]TAAGGGCAGAGTCACACTGGGGCAGCTGATACAAATAAAATGCAGAAAAGAGAGCTTAAT GATAATATTGTGGTGCCACAAATAAAATGGATTTATTAGAATTCATATGAC
WI-7689	121	G	A	TCCCATAAACGGCTGATTCTCAGGGTCTCTGCTGCGCCCCACCCAGATGGGGGAAAGCACAGGTGGGC TTCCCAGTGGCTGGCTGCTGCCCAGGACCTTCTAGGACGCCCACCCAGACTGTGTAAAAAGAGACTTAAT AATAAGGGCAGAGTCACACTGGGGCAGCTGATACAAATAAAATGGATTTATTAGAATTCATATGAC GATAATATTGTGGTGCCACAAATAAAATGGATTTATTAGAATTCATATGAC
WI-7690	45	G	A	TGGAGAACATTCAATCTTGCCGTCCACTATTCATCAATGAAGATTA[G/A]CACTGAGATCCAGAGAGG CTGGATGACTTGCTCAAGTTCACCAGCACATGGTAGTGGCAAAGAGAGGTCCAGAGTCCTGGCCCTTGAT GCCCAGCTCAGTGCCACAAAGCTCAGTGAGGAGGATGTTCCAGTGAGGGCCACCAGGAAGCAC AGGTCCAAGGCGTGGTCTCCCACACTTATCAGCAGCAACAACTGTCAGTTCATCC
WI-7703b	164	T	C	ACAGAAAAGTTGAATTTACATGGCTGGAGCTAGAATTTGATATGTGAACAGTTGTGTTGAAGCAC AGTGATCAAGTTATTTAATTTGGTTTCACATTGGAAACAAGTCAGTCATTCAGATATGATTCAAA TGTCTATAAACCAAACTGATGATGTAAGTAAA[T/C]GGTCTCTCCACTTGTTTATTTAACCTCTAAATTCT TTCATTTTAGGGGTAGCATTTGTGTTGAAGAGGTTTTAAAGCTTCCATTGT
WI-7703	156	T	C	ACAGAAAAGTTGAATTTACATGGCTGGAGCTAGAATTTGATATGTGAACAGTTGTGTTGAAGCAC AGTGATCAAGTTATTTAATTTGGTTTCACATTGGAAACAAGTCAGTCATTCAGATATGATTCAAA TGTCTATAAACCAAACTGAT[GT/C]AAGTAAAATGGTCTCTCTGTTTATTTAACCTCTAAATTCT TTCATTTTAGGGGTAGCATTTGTGTTGAAGAGGTTTTAAAGCTTCCATTGT
WI-7743e	106	C	A	TTAAATGAGTGTGTTGTCACCGTTGGGGAATTGGGGAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTCAGAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC[C/A]CCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAATTCTGCTACCTCACTGGGGTCCTCCGGAGCCTCATCCGAGGCAGGGTCAGGA GAGGGGCAGAACAGCCGGCTCCTGTCTGCCAGCCAGCCTCTCAGCC
WI-7743d	275	C	T	TTAAATGAGTGTGTTGTCACCGTTGGGGAATTGGGGAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTCAGAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAATTCTGCTACCTCACTGGGGTCCTCCGGAGCCTCATCCGAGGCAGCGTCAGGAGAG GGGCAGAACAGCCGGCTCCTGTCTGCCAGCCAGCCTCTCAGCCAACG
WI-7743e	106	C	A	TTAAATGAGTGTGTTGTCACCGTTGGGGAATTGGGGAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTCAGAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC[C/A]CCGGAGTCCCTGGTAATAAGTACT GTGTACAGAATTCTGCTACCTCACTGGGGTCCTCATCCGAGCCGCAGCCAGCCTCTCAGCC GAGGGGCAGAACAGCCGGCTCCTGTCTGCCAGCCAGCCTCTCAGCC

WI-7743d	275	C	T	---	TTAAATGAGTGTGTTTGTCACCGTTGGGGATTGGGGAAGACTGTGGCTGCTGCCAAGG GTTCAGAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAATTCTGCTACCTCACTGGGGTCCTGGGCCTCGAGCCTCAGCAGCCAGCTCTCAGCCCAACG GGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCCAGCTCTCAGCG
WI-7743e	106	C	A	---	TTAAATGAGTGTGTTTGTCACCGTTGGGGATTGGGGAAGACTGTGGCTGCTGCCAAGG GTTCAGAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC[C/A]CCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAATTCTGCTACCTCACTGGGGTCCTGGGCCTCGAGCCTCAGCAGCCAGCTCTCAGCGA GAGGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCCAGCTCTCAGCC
WI-7743d	275	C	T	---	TTAAATGAGTGTGTTTGTCACCGTTGGGGATTGGGGAAGACTGTGGCTGCTGCCAAGG GTTCAGAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACC[C/A]CCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAATTCTGCTACCTCACTGGGGTCCTGGGCCTCGAGCCTCAGCAGCCAGCTCTCAGCGA GAGGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCCAGCTCTCAGCCCAACG
WI-7743c	106	C	A	---	TTAAATGAGTGTGTTTGTCACCGTTGGGGATTGGGGAAGACTGTGGCTGCTGCCAAGG GTTCAGAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC[C/A]CCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAATTCTGCTACCTCACTGGGGTCCTGGGCCTCGAGCCTCAGCAGCCAGCTCTCAGCC
WI-7743b	275	C	T	---	TTAAATGAGTGTGTTTGTCACCGTTGGGGATTGGGGAAGACTGTGGCTGCTGCCAAGG GTTCAGAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAATTCTGCTACCTCACTGGGGTCCTGGGCCTCGAGCCTCAGCAGCCAGCTCTCAGCCCAACG
WI-7743	106	C	A	---	TTAAATGAGTGTGTTTGTCACCGTTGGGGATTGGGGAAGACTGTGGCTGCTGCCAAGG GTTCAGAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC[C/A]CCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAATTCTGCTACCTCACTGGGGTCCTGGGCCTCGAGCCTCAGCAGCCAGCTCTCAGCC
WI-7743	275	C	T	---	TTAAATGAGTGTGTTTGTCACCGTTGGGGATTGGGGAAGACTGTGGCTGCTGCCAAGG GTTCAGAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAATTCTGCTACCTCACTGGGGTCCTGGGCCTCGAGCCTCAGCAGCCAGCTCTCAGCGAGGAGAG GGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCCAGCTCTCAGCCCAACG
WI-7758	144	A	G	---	TGACATTTATTCAAAGTTAAAAGCAAACACTTACAGAATTATGAAGAGGTATCGTTAACATTCC TCAGTCAAGTTCAGAGTCTTCGTAATTAAAGGAACAGAGTGAGAGACATCATCAAGTG GAGAGAAATC[A/G]TAGTTAAACTGCATTATAAATTTATAACAGAATTAAAGTAGATTTTAAAA GATAAAATGTGTAATTTGTTTATTTTCCCATTTGGACTGTAACTGACTGCC

Label	Pos		
NI-7765b	126	G	C

ACAGGGCCTTTGGCAGGTGCAGCCCCCACTGCCTCCCCTTGACCTGCCTCCCCTTCATGCATGGAAATTCCCT
TCATCTGGAACCATCAGAAACACCCTCACACTGGGACTTGCAAAAGGGTCAGTATGG[G/C]TTAGG
GAAAACATTCCATCCTTGAGTCAACTTCAATTCTCCTATCTTTGCCACCCTCATGCTGTGTG
ACTCAAACCAAATCACTGAAACTTTGCTGAGCCTGTAAAATAAAGGTCGGA

| NI-7773b | 237 | C | G |

TTAATTTACTGATTCCAGCAAGACCAAATCATTGTATCAGATTATTTTAAGTTTTATCCGTAGTTTT
GATAAAAGATTTCCTATTCCTTGGTTCTGTCGTGCAGAGAACCTAATAAGTGCTACTTTGCCATTAAGGCA
GACTAGGGTTCATGTTCATTTTACCCTTTNNNNNNNNNTGTAAAAGTCTAGTTACCTACTACTTTTTCTTT
GATTTTCGACGTTTGACTAGCCATCCAAGCAA[C/G]TTTGACGTTTGA

| NI-7774b | 170 | T | C |

TGCAACCTCTTTCGTGATGGGCAGCCTGCTGGTCAGATCCCAGCTCTCCAGTAGGCAGGACGGCACCCAGAAT
CAGATCCCAGCTCTCGGCATTGATCAGACAAACAGTGCTGTTTCCGGGGAGGAAACACTTTTTAA
TTACCCTTTGCAGGCACCACCTTAATCTGTTT[T/C]ATACCTTGCTTATTAAATGAGCGACTTAAA
ATGATTGAAAATAAATGCTGTCCTTTAGTAGCAAGTAAAATGTGTCTTGCT

| WI-7785c | 165 | G | |

GCAGAGACCTTCCAAGGACATATTGCAGGATTCTGTAATAGTGAACATATGGAAAGTATTAGAAATA
TTTATTGTCTGTAAATACTGTGAATGTCATTGGAATAAAACTGTCTCCCCCATTGCTCTATGAAACTGC
ACATTGGTCATTGTGAATANNNNNNNNNGCCAAGGCTAATCCAATTATTATTATCACATTTACCA
TAATTTATTTATTTTGTCCATTGATGTATTTATTTTGTAAATGTATCTTGGTGCTGC

| WI-7785b | 165 | G | |

GCAGAGACCTTCCAAGGACATATTGCAGGATTCTGTAATAGTGAACATATGGAAAGTATTAGAAATA
TTTATTGTCTGTAAATACTGTGAATGTCATTGGAATAAAACTGTCTCCCCCATTGCTCTATGAAACTGC
ACATTGGTCATTGTGAATANNNNNNNNNGCCAAGGCTAATCCAATTATTATTATCACATTTACCA
TAATT[T/A]TTTATTTTGTCCATTGATGTATTTATTTTGTAAATGTATCTTGGTGCTGC

| NI-7785 | 156 | - | T |

GCAGAGACCTTCCAAGGACATATTGCAGGATTCTGTAATAGTGAACATATGGAAAGTATTAGAAATA
TTTATTGTCTGTAAATACTGTGAATGTCATTGGAATAAAACTGTCTCCCCCATTGCTCTATGAAACTGC
ACATTGGTCATTGTGAATANN[-/T]NNNNNNNGCCAAGGCTAATCCAATTATTATTATCACATTTACCA
TGTATTTATTTTGTAAATGTATCTTGGTG

| NI-7789c | 84 | G | A |

TCTCCCCTCATCCAACTCCGAAAGTCTGAATCTCCCAAGGAGGGCACCATCTCCCAAGGAGGGCACCATCTTACAGAGACTCTCCC
TGACGGTGGAATTTAA[G/A]TTAGGGTCCCTAAAAGCATTTGAGGTCCCTAAAAGCATTTGACACACAGTTGGACACACAGTTGTTGAATGACTGAC
GCCCTCCTGGTGACTCGGGGGCTGTCCCTTGAGTGAAGCTCCCTTGAGTGAAGCGCCCGCTGCCCTAGGATAT

| NI-7789b | 84 | G | A |

TCTCCCCTCATCCAACTCCGAAAGTCTGAATCTCCGAAAGTCTGAA
TGACGGTGGAATTTAA[G/A]TTAGGGTCCCTAAAAGCATTTGAGGTCCCTAAAAGCATTTGACACACAGTTGGACACACAGTTGTTGAATGACTGAC
GCCCTCCTGGTGACTCGGGGGCTGTCCCTTGAGTGAAGCTCCCTTGAGTGAAGCGCCCGCTGCCCTAGGATCT

ID	Pos			Sequence
Il-7789	73	G	A	TCTCCCCCTCCATCCAACTCCGAAAGTCTGAATCTCCAAGGAGGGCACCATCTTACAGAGAGACTCTCCC TGACG[G/A]TGGAATTTAAGTTTAGGGTCCCTAAAAAGCATTGACACACAGTTGTTGAATGACTGAC CCAAAAATGTGAATGAAGCTAATGTGAGTGAAGCTCCCTCAGCGCCCGCTGCCCTAGGATAT GCCCTCCTGGTGACTCGGGGGCTGTCTCAGACGACTAGCCCAGGACCCATCT
Il-7790b	190	C	T	AATTGTCAGTCACTTCTTCAAAACCTTACAGTCCTTCCTAAGGTTACTCTTCATGAGAATTCATCCATT TACTAATACTGTATTTTTGGTGGACTAGGCTTGCCTATGTGCTTATTTTCTTGAACTC[C/T]TTCTATACTTT TGTGATTAAGTGGTGATCAAGGTAGGAAAAGTTGTGTTCTATTTTCTTGTAGCTTTTACTTTTTATGG AAGATACTCTATTTTAAAACACTATCTGCAAACTCAGGACACTTAAC
Il-7790	190	C	T	AATTGTCAGTCACTTCTTCAAAACCTTACAGTCCTTCCTAAGGTTACTCTTCATGAGAATTCATCCATT TACTAATACTGTATTTTTGGTGGACTAGGCTTGCCTATGTGCTTATTTTCTTGAACTC[C/T]TTCTATACTTT TGTGATTAAGTGGTGATCAAGGTAGGAAAAGTTGTGTTCTATTTTCTTGTAGCTTTTACTTTTTATGG AAGATACTCTATTTTAAAACACTATCTGCAAACTCAGGACACTTAAC
Il-7795b	81	C	A	CAGATGTTCTGGTAAACTGATTGCTGGCAACAACAGATTCTCTTGGCTCATATTTCTTTCTTTCTCAT CTTGATGATGAT[C/A]GTCATCATCAAGAATTAATGATTAAAATAGCATGCCTTTCTCCTTCTCTTCTCT TAATAAGCCCACATATAAATGTACTTTTCTTCCAGAAAAATTCTCCTTGAGGAAAAATGTCCAAAA TAAGATGAATCACTTAATACCGTATCTCTAAATTTGAAATATAATTCTG
I-7795	81	C	A	CAGATGTTCTGGTAAACTGATTGCTGGCAACAACAGATTCTCTTGGCTCATATTTCTTTCTTTCTCAT CTTGATGATGAT[C/A]GTCATCATCAAGAATTAATGATTAAAATAGCATGCCTTTCTCCTTCTCTTCTCT TAATAAGCCCACATATAAATGTACTTTTCTTCCAGAAAAATTCTCCTTGAGGAAAAATGTCCAAAA TAAGATGAATCACTTAATACCGTATCTCTAAATTTGAAATATAATTCTG
-7814c	41	G	A	TTCTCTCTCATTTATCCCTCACCTGTAGCATGCCAGTCCC[G/A]TTTCATTTAGTCATGTGACCACTC ATTGCTTACAAGCCTAAGAATCTTAGAGAAGTGCTAACATCTAAAAATAGACTTAAATCTC TTTCTTTTCTCTGGTAATATTGACTTGTATATTTAAGAAATAACAGAA
7814b	41	G	A	TCTCTCTCATTTTATCCCTCACCTGTTGTTTCCACAGCCTGCAAGTTCATT[G/A]TTCATTTAGTCATGTGACCACTC ATTGCTTACAAGCCTAAGAATCTTAGAGAAGTACATCTAAAAATAGACTTAAATCTC TTTCTTTTCTCTGGTAATATTGACTTGTATATTTAAGAAATAACAGAA
314	28	G	A	TTCTCTCTCATTTTATCCCTCACCTGTTGTTTCCACAGCCTGCAAGTTCATTTAGTCATGTGACCACTC TGTCTTGTGTTCCACAGCCTGCAAGTTCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAATATTGACTTGTATATTTAAGAAATAACAGAA TTTCTTTTCTCTGGTAATATTGACTTGTATATTTAAGAAATAACAGAA

		Sequence
WI-7830d	150 C/T	GCAGGAAATAGTCACTCCACTCCACATAAGGGGTTTAGTAAGAGAAGTCTGTCTGTCTGATGATGGATAGGGGGCAAATCTTTTCCCTTCTGTGTTAATGTACACATTGCATTTGATAAAATTAATTTTGTTGCGTGTGGAATCCATAACTTTAGTT[C/T]TAATGTACACATTGCTGCACTTTTTACTTTTTTGCGTGTGGAAGGTTGATCGTTGTGTGTTGCTGCACTTTTTACTTTTTTGCGTGTGGA AGGTTGATCGTTGTGTGTTGCTGCACTTTTTACTTTTTGTTTCCTTTG
WI-7830c	54 G/A	GCAGGAAATAGTCACTCCACTCCACATAAGGGGTTTAGTAAGAGAAGTCTG/A]TCTGTGATGATGGATAGGGGGCAAATCTTTTCCCCTTCTGTTAATGTACACATTCTTAATGTACACATTGCATTTGATAAAATTAATTTTGTTGCGTGTGGAACGATCCATAACTTTAGTCATCACATTCTATGCCAAACAGGAAGGTTGATCGTTGTGTGTTGCTGCACTTTTTACTTTTTGCGTGTGGA
WI-7830b	134 G/A	GCAGGAAATAGTCACTCCACTCCACATAAGGGGTTTAGTAAGAGAAGTCTGTCTGTCTGATGATGGATAGGGGGCAAATCTTTTCCCTTCTGTGTTAATGTACACATTGCATTTGATAAAATTAATTTTGTTGCGTGTGGAG/A]ATCCATAACTTTAGTCTTAATGTACACATTGCTGCACTTTTTACTTTTGTTTCCTTTG
WI-7830	44 A/G	GCAGGAAATAGTCACTCCACTCCACATAAGGGGTTTAGTA[A/G]GAGAAGTCTGTCTGTCTGATGATGGATAGGGGGCAAATCTTTTCCCTTCTGTGTTAATGTACACATTGCATTTGATAAAATTAATTTTGTTGCGTGTGGAACGATCCATAACTTTAGTCATCACATTCTATGCCAAACAGGAAGGTTGATCGTTGTGTGTTGCTGCACTTTTTACTTTTTGCGTGTGGA
WI-7865e	25 C/T	CCACTTCCTATCTGATTTTTCCCAG[C/T]AAATGAGGCAGGCAATTCTAGTCTTCCACAAAACATCTAGCCGGTATGGTACTCATAAGATTCAGGGTGTCTTCCAACTAGCTAGCTATTAGAGGGTGGTTGGCTGAAATCACATGCCTATGTAAGGAAAGTGCTATTCAATGTTCTCAGTACGAAAAACCCAA
WI-7865d	191 C/T	CCACTTCCTATCTGATTTTTCCCAGC[C/T]AAATGAGGCAGGCAATTCTAGTCTTCCACAAAACATCTAGCCGGTATGCTACTCATAAGATTTCAGGGTGTCTTCCAACTAGCTAGCTATTAGAGGGTGGTTGGGGTCTGAAATCACATGCCTATGTAAGGAAAGTGCTATTCAATGTTCTCAGTA[C/T]GAAAAACCCAA
WI-7865c	25 C/T	CCACTTCCTATCTGATTTTTCCCAGC[C/T]AAATGAGGCAGGCAATTCTAGTCTTCCACAAAACATCTAGCCGGTATGCTACTCATAAGATTTCAGGGTGTCTTCCAACTAGCTAGCTATTAGAGGGTGGTTGGCTGAAATCACATGCCTATGTAAGGAAAGTGCTATTCACCCAGTAAACCCAA
WI-7865b	191 C/T	CCACTTCCTATCTGATTTTTCCCAGCC AAATGAGGCAGGCAATTCTAGTCTTCCACAAAACATCTAGCCATCTAAAATGGAGAGATGAATCATTCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTTGGGGTCTGAAATCACATGCCTATGTAAGGAAAGTGCTATTCAATGTTCTCAGTA[C/T]GAAAAACCCAA

WI-7865	25	C/T	CCACTTCCTATCTGATTTTCCCAG[C/T]AAATGAGGCAGGCAATTCTAGTCTTCCACAAAACATCTAGCCATCTAAAATGGAGAGATGAATCATTCTACCTATACAACAGCTAGCTATTAGAGGGTGGTTGGGGTATGCTACTCATAAGATTCAGGGTGTCTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAACCTGAAATCACATGCCTATGTAAGGAAAGTGCTATTCACCCAGTAAACCCAAA
WI-7865	191	C/T	CCACTTCCTATCTGATTTTCCCAGCAAATGAGGCAGGCAATTCTAGTCTTCCACAAAACATCTAGCCAATCTAAAATGGAGAGATGAATCATTCTACCTATACAACAGCTAGCTATTAGAGGGTGGTTGGGGTATGCTACTCATAAGATTCAGGGTGTCTCCAACTGAAATCTCAATGTTCTCAGTA[C/T]GAAAAACCTGAAATCACATGCCTATGTAAGGAAAGTGCTATTCACCCAGTAAACCCAAA
WI-7867c	92	A/C	TTCAAACACCTGTCTTCCCACCCTCCCACCATCTGTGCAATCACTCACCCTTCAGCCTCACTAGTCCCCCTAACAATTACCCTGTCAAGAGG[A/C]GAGTGCAGCTCAGGTGGATTAATGTGGGTTTAATATGGCCTGTTGAGTTTAATGTTAATGTTCTTTAAGTAACCATTCTGTTCTTGCTATAAATCTATGTCTATATGTCTATGCTTAATTTGGATGATGAAGGCAACTTGGATTTAAGG
WI-7867b	92	A/C	TTCAAACACCTGTCTTCCCACCCTCCCACCATCTGTGCAATCACTCACCCTTCAGCCTCACTAGTCCCCCTAACAATTACCCTGTCAAGAGG[A/C]GAGTGCAGCTCAGGTGGATTAATGTGGGTTTAATATGGCCTGTTGAGTTTAATGTTAATGTTCTTTAAGTAACCATTCTGTTCTTGCTATAAATCTATGTCTATATGTCTATGCTTAATTTGGATGATGAAGGCAACTTGGATTTAAGG
WI-7868c	173	C/T	TTGATCGATCTTTTCCCACCCTGTCACTCAACGTGGTCCCTAGAACAAGAGAGGCTTAAAACCGGGCTTTCACCCAACCTGCTCCCTCTGATCTCCATCAGGGCCAGATCTTCCACGTCTCCAGTACACAATCATTTAATATATTCCCTGTCTTAACCCTATTCAAGCAA[C/T]TTAGAGGCCAGAAAATGGGCAAATTATCACTAACAGGTCTTTGACTCAGGTTCCAGTAGTTCATTCTAATGCCTAGAT
WI-7868b	173	C/T	TTGATCGATCTTTTCCCACCCTGTCACTCAACGTGGTCCCTAGAACAAGAGAGGCTTAAAACCGGGCTTTCACCCAACCTGCTCCCTCTGATCTCCATCAGGGCCAGATCTTCCACGTCTCCAGTACACAATCATTTAATATATTCCCTGTCTTAACCCTATTCAAGCAA[C/T]TTAGAGGCCAGAAAATGGGCAAATTATCACTAACAGGTCTTTGACTCAGGTTCCAGTAGTTCATTCTAATGCCTAGAT
WI-7868	66	T/C	TTGATCGATCTTTTCCCACCCTGTCACTCAACGTGGTCCCTAGAACAAGAGAGGCTTAAAACCGGGCTT[C/T]CACCCAACCTGCTCCCTCTGATCTCCATCAGGGCCAGATCTTCCACGTCTCTCAGTACACAATCATTTAATATATTTCCCTGTCTTAACCCTATTCAAGCAACTAGAGGCCAGAAAATGGGCAAATTATCACTAACAGGTCTTTGACTCAGGTTCCAGTAGTTCATTCTAATGCCTAGAT
WI-7870b	85	T/C	ATCTTTGTCCCTGCAAGAAATCAGCCATAAGAAAGCACTATTAATACTCTGCAGTGATTAGAAGGGGTGGGGTGGCGGGAATCCT[C/T]ATTTATCGACAACTAAATATTGAATATAAATGTTTACTCAGAGGAGCTGCAAATTGCCTGCAAAATGAAAATCCAACAATGAGCACTAGAATATTTAAAACATTACTTACTGCCATCTTTATCATGAAGCAACATCAATTACAACGCTGTAGACCTAATATCAATTTG

WI-7870	76	C/T	ATCTTTGTCTCCCTGCAAGAAATCAGCCATAAGAAAGCACTATTAATACTCTGCAGTGATTAGAAGGG GTGGGGTGG[C/T]GGGAATCCTATTTATCAGACTCTGTAATTGAATATAAATGTTTACTCAGAGGAG CTGCAAATTGCCTGCAAAAATGAAATCCAATTACAAGCTGTGAGACCCACCTAATATCAATTTG TTTATCATGAAGCACATCAATTACAAGCTGTGAGACCTAATATCAATTTG
WI-7889c	54	C	TTAGGTCTCATGCCCACTCCCCAGGAGCAGCTGGCACTGACAGCCTGGGGGGCCGCTCTCCCCCTG CAGCCGGTGCAGGAGCTCTAGCTCATGAGTGGAAAGTCACCTACAGGACTGGGCCCGGGCCCTCT GGCTTCCCTGCCCAATCCTCCCTGGAGAAGGGACATGGAATGAATGAAATGGGGCGCTGGACACC TACAGCAGCACGCATGTCCCCTCCAAGGCTGTCTTCTCCCAGAGCACAGAAG
WI-7889b	54	C	TTAGGTCTCATGCCCACTCCCCAGGAGCAGCTGGCACTGACAGCCTGGGGGGCCGCTCTCCCCCTG CAGCCGGTGCAGGAGCTCTAGCTCATGAGTGGAAAGTCACCTACAGGACTGGGCCCGGGCCCTCT GGCTTCCCTGCCCAATCCTCCCTGGAGAAGGGACATGGAATGAATGAAATGGGGCGCTGGACACC TACAGCAGCACGCATGTCCCCTCCAAGGCTGTCTTCTCCCAGAGCACAGAAG
WI-7894c	142	A G	AGCCCACCCCCAAATATAACTGTTATCCAGAAGCTGTGTATGTCCTGTTCCATACATGTTTTGTACT TTTACTATATCTACATACATCAATTAAACTTATGTCCTATTGTTTGTGAATTTATATTTGCGTATAC ATTATC[A/G]TATGTAAAATTTGCATTTTTTATTGAAAATTATGTTTCTTGAGATTTATCCACATTG AAACATGGAGCTCTAAATCGTTAATTTAACCGCTATAGAGTATTCCATA
WI-7894b	142	A G	AGCCCACCCCCAAATATAACTGTTATCCAGAAGCTGTTATGTCCTGTTCCATACATGTTTTTGTACT TTTACTATATCTACATACATCAATTAAACTTATGTCCTATTGTTTGTGAATTTATATTTGCGTATAC ATTATC[A/G]TATGTAAAATTTGCATTTTTTATTGAAAATTATGTTTCTTGAGATTTATCCACATTG AAACATGGAGCTCTAAATCGTTAATTTAACCGCTATAGAGTATTCCATA
WI-7900e	84	C T	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAAACAAGTGACCTTCAGAGCAGCT GCCACAACTGGCCATG[C/T]CCTGCCATTGAAACAGTGATTAAGTTTGATCAAGCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCAGTGAAA TATGATGTATTTCTGAGCTAAAAACTCAACTATAGAAGACATTAAAAGAAATC
WI-7900d	128	C T	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAAACAAGTGACCTTCAGAGCAGCT GCCACAACTGGCCATGATTGATCAAGCAGTGATTAAGTTTGATCAAGCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCAGTGAAA TATGATGTATTTCTGAGCTAAAAACTCAACTATAGAAGACATTAAAAGAAATC
WI-7900e	84	C:T	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAAACAAGTGACCTTCAGAGCAGCT GCCACAACTGGCCATG[C/T]CCTGCCATTGAAACAGTGATTGATCAAGCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCAGTGAAA TATGATGTATTTCTGAGCTAAAAACTCAACTATAGAAGACATTAAAAGAAATC

WI-7900d	128	C	T	GCTCACTGTGACCACCATCCTTACTCTACTTGGCCAGGCCACAGTAAAACAAGTGACCTTCAGAGCAGCT GCCACAACTGGCCATGGCCCTGCCATTGAAATAGGAGCCCATGCTAAAACTCAACTATAGAGACATTAAAGAAAC[C/T]ACA AAAATGCATTGATCATGAATAGGAGTACATTCTCTCAGATTTGAACCAGTGAAA TATGATGTATTTCTGAGCTAAAACTCAACTATAGAGACATTAAAGAAATC
WI-7900e	84	C	T	GCTCACTGTGACCACCATCCTTACTCTACTTGGCCAGGCCACAGTAAAACAAGTGACCTTCAGAGCAGCT GCCACAACTGGCCATGGCCCTGCCATG[C/T]CCTGCCATTGAAACAGTGATTAAGTTGATCAAGCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCAGTGAAA TATGATGTATTTCTGAGCTAAAACTCAACTATAGAGAAGACATTAAAGAAATC
WI-7900d	128	C	T	GCTCACTGTGACCACCATCCTTACTCTACTTGGCCAGGCCACAGTAAAACAAGTGACCTTCAGAGCAGCT GCCACAACTGGCCATGGCCCTGCCATTGAAACAGTGATTAAGTTGATCAAGCCATGGTGA[C/T]ACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCAGTGAAA TATGATGTATTTCTGAGCTAAAACTCAACTATAGAGAAGACATTAAAGAAATC
WI-7900c	84	C	T	GCTCACTGTGACCACCATCCTTACTCTACTTGGCCAGGCCACAGTAAAACAAGTGACCTTCAGAGCAGCT GCCACAACTGGCCATG[C/T]CCTGCCATTGAAACAGTGATTAAGTTTGATCAAGCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCAGTGAAA TATGATGTATTTCTGAGCTAAAACTCAACTATAGAGAAGACATTAAAGAAATC
WI-7900b	128	C	T	GCTCACTGTGACCACCATCCTTACTCTACTTGGCCAGGCCACAGTAAAACAAGTGACCTTCAGAGCAGCT GCCACAACTGGCCATGGCCCTGCCATTGAAACAGTGATTAAGTTTGATCAAGCCATGGTGA[C/T]ACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAAAACTCAACTATAGAGAAGACATTAAAGAAATC TATGATGTATTTCTGAGCTAAAACTCAACTATAGAGAAGACATTAAAGAAATC
WI-7900	84	C	T	GCTCACTGTGACCACCATCCTTACTCTACTTGGCCAGGCCACAGTAAAACAAGTGACCTTCAGAGCAGCT GCCACAACTGGCCATG[C/T]CCTGCCATTGAAACAGTGATTAAGTTTGATCAAGCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCAGTGAAA TATGATGTATTTCTGAGCTAAAACTCAACTATAGAGAAGACATTAAAGAAATC
WI-7901c	33	C	T	AGACTTAGGTACAATTGCTCCCCTTTTATATA[C/T]AGACACACAGGACACATATTAAACAG ATTGTTCATCATTGCATCTATTTCCATATAGTCATCAAGAGACCATTTATAAAACATGGTAAGAC CCTTTTTAAAACAAACTCCAGGCCCTTGGTTCGCGGTCGCTGGGTTATTGGGCAGCGCGTGGTCGT CACTCAGTCGCTCTGCTCATGCTCTCTGTCATACAGACAGGTAACCTAGTTCT
WI-7901b	33	C	T	AGACTTAGGTACAATTGCTCCCCTTTTATATA[C/T]AGACACACAGGACACATATTAAACAG ATTGTTCATCATTGCATCTATTTCCATATAGTCATCAAGAGACCATTTATAAAACATGGTAAGAC CCTTTTTAAAACAAACTCCAGGCCCTTGGTTCGCGGTCGCTGGGTTATTGGGCAGCGCGTGGTCGT CACTCAGTCGCTCTGCTCATGCTCTCTGTCATACAGACAGGTAACCTAGTTCT

WI-7901	33	C T	AGACTTAGGTACAATTGCTCCCCTTTTATATA[C/T]AGACACACACAGGACACATATATTAAACAG ATTGTTCATCATTGCATCTCATTTCCATATAGTCATCAAGAGACCATTTTATAAAACATGGTAAGAC CCTTTTAAAACAAACTCCAGGCCCTTGGTTCGCGTCGCTGGGTTATTGGGCAGCGCCGTGGTCGT CACTCAGTCGCCTCTGCATGCTCTCTGTCATACGACAGGTAACCTAGTTCT
WI-7901	271	T G	AGACTTAGGTACAATTGCTCCCCTTTTATATACAGACACACACAGGACACATATATTAAACAGATT GTTCATCATTGCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAAACATGGTAAGACCCT TTTAAAACAAACTCCAGGCCCTTGGTTCGCGGTCGCTGGGTTATTGGGCAGCGCCGTGGTCGTCAC TCAGTCGCCTCTGCATGCTCTCTGTCATACGACAGGTAACCTAGTTCTGTGT
WI-7926c	150	C A	CATTCCGCATCTGTCAACCAGGACAGAAAGCATGGACAAGGGGATGAGCTTTACAAAGATGACT TTGGAGATCAGAAAATTCATATTTAAGCAAAGTGATACAAACACAGTGATTTGGGAATGCCTTCATT TACAATGCAATACTTA[C/A]ATTTAATACTCTTGTGAGGAGAAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAATTACACTGTGGGAA
WI-7926b	28	A T	CATTCCGCATCTGTCAACCAGGACAGAAA[A/T]GCATGGACAAGGGATGAGCTTTACAAAGATGATGC ACTTTGGAGATCAGAAAATTCATATTTAAGCAAAGTGATACAAACACAGTGATTTGGGAATGCCTTCATT ATTACAATGCAATACTTACATTTAATACTCTTGTAGGAGAAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAATTACACTGTGGGAA
WI-7926	150	C A	CATTCCGCATCTGTCAACCAGGACAGAAAGCATGGACAAGGGATGAGCTTTACAAAGATGATGC TTGGAGATCAGAAAATTCATATTTAAGCAAAGTGATACAAACACAGTGATTTGGGAATGCCTTCATT TACAATGCAATACTTA[C/A]ATTTAATACTCTTGTAGGAGAAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAATTACACTGTGGGAA
WI-7947b	203	G T	AAGAGCCAGCAGGTCAAAAGGCCAACACACAACCATAAGCAGCCCACAAGGCCAGGTCCTGT GCTATCACAGGGTCACCTCTTTTACAGTTAGAAAACACCGGAGGCCACAGAATCCCATCCCCTTCC TGAGTCATGGCCTCAAAAATCAGGGCCACCATTGTCTCAATTCAAATCCATAGATTTCGAAGCCACA GA[G/T]TCTCTCCCTGGAGCAGCAGACTATGGGCAGCCCAGTGCTGCCACCTG
WI-7947	203	G T	AAGAGCCAGCAGGTCAAAAGGCCAACACACAACCATAAGCAGCCCACAAGGCCAGGTCCTGT GCTATCACAGGGTCACCTCTTTTACAGTTAGAAAACACCGGAGGCCACAGAATCCCATCCCCTTCC TGAGTCATGGCCTCAAAAATCAGGGCCACCATTGTCTCAATTCAAATCCATAGATTTCGAAGCCACA GA[G/T]TCTCTCCCTGGAGCAGCAGACTATGGGCAGCCCAGTGCTGCCACCTG
WI-7963b	145	T C	CATGTGCTGCATGAAGAGCTAATTTAAAAAAGCAAAGTAAGACTAATTATTTAAAATAAAAAATGCC ACAAATTTCATTTCTCCTTCTAAGTATTACAATGGAGTTTATTCTCTGCCTAAAAAGTGGAAGAAAT TGAGTGAATGA[T/C]AATTTGTAATTTAGGATAAGATCCAAGTTATTTCCCAACTCTGTTTCCC CCATAAAGTTAGGCATGAGGAGGCACTCATTAAAGGCAGAAGACGGAAAA

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WI-7972c	268	T	G	GGAGTTCTGGTTCCTACTGGGGGCAACCCTGGTGACCAGCACCATCTCTCCTCCTTTCACAGTTCTCT CCTTCTTCCCCCGCTGTCAGCCATTCCCATGAGATGATGCCATGGGTCTCAGCAGGGGAGG GTAGAGCGGAGAAAGGAAGGGCAGCATGCGGGCTTCCTCCTGGTGTGGAAGAGCTCCTTGATATCCT CTTTGAGTGAAGCTGGGAGAACCAAAAGAGGCTATGTGAGCACAAAGGTA
WI-7972b	268	T	G	GGAGTTCTGGTTCCTACTGGGGGCAACCCTGGTGACCAGCACCATCTCTCCTCCTTTTCACAGTTCTCT CCTTCTCCCCCGCTGTCAGCCATTCCCATGAGATGATGCCATGGGTCTCAGCAGGGGAGG GTAGAGCGGAGAAAGGAAGGGCAGCATGCGGGCTTCCTCCTGGTGTGGAAGAGCTCCTTGATATCCT CTTTGAGTGAAGCTGGGAGAACCAAAAGAGGCTATGTGAGCACAAAGGTA
WI-7972	268	T	G	GGAGTTCTGGTTCCTACTGGGGGCAACCCTGGTGACCAGCACCATCTCTCCTCCTTTTCACAGTTCTCT CCTTCTTCCCCCGCTGTCAGCCATTCCCATGAGATGATGCCATGGGTCTCAGCAGGGGAGG GTAGAGCGGAGAAAGGAAGGGCAGCATGCGGGCTTCCTCCTGGTGTGGAAGAGCTCCTTGATATCCT CTTTGAGTGAAGCTGGGAGAACCAAAAGAGGCTATGTGAGCACAAAGGTA
WI-7981	261	T	G	AACCCCTGAAATCGGAAGGGACTTCCTCTTCTCTCTCCCTGTTTAAATTATAAGATGTCAT CCCCTTGTGTCAGAGACAGACCCCCTTGCTTTGCTTGGCAGAGAGGACCCCACTGGACTGGGTTTG TCTCTGCATCTCATTGTAGAGCTTGGTGGCTGAGCTTGGCCCTATTAAGATAAATAGAGTTCCAAATA AGGATTGTTCACATGCCATCATAACCATTCCCATTGGTTCTCCTAAAACAT
WI-7992b	62	A	G	GAGCTTCCACAGTGAAGATGGAGAAGGTGAACTGCTTGTTTCTTCTTCACGAAATATNCCAGATTGTTTGGTC[A/G]T GCGTATGGCAGTGAGCAGGTATGTGTTTCTTCTTCACGAAAAATTAAATTGCTATCAAGAGCAAAC TATGAAACATTATATTCAAGATGTCTCCAGAGTGAAGATGCCGAGGATGAACTTGCATTGAACATTCC AGATGTGTGAGATCATGTGTATTGCAGTGGGCAGGTATTGCTTTGCTTGC
WI-7992	62	A	G	GAGCTTCCACAGTGAAGATGGAGAAGGTGAACTGCTTGAATATNCCAGATTTGTTTGGTC[A/G]T GCGTATGGCAGTGAGCAGGTATGTGTTTCTTCTTCACGAAAAATTAAATTGCTATCAAGAGCAAAC TATGAAACATTATATTCAAGATGTCTCCAGAGTGAAGATGCCGAGGATGAACTTGCATTGAACATTCC AGATGTGTGAGATCATGTGTATTGCAGTGGGCAGGTATTGCTTTGCTTGC
WI-8004b	183	C	T	ACTAAGAAATTATTATTGGTGGCCTATAAAACTCTGTTCAGTCTTTACTTGCTAATGATTTATTT CATTAAAGTAAATAATGATCATCTTGGGGAGGCATTTATAAAAACATATTTAGGAGAAATTTCTTTGA TTTATGCTATAAGGTAAATGTTGCATAATTTCTTGCCTATGTGAATTG[C/T]AGGTTTCCACTTTGAG AGAATTCTCTCAATCTAATAATAAAGACCAAGGGCCAGAAAACACTAAGATA
WI-8021c	57	C	T	ACAATCTCAGAAGGACTGTGCAAGTCAATGAGTCGCTTGTGAATTCTCATCTGGAAA[C/T]GATCCC ACGTCTTAGAACCTTCACCACCAAGGAGTTTTTCTGTGAGTGATTCTCAAGTCTTGGTAGGCATTCGA ACTGGTCCTTCACTTTGAGATTCTTTCTTTGCGCCTCTTATCAAGTCAGCACACCTTTCCAAG GATTTTACGTTGCGGCCTTGTTGAGGGGTGATTCGGTGAATTGCCA

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WI-8021b	57	C	T	ACAATCTCAGAAGGACTGTGCCAAGTCAATGAGTCGCTTGTGTGAATTCTCATCTGGAAA[C/T]GATCCC ACGTCTTAGAACCTTCACCACAACAAGGAGTTTTCTTGTAGTGATTCTCAAAGTCTTGGTAGGCATTCGA ACTGGTCCTTCACTTTGAGATTCTTTCTTTGCGCCCTCTATCAAGTCAGCACACCTTTCCAAG GATTTACGTTGCGGCTTGGTTAGGGGTGATTCGAATTCGGTGAATTGCCA
WI-8021	57	C	T	ACAATCTCAGAAGGACTGTGCCAAGTCAATGAGTCGCTTGTGTGAATTCTCATCTGGAAA[C/T]GATCCC ACGTCTTAGAACCTTCACCACAACAAGGAGTTTTCTTGTAGTGATTCTCAAAGTCTTGGTAGGCATTCGA ACTGGTCCTTCACTTTGAGATTCTTTCTTTGCGCCCTCTATCAAGTCAGCACACCTTTCCAAG GATTTACGTTGCGGCTTGGTTAGGGGTGATTCGAATTCGGTGAATTGCCA
WI-8024c	206	A	G	CTGAAAATTTACTATGCTCTCCACAACAAGAGCTCCCATTTCCACAGACACAGTCAATGTCAGTCA GCTTGTATTCAGGAGGACAGGGGCAGAGGGATCCCAGTGGCACTTCCCATGGGAAGACAGAAGAGAGT GGGCCCCAGAGATGGAAGGAACCCCAGTGTCATCACCAAACAACCATTTCAGCCGCCTCTAGCCTCTAA TTCCC[A/G]CTCTAGAACAGCTGGCCCTGGTCGTCAGTACACAAGGAAAGAGC
WI-8024b	206	A	G	CTGAAAATTTACTATGCTCTCCACAACAAGAGCTCCCATTTCCACAGACACAGTCAATGTCAGTCA GCTTGTATTCAGGAGGACAGGGGCAGAGGGATCCCAGTGGCACTTCCCATGGGAAGACAGAAGAGAGT GGGCCCCAGAGATGGAAGGAACCCCAGTGTCATCACCAAACAACCATTTCAGCCGCCTCTAGCCTCTAA TTCCC[A/G]CTCTAGAACAGCTGGCCCTGGTCGTCAGTACACAAGGAAAGAGC
WI-8077	167	A	G	GAATGAGCCTTCCTAGCCGCCGAGGGGACCTGCTGCTGTTGGCCTCGCACATGCATTCTATGGAATGC TTTTTGGCCAAGCGGGGGCACTGAGGACTAAGCTCTGANNNNNNNNNATCTCGCCCAAACTCCTTCT AAGGAGTCTGGGGTGTCATGCCCTACAAACC[A/G]TAAATTCTCATCAGATGGATTTATTTAACGTT GTGTATTGTGACTTACTTCCAATCTGACTCTGGCATAACAAGGGAAAA
WI-8118f	114	G	C	TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTTGGAATGACCACTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAAACTGGCAAATACAGAATGTAGCTTGTT[G/C]TTTTCTTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTTCTGATTTCCCTGCTCCTCCTATTCCTTCCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118e	40	A	G	TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTTGGA[A/G]TGACCACTCCCTTGCTAAGGAAGC TATGTACTTCATGCTGTGGAAACTGGCAAATACAGAATGTAGCTTGTTGTTTTCTTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTTCTGATTTCCCTGCTCCTCCTATTCCTTCCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118d	118	T	G	TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTTGGAATGACCACTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAAACTGGCAAATACAGAATGTAGCTTGTT[T/G]CTTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTTCTGATTTCCCTGCTCCTCCTATTCCTTCCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA

ID	Pos	B1	B2	Sequence
WI-8118c	44	C	T	TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTGGAATGA[C/T]CACTCCCTTGCTAAGGAAGCTATGTACTTCATGCTGTGGAAACTGGCAAATACAGAATGTAGCTTGTTTGTTTTCTGATTCCCTGCTCCTCCTATTCCTTCCTTGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTTCTGATTCCCTGCTCCTCCTATTCCTTCCTAAAAATCAGACTCATTGTGACCAGTCTTGAGGACTCAAGCTGAATGA
WI-8118b	88	T	C	TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTGGAATGA[T/C]GGCAAATACAGAATGTAGCTTGTTTGTTTTAGCCTTGAAGAGTACTTCATGCTGTGGAAAC[T/C]GGCAAATACAGAATGTAGCTTGTTTGTTTTAGCCTTGAAGATGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTTCTGATTCCCTGCTCCTCCTATTCCTTCCTAAAAATCAGACTCATTGTGACCAGTCTTGAGGACTCAAGCTGAATGA
WI-8171d	299	C	T	TTTCTCTCCTTCCGGGGGACCAAGGTACCTTCTGGGGCATACAAC[A/G]TGGCAGCAGGGCCTCGGGAAGAGGGGTAGGAGGACCGAGCAGCAGCATTCTCTGTAGAGGAAGACAGGAAAGGAGACCCTCTTGGCACACATTTATGGAGGGTTGTCCCTGAAGAGAAGGGCAGGTGGGGAGAGGTTCCCTGTTACTTAAGAGAAGGCACCAGTGGGCAAAGAGCACAATGAAGAGGATGATGATAAAAACAATCAC
WI-8171c	46	A	G	TTTCTCTCCTTCCGGGGGACCAAGGTACCTTCTGGGGCATACAAC[A/G]TGGCAGCAGGGCCTCGGGAAGAGGGGTAGGAGGACCGAGCAGCAGCATTCTCTGTAGAGGAAGGCAGGTGGGGAGAGGTTCCCTGTTACTTAAGAGAAACATTTATGGAGGGTTGTCCCTGAAGAGAAGGGCAGGTGGGGAGAGGTTCCCTGTTACTTAAGAGAAGGCACCAGTGGGCAAAGAGCACAATGAAGAGGATGATGATAAAAACAATCAC
WI-8171a	46	A	G	TTTCTCTCCTTCCGGGGGACCAAGGTACCTTCTGGGGCATACAACATGGCAGCAGGGCCTCGGGAAGAGGGGTAGGAGGACCGAGCAGCAGCATTCTCTGTAGAGGAAGACAGGAAAGGAGACCCTCTTGGCACACATTTATGGAGGGTTGTCCCTGAAGAGAAGGGCAGGTGGGGAGAGGTTCCCTGTTACTTAAGAGAAGGCACCAGTGGGCAAAGAGCACAATGAAGAGGATGATGATAAAAACAATCAC
WI-8171b	298	T	C	TTTCTCTCCTTCCGGGGGACCAAGGTACCTTCTGGGGCATACAACATGGCAGCAGGGCCTCGGGAAGAGGGGTAGGAGGACCGAGCAGCAGCATTCTCTGTAGAGGAAGACAGGAAAGGAGACCCTCTTGGCACACATTTATGGAGGGTTGTCCCTGAAGAGAAGGGCAGGTGGGGAGAGGTTCCCTGTTACTTAAGAGAAACCAGTGGGCAAAGAGCACAATGAAGAGGATGATGATAAAAACAATCACGGGCA
WI-8314b	85	G	C	GAGGGGAAATGACATCTGGAGATCTAGGTATGTGGCCCATTGCAATTGAGCACATTTCTTGGGTCTGTTTCTCTATCT[C/G]AGTCTCAAAATCTCAAAATACGACACTAACATGATGAACATGCATGAGCTTGAAAGTGCTCTGTGTAGTCTTATGATGATCTCCAATAGAACTTTCTGTGATGATGAAAAGATTCTACTTCTGACCTATTCAATAGGGGTAACCACT
WI-8314	78	C	G	GAGGGGAAATGACATCTGGAGATCTAGGTATGTGGCCCATTGCAATTGAGCACATTTCTTGGGTCTGTGCATGAGCTTGAAAGTGCTCTGTGTAGTCTTATGATGATCTCCAATAGAACTTTCTGTGATGATGAAAAGATTCTACTTCTGACCTATTCAATAGGGGTAACCACT

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WI-8321	178	G	A	---	TTTTAAATATGCCCGTTTAGAGCAGACAGTCACAATAAAAGTTAAAAAGTTACAATGTGTCCAG TGTATATACCCAGGNAATCCATTCTTGGTACTTTCAGAGCTGCTGTTATACTGAGTCTCTGAGAAG TCCCCTTAGATAATAGCTGCCACTTTCAGTATGGTTCAGAAT[G/A]AGTATCTTAGTATTCTTTCTA TTTTGCTATGGTTCTAGTTTATCAACCTACTTTATTAGCTGAACTGTTGGC
WI-8321	178	G	A	---	TTTTAAATATGCCCGTTTAGAGCAGACAGTCACAATAAAAGTTAAAAAGTTACAATGTGTCCAG TGTATATACCCAGGNAATCCATTCTTGGTACTTTCAAGAGCTGCTGTTATACTGAGTCTCTGAGAAG TCCCCTTAGATAATAGCTGCCACTTTCAGTATGGTTCAGAAT[G/A]AGTATCTTAGTATTCTTTCTA TTTTGCTATGGTTCTAGTTTATCAACCTACTTTATTAGCTGAACTGTTGGC
WI-8332b	123	A	C	---	TATGTACTCACTTTCAGTTACCCCCGTGCCTCCAGAATCGCATGTTGCTCCACCTGGGGGCGGATATA AATTACCTCTAGATTGTCCAAAGCCCAGTCTTTCCCTTGTGCAGCCTTAGA[A/C]ACTAAGTAG CAGTACTGTTGGTGTGTTTGTTCTTCCCCAGCAATGCCTACTGCAGCTACTTAGTAACAACTAG AGGTGGAGGGINTCCGGGGAAGCAGTTAGATGAGTTAAGTGTGATGCACA
WI-8332	114	A	C	---	TATGTACTCACTTTCAGTTACCCCCGTGCCTCCAGAATCGCATGTTGCTCCACCTGGGGGCGGATATA AATTACCCTCTAGATTGTCCAAAGCCCAGTCTTTCCCTTGTGC[A/C]GCCTTAGAAACTAAGTAG CAGTACTGTTGGTGTGTTTGTTCTTCCCCAGCAATGCCTACTGCAGCTACTTAGTAACAACTAG AGGTGGAGGGINTCCGGGGAAGCAGTTAGATGAGTTAAGTGTGATGCACA
WI-8378b	311	T	C	---	TGCGGGCTTAACAGGAAGCATGACTGGGAGGCCTCAGGAAGCTTATAATCATGGCAGAAGGCGAAGG GGAAGCAAGGACCTTCTTCACATGGCAGCAGGAGGAAAGAGAAGGGAGAAGTCTACACACTTT AAACAACCAGATCTCATGAGANTTCCATCACCNTCACCAGGCCCCTCCTCCAACACGTGGGG AACTGCCCCCATGATCCAATCAACCTNTCACCAGGCCCCTCCTCCAACACGTGGGG
WI-8378	308	T	C	---	TGCGGGCTTAACAGGAAGCATGACTGGGAGGCCTCAGGAAGCTTATAATCATGGCAGAAGGCGAAGG GGAAGCAAGGACCTTCTTCACATGGCAGCAGGAGGAAAGAGAAGGGAGAAGTCTACACACTTT AAACAACCAGATCTCATGAGANTTCCATCACCNTCACCAGGCCCCTCCTCCAACACGTGGGG AACTGCCCCCATGATCCAATCAACCTNTCACCAGGCCCCTCCTCCAACACGTGGGG
WI-8426	184	T	G	---	TTTAGCACATATTAGCATTAAGCCTCAAACGATACAGCAATATGTTACATTCTCTTGTGAAAACAG TTGTTGTAGACTGTTAANNNNNNNNAAATGTAACTCCGACTTGTGCCTAATAGGATTTGACCNTTAA GAGGNTTCTTTGCTGTGGANGGGGTGGCTTGCCCTTGAACTTCCATTCGT[T/G]GCCTTGTAGCTGGTG AGGCTGGGAGTATGGGANGGNCCCGGGGCCCTTGGCNATNGNATTCAGTGAG
WI-8450h	61	C	A	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTTACATTTTAACAGCCCTTCTACATACACTTC/AJCA TCTTCTCTATCTTAGTTCCAAGTTTTAGTTTCAATCCCAATTATACCAATTCCATTGTATTTTAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCCTCCACTACCCAGCAAACTAC AGAGAGGAGGATGGGGAGTGTAATATGAGCAGTACAGAGTCTTAATGCAATTCAT

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WI-8450g	55	T	C	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAACAGCCCTTCTACA[T/C]ACACTCCAT CTTCTCTATCTTAGTTCCAAGTTTTAGTTTTCAATCCCAATTATACCAATTCCATTGTATTTAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGAGCAGTACAGAGTCTTAATGCAATTCAT AGAGAGGATGGGAGTGTAATATGAGCAGTACAGAGTCTTAATGCAATTCAT
WI-8450f	108	T	A	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTACATTTTAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCAAGTTTTCAATCCCAATTA[T/A]ACCAATTCCATTGTATTTTAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCCTCCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAATATGAGCAGTACAGAGTCTTAATGCAATTCAT
WI-8450e	125	T	C	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCAAGTTTTCAATCCCAATTATACCAATTCCATTGTTA[T/C]TTTAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCCTCCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAATATGAGCAGTACAGAGTCTTAATGCAATTCAT
WI-8450d	125	T	C	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCAAGTTTTCAATCCCAATTATACCAATTCCATTGTTA[T/C]TTTAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCCTCCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAATATGAGCAGTACAGAGTCTTAATGCAATTCAT
WI-8450c	108	T	A	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAACAGCCCTTCTACATACACTCCATCTT TCTCTATCTTAGTTCCAAGTTTTCAATCCCAATTA[T/A]ACCAATTATACCAATTCCATTGTATTTTAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCCTCCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAATATGAGCAGTACAGAGTCTTAATGCAATTCAT
WI-8450b	61	C	A	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAACAGCCCTTCTACACT[C/A]CA CTTCTCTATCTTAGTTCCAAGTTTTAGTTTTCAATCCCAATTATACCAATTCCATTGTATTTTAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCCTCCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAATATGAGCAGTACAGAGTCTTAATGCAATTCAT
WI-8450a	55	T	C	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAACAGCCCTTCTACA[T/C]ACACTCCAT CTTCTCTATCTTAGTTCCAAGTTTTAGTTTTCAATCCCAATTATACCAATTCCATTGTATTTTAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCCTCCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAATATGAGCAGTACAGAGTCTTAATGCAATTCAT
WI-8458b	60	A	G	CAAGGAAAGCTGTCAGTCTTCATAAACTTCAAAGAGTTACAAAAATACGTATTTTTTAA[A/G]CTA CAATTCAAGATTAGCATCCAAACCTACAAAACATGATGTCGTCACACCATACAACCTTCAC ACCTGGCTACAGCAATGTTGACTTACATCACCATTGTTTATACTTGTGAAAACTTTATTGTGCACAGT GACATCCATTCCGCCAGACTTAATGTTATAAAGCAGCTGAGCAGAGTTCTCA

WI-8461c	105	A T	CTTCCTCCTCCAAAATCTCTACATGATAATACTTGAAGAGACAATATAACTACAACCTTACAAATGCCAATTA GACAAAGAGANTAAATGATATAAATATAAATCATTTTT[A/T]NNNNNNNNNNCCTTGTCTTATTCACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTTAACAACATTACAANTTTNTTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAAGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461b	38	T C	CTTCCTCCTCCAAAATCTCTACATGAATACTTGAAGACAA[T/C]ATAACTACAACCTTACAAATGCCAA TTAGACAAAGAGANTAAATGATATAAATCATTTTTNNNNNNNNNNCCTTGTCTTATTCACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTTAACAACATTACAANTTTNTTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAAGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461	38	T C	CTTCCTCCTCCAAAATCTCTACATGAATACTTGAAGAGACAATATAACTACAACCTTACAAATGCCAATTA TTAGACAAAGAGANTAAATGATATAAATATAAATCATTTTT[A/T]NNNNNNNNNNCCTTGTCTTATTCACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTTAACAACATTACAANTTTNTTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAAGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461	105	A T	CTTCCTCCTCCAAAATCTCTACATGAATACTTGAAGAGACAATATAACTACAACCTTACAAATGCCAATTA GACAAAGAGANTAAATGATATAAATATAAATCATTTTT[A/T]NNNNNNNNNNCCTTGTCTTATTCACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTTAACAACATTACAANTTTNTTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAAGAAAANTCAAGGATTTGCAAAAAGGGGG AATAACATGTTATGAAACAAGCTGGTTACAAGTAGTAGGTAGATGACTTAATTTTTGATAAAAAT TAAAAAGCAT[A/G]AACATGCATATAAAAATTAGATTATGTACAAAATACCAACAGTATTTACTTC TGCTCAGTAATTAAATATTCTTCCCTTGTTTGTCTTTTAAAAAACATTATTTCTGAAAAAAAAA ATCAGAAAAACATGATCGTCGTGGAGAATTATTA
WI-9438	77	A G	ACAGAAAAATTGACCTTTATTTGTTGTACTAAAGCCTGTTTAACTTTGATACAAAGTAACATTTTAGTA CAGAAAAATCCCAGTCTGTCAGCTACCTGT[C/T]TGTGCACACTGTACCATCTCAGTCCCACTCT GCCTGTAACTTAGAAAACAGCCCCTACCCCCAGAGGGTCTGCGAGTTAATACCTTGAGAATAGTCTA CAGTTTTTCATAGTTTGTCTGAGCTAGAAAACTTGTACCTGTAAAACAAAG
WI-9439b	101	C T	ACAGAAATTGACCTTTATTTGTTGTACTAAAGCCTGTTTAACTTTGATACAAAGTAACATTTTAGTA CAGAAAAT[C/T]CCAGTCTGTCAGCTCAGTCAGTACCTGTCTGTGCACACTGTACCATCTCAGTCCCCACTCT GCCTGTAACTTAGAAAACAGCCCCTACCCCCAGAGGGTCTGCGAGTTAATACCTTGAGAATAGTCTA CAGTTTTTCATAGTTTGTCTGAGCTAGAAAACTTGTACCTGTAAAACAAAG
WI-9439a	76	C T	GAAGGCTTGATTAAGGGAGGNTTTATTTGATGTNAACTTACCATTCCATAGACTATAAAGANCATTA TAAAAAAAT[T/C]CCTCTAAAAGNGACACATGCCCCAAAATGACCANGNCATAAGCAAACCTTTAAAT TACTCATCTTTCATATGTGTTTGTNCCCCTACTNTTATCACTGTCTTGTCTTCTGTCTTTTGTCTACCTA TGNGAACTGCACACTATCTCGTGTGGCAATATTGT
WI-9446b	75	T C	

ID	Position	Alleles	Sequence
WI-9446	75	T C	GAAGGCTTGATTAAGGGAGGNTTATTTGATGTNAACTTACCATTCCATAGACTATAAAGANCATTA TAAAAAAAT[T/C]CCTCTAAAGNGACACATGCCCCAAATGACCAANGNCATAAGCAAACCTTTTAAAT TACTCATCTTTCATATGTGTTGTNCCCCTACTNTATCACTGTGTCTTCTGTCTTTTGTCTACCTA TGNGAACTGCACACTCTGTGGCAATATTGT
WI-9497b	185	A	ATTAAAAATGTCAAGGTTCATGTTACATTTTCTTATATCAAGTACAATGGTATATATACTTTTTTTT GAGATAATTATTCTAGATTCCAGGCTTTCTTCTCTAGAGTGTAAGTNCCTAAAGCTTATAGTTTACATTGA TATCTAGACATATATCTTAAAACAGTCTCCAAATTTNCTTAATTAATCAAAGTATGTTAATGTCACTT GGAATTCTACATGGAAAAGCCAACAAAATAACTAAAACTTGACTAATGAAG
WI-9497	185	A	ATTAAAAATGTCAAGGTTCATGTTTACATTTTCTTATATCAAGTACAATGGTATATATACTTTTTTT GAGATAATTATTCTAGATTCCAGGCTTTCTTCTCTAGAGTGTAAGTNCCTAAAGCTTATAGTTTACATTGA TATCTAGACATATATCTTAAAACAGTCTCCAAATTTNCTTAATTAATCAAAGTATGTTAATGTCACTT GGAATTCTACATGGAAAAGCCAACAAAATAACTAAAACTTGACTAATGAAG
WI-9523b	193	C A	GTGAAAAAGTTTCTATTCATTCCATCAATAGATTGTGCTAAGGATCATCATTTTGGAAGAATGTG CAGCATTCAGAAGTTGTATCTCATCATGCAGTCAGCATTTATCTAAAAGTACGTGCACA GACTCAGAGACAATTACAAACTATTCAGCCATGATCTATGGTGATTTCCACACATTGTA[C/A]AGTG AAAGCTCTTCAGCTTGGGAACAACTGTCAAGGCAGCAGTGCATGCACATATAT
WI-9523a	47	G A	GTGAAAAAGTTTCTATTCATTCCATCAATAGATTGTGCTAAG[G/A]ATCATTTTGGAAGAAT GTGCAGCATTCAGAAGTTGTATCTCATCATGCAGTCACTCAGCAGCATTTATCTAAAAGTAGCGTGCA CAGACTCAGACAATTACAAACTATTCAGCCATGATCTATGGTGATTTCCACACATTGTACAGTGA AAGCTCTTCAGCTTGGGAACAACTGTCAAGGCAGCAGTGCATGCACATATAT
WI-9554	202	T C	AAAAACACAAGTTCATACATCACAAAAAACCTTCCATTATAAACACAGAAGTGATTATTACCAGAC AAGCATCAGTGATGTATACTGCCTTNCTAGTTGTTATTGTAACAATGCTGTAGATAATGCAGCCCATG CAATACACCCAAGAACACTAGAGTCCTACACCCAAGTAGCCTACATAATGATAAAGCAGCCCTCTGCAAGTG G[T/C]CGCTGGATACCCACTAAGGAAGTCTACTGCAGCCATGTTGGTTATGATTT
WI-9555	97	G A	CCAAAAGCCAAACCATTCATATGTCATATGTGGATTTCATAAACATTTATTGATCCTTTTTGAGGTAAGTAT AAATACCTTTACATGTGGCTAACCTTCTAAC[G/A]CTTGAAAAATCAATTTCAAGGGACTCTTAATCA GTTAAATAATCTGCTTTAGAAGGCACAAATGATCATACTTCAGATTAAAATACAGGTAAGTATTCAG GGNTAAAATGGTACAAAAAGGCTGTAACTCTTTTNCTTCACATTGATCACA
WI-9625b	172	A T	TTGAACATTTAATGAATGACAAAGAACATAACATCCTCTGAAAATCTGCAAGTAAATCAATCATTTT TAAACAATAGCTACCATATATTTGTATCTNCTCNTCCTTGGGAAAAAACTTGGAAAAAAAACACGCACA TAAGTATCATAACTGAGGGTTGTGGACAAGTTACTTCT[A/T]GTTACCAATTTTATATTGACATAA AGTAGCACAGAGACTAGTTATTTCATTTAAAAAAAACACTGACAAATCTTTTC

ID	Pos	Allele 1	Allele 2	Sequence
WI-9625	172	A	T	TTGAACATTTAATGAATGACAAAGACATAACATCCTCTGAAAAATCTGCAAGTAAATCAATCATTTT TAAACAATAGCTACCATATATTGTATCTNCTCCTTGGGAAAAAACTTTGGAAAAAACACGCACA TAAGTATCATAACTGAGGGTTGTGGACAAGTTACTTCT[A/T]GTTACCAATTTTATATTGACATAA AGTAGCACAGACTAGTTATTTCATTAAAAAACACTGACAAATCTTTC
WI-9647	144	C	T	TTTTTCTGAGATTCAAAGAGCTACATTTTGGTTAGTGTAGTGTCTACTATACCTTTTTCATCCTTTCA ACATCTTTTGTCACATTTAGGTGATGCTCTGTGTAAACAGTGTATTGCTAGACCTAAAAATCCAAGCT TACAACT[C/T]GTCCTTTACCTGATACATTTATTCCATTTACTTCATTTGATTTTTAAAAATGTTA ACTTAATACGTCTCTTTCAGATGTCCCTGCTTTTAGTTAATTGTGTT
WI-9676n	114	A	G	GGCCACTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCA[A/G]GATGTGGCTTCCTGCC CCCATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAATCCTATGCATTGTTTGTT
WI-9676m	184	G	T	GGCCACTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTCCTGCCCCC ATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGC[G/T]CATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAATCCTATGCATTGTTTGTT
WI-9676l	84	A	C	GGCCACTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGGTACCAAGGNTCTG[A/C]GTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTCCTGCC CCCATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAATCCTATGCATTGTTTGTT
WI-9676k	202	C	T	GGCCACTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTCCTGCCCCC ATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGAGGG[C/T]CAGGGTCTCTCAGCTTTAAAGCCTTGGAATCCTATGCATTGTTTGTT
WI-9676j	92	C	T	GGCCACTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTTGTA[C/T]GGTCTTTATAAATGCAGAGCAAGATGTGGCTTCCTGCC CCCATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAATCCTATGCATTGTTTGTT
WI-9676i	173	T	C	GGCCACTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTCCTGCCCCC ATTTCACCTCAAGGCATCTCTTCAGCAACCCACATGGCT[T/C]CCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAATCCTATGCATTGTTTGTT

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WI-9676h	134	C	A	GGCCACTGTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTAGGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCCCC[C/A]ATTTCACCTCAAGGCATCTTCAGCTTTAAAGCTTCTCTATGCATTGTTTGTTTAGGCCAGGGGTCTCTCAGCTTTAAAGCTTCTCTATGCATTGTTTGTTT
WI-9676g	202	C	T	GGCCACTGTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTAGGGGTACCAAGGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCCCCCATTTCACCTCAAGGCATCTTCAGCAACCCCACATGGCTTCCCTCTGTGCGCCATGAAATAACTTGAGG[C/T]CAGGGGTCTCTCAGCTTTAAAGCTTCTCTATGCATTGTTTGTTT
WI-9676f	184	G	T	GGCCACTGTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTAGGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCCCCCATTTCACCTCAAGGCATCTTCAGCAACCCCACATGGCTTCCCTCTGTGC[G/T]CATGAAATAACTTGAGGGGTCTCTCAGCTTTAAAGCTTCTCTATGCATTGTTTGTTT
WI-9676e	173	T	C	GGCCACTGTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTAGGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCCCC[T/C]CCCTCTGTGCGCCATGAAATAACTTGAGGGGTCTCTCAGCTTTAAAGCTTCTCTATGCATTGTTTGTTT
WI-9676d	134	C	A	GGCCACTGTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTAGGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCCCC[C/A]ATTTCACCTCAAGGCATCTTCAGCAACCCCACATGGCTTCCCTCTGTGCGCCATGAAATAACTTGAGGCCAGGGGTCTCTCAGCTTTAAAGCTTCTCTATGCATTGTTTGTTT
WI-9676c	114	A	G	GGCCACTGTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTAGGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCA[A/G]GATGTGGCTTTCCTGCCCCCATTTCACCTCAAGGCATCTTCAGCAACCCCACATGGCTTCCCTCTGTGCGCCATGAAATAACTTGAGGCCAGGGGTCTCTCAGCTTTAAAGCTTCTCTATGCATTGTTTGTTT
WI-9676b	92	C	T	GGCCACTGTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTAGGGGTACCAAGGNTCTGAGTTTGTA[C/T]GGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCCCCCATTTCACCTCAAGGCATCTTCAGCAACCCCACATGGCTTCCCTCTGTGCGCCATGAAATAACTTGA
WI-9676a	84	A	C	GGCCACTGTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTAGGGGTACCAAGGNTCTG[A/C]GTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCCCCCATTTCACCTCAAGGCATCTTCAGCAACCCCACATGGCTTCCCTCTGTGCGCCATGAAATAACTTGA

ID	Pos			Sequence
WI-9738b	40	C	A	TGGACCAAACACAGACAGATGTATTCCTGGTGCCTGTGTA[C/A]ATTACAACTCATTGATCACATGC AGCAACATCAACATCTCAAGGAGTCCATTGTTCAAAACACAGTAAATGACTCCACATTTCCCTTT GAGTCAACAAAAGACTCTGCTTGTCACCTTGCCTGGGGCACATGTCTGTATTGCTGTCC TCTTTTATTTCTGTCCCTTATGTTGGTGGGCACATGTCTGTATTGCTGTCC
WI-9738	40	C	A	TGGACCAAACACAGACAGATGTATTCCTGGTGCCTGTGTA[C/A]ATTACAACTCATTGATCACATGC AGCAACATCAACATCTCAAGGAGTCCATTGTTCAAAACACAGTAAATGACTCCACATTTCCCTTT GAGTCAACAAAAGACTCTGCTTGTCACCTTGCCTGGGGCACATGTCTGTATTGCTGTCC TCTTTTATTTCTGTCCCTTATGTTGGTGGGCACATGTCTGTATTGCTGTCC
WI-9756	47	A	-	ACTGAAATGTAAATGGCCAAGCACCCAGGACCTTAAAAATCATAAGAAGTTAATCTGTGGGAAAA GAGTAACTACAAAAGCATCTAAACAAGAGCAGGATGTGAATGTGTCCCCTTATCACTTTAGTC AGTAAAGATAAGAAAGCCCTGGTAGTATCCACTTCCACAAACACACAGAATATACACTTTTGGAAG ATTTCCACTTAACCACTGTGATTCTTCACTTTTTATGATTTAAAACTCTCCGTGG
WI-9758	135	A	G	GATGGTCCCTTAAGGATTTGCATTGGTTAATGGCAGACTGGTGCAAAAGAGGCTGAATTGAATAAT TAGGAAACTGGGGAGAATTCAATTCAAAGAAGAGAATTCTTGTTCGCAAGGTCAATTTTATACTATTTA A[A/G]TAAAATAACTCTGGTAGTTCTATAGCAAATGCTAAGTAAGTAACCGCTGGTTTCTAAATT ATTACG
WI-9778	127	G	A	ATTTAAATCCAGGCAGCGGGGGAAATGGATACTTTCATATGTCTGTACCCAACTATAAACTTTTG GTTCTCATGCACCATTTCATTTTGCCTCTCCAAGTACCTGATTTTACCAATT[G/A]CTCTC ATAATTGACTTTGCTACTGGAAGAAACTCTTAGAATGTTGGAATTTCTCTATTACACACTTTGCCTCA AAGAATGTGTCAGTCAGGACTAAAGGCAATAGTCTCAGGGCAGACAGCC
WI-9832	116	C	A	TCTCCCCTTTGCCTCCTCATGCCCACTCCCCTCCAGCCTGCACAGAGCGTTTCTCCAGTGTAGTCTCTGGT CCATCTGCATCAAAATCACCTGCAGGACTTGCTGACAATGCAGTTTC[C/A]TGGATCCCACCAGGA CTCAAAAAACTAGGAATTGGGAGAAGAGGGACCTGGAATCGGTGTTGCTAGCAAGCCCCCAGGTGG TTTGTAAGTGGACTAAAGTTTGAGGACCAGACATGGAAGGTTGGCTTGGC
WI-9841	101	A	G	TGGAAAAATAGCTTTATCAATCTGTGATTAATCAATCTCTGATAATGCATGGAGAAATGCAGAATGGCATGA TATGAAGAATTCCATTTTGAATGAATAAAAATATAC[A/G]TGTGTATGTATATAACTTATTAACACTT AGGATTATATACACACAATAAAAACGTCTGTAAGGATAAACTAAGGTTCTATCAGTGGGAAATGAGA TTGAAAAGAGGGGGATGTGTTACTTGTTACTCTGTTG
WI-9880c	222	G	A	GAACTAACACCTTTCTTGCATGGATTTTCTTGATTATTGGCAGTTAACAATAAAAATGTTATTAGATC ACTGGTGCTTCTGTGTGGGGTTGAGTTTTTATGATATCTCCTGTTTAAAATTATATTTTATATAAGCACTGTGA GTTGTTTTCTACATCCTTGGACTATATAAGATCCTCTTTAAAATTATATTTTATATAAGCACATGAA AATGGGAATGAAATAATGA[G/A]ATTGACATAGGAATTACCTACATATTTTG

ID	Pos				Sequence
WI-9880b	157	C	A	---	GAACTAACACCTTCTTGCATGGATGATTTTCTTGATTATTGGCAGCAGTTAACAATAAAAATGTTATTAGATCACTGGTGCTTCTGTGTGGGGGTTGAGTTTTATGATATCTCCTGTTAGACCCATAAGGGAGGCTGTGAGTTGTTTTCTACATCCTTGGA[C/A]TATATAAGATCCTCTTTAAAATTATATTTATATAAGCACATGAAAATGGAATGAAATAATGAGTTGACATAGGAATTACCTACATATTTG
WI-9880a	108	C	T	---	GAACTAACACCTTCTTGCATGGATGATTTTCTTGATTATTGGCAGTTAACAATAAAAATGTTATTAGATCACTGGTGCTTCTGTGTGGGGGTTGAGTTTTATGATATCT[C/T]CTGTTAGACCCATAAGGGAGGCTGTGAGTTGTTTTCTACATCCTTGGACTATATAAGATCCTCTTTAAAATTATATTTATATAAGCACATGAAAATGGAATGAAATAATGAGTTGACATAGGAATTACCTACATATTTG
WI-10183	127	C	T	---	ACACTGCAGGCACTCCAAATCCTNACAGACATATGCACTTCGGAATCAACTCAGGCATGCACAGCATCCCTGTCTGCTGGAGTTTATTTAAAAAACAACGCCCCAGTTATCACAGTTCTNTTTGT[C/T]CACCATTTTCCATAACAAAAGAAGCTACACAAAATTNGGGGGAGANACTCTCTTTGGAGACTGACACATTTGCAGAGGGGTCATGAATAATGATTCCAAA
FB25G10b	109	A	G	---	TCCCTCAATGACAGATGAACTAAATTTCTCTTGGGTAAGAAATACTTATGTCCATTGTGATTAAAAAGTCAGATTCAAGACACACTGCTTTATGTACAAGAAAATGGAA[A/G]TGATTTAGATCCTCCCCAGTGACAAGTAAACTGAACTGACCATATTTATACATAAAAATGGAATGTAAGAACCTATTTTGGATATCCCGGAC
FB25G10	109	A	G	---	TCCCTCAATGACAGATGAACTAAATTTCTCTTGGGTAAGAAATACTTATGTCCATTGTGATTAAAAAGTCAGATTCAAGACACACTGCTTTATGTACAAGAAAATGGAA[A/G]TGATTTAGATCCTCCCCAGTGACAAGTAAACTGAACTGACCATATTTATACATAAAAATGGAATGTAAGAACCTATTTTGGATATCCCGGAC
IB3071	102	C	A	---	ACAACGCTGAACTTCCATAACAGTACAGTCAATGGTACAGTCAAACATCACAGAGAACACACAATTTAGATGAACTGAAATTATAAGNTAAATAAAATAAAAT[C/A]CAATTTCAGNAACAAAATCAAAACATTAAGGNTCCCTGNNATATTCTTAAACCCTAATGAGATTTCACTGGNCTCAAGTCATTTTGTAGTGAGGCATTCACAATATGACCCTATTAACCCAGTCTAGGGATTCTG
NIB551	161	C	T	---	CGTCCTTTCCTTTTGAGATTGCAATTAAGTAGTAGATAATATGAGAGGAGAACTGACAATTGGGGTTGTCCCTACTGAGCTTGGGGCCCAGGTGGTGTACTTAGGAACCCAATCCCACCCAGAGAGACTCATCTATGTTAACACTAAGGATGCCCTGGAGGAGGTC[C/T]TGACCACCACATCAGCGGCCATGCGGGCCATTGTTGATTTCAGCTTTGCAAGCAGCGTAGTGACAAGTGAGAAAACCAAAGCTTGTCC
S722904	51	G	T	---	AGCATAGAAAGTGATTTATATTTTTAAATGGTTTCAAGTGGAAGTTCCTTT[G/T]AATTTGTCAGTTCATTCCTGGAAAATCTTTTGAGTTAAAATAAGGATCCTAGGACAGTACCTGAACTACAGGCCCTAAAGAGAAATTGCCTCAAACCACACAAGTGCTGTAACTTCCTCCCCTTTCTGTCAAATTGGTTGTCTTTAAATATTGCAAAAGTCCTGATGTCTAAACAGTATTTGGAGTGTTTTCAGTGTCTGTA

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UTR-00481	115	C	T	TATTCTTTTATCCTGGGGCCACAGTTCTTGATATTATTCCTCTCTGTGGTTAAAGACTGAATTTGTAAACCCATTCAGATAAATGGCAGTACTTTAGGACACACAAACACACAGA[C/T]ACACCTTTTGATATGTAAGCTTGACCTAAAGTCAAAGGGGACCTGTGTAGCATTTCAGATTGAGC
ESTC1	33			CCCTGTGTAGCAGTCTTCAGCCTCCTCCTCTACCCTACNAGATCTGGAGCAACAGCTAGGAAA
ESTC102	37			GCTACTACCAGGCGGCTGCTTCGTTGGACAAAAATAACNAGGAGGCATCCACGGGATTAGTTA
ESTC103	21			GCCATCAAAATTTCCTTCACANTCAATACTGTTGAACAACAAGATAACACATCTTCTTGCTCATCCCACTTGAA
ESTC107	20			TGCTGGCTCACTTCCTCACANGCTGTATTACCTTTCAGAGCTGAGTGAGGCTGTGCT
ESTC109	35			AAAACCAGGAAGGCCCTGCCCCGCAGAGGCACATGNACAGGGCAGTGCACAGTGACC
ESTC110	23			AAACCTCACACAGAAAAGAGGANAACACTCAGAAAATGTGATTACAGATTAGGCA
ESTC113	37			AAGGGACACAGTGTTGCTGACAAGGTGACACTGAACACANAACAGTTTCCTTAATTGTAAAAGCGGGCATCG
ESTC117	24			AATTGGCTCTTCTCCACATGATACNTAAGTTCAAGGTCCAAAGTTCCTATCACAATTTACAAAAAGCCTCCA
ESTC119	24			TGTCAAGCAGATCTTGAGGGTTATNGTTAAGCCTGATAACAGCCTCTT
ESTC122	34			GACAATAAACAGCTAAGCTACTGACATAAAATATNCAATAAATTTATGAGATATAAGGTACAGATGAGAAAATCTGAAA
ESTC123	21			GAAGCCAGTATGTTGTGGCAANATTCGAGAAAACACTGAAAAA
ESTC128	42			GCAGAGGCATCAGATAAAGGCCTCAGAAAAGCCCAGGCCATCATNTTCCATGGGACCAGGCTGGCTCAATGTGGAACTGG
ESTC129	20			AGTCACCATGCCCAGCCTAGNATGAGTTTAGTAAGATTTGGTTATGCTGGGGAG
ESTC13	46			GTGTATCTGGGCTTCATGGGATGCATAAAATTTTCCAGTTGGTAAGNAGCAGGTGCCGAGGGTCTGGATCAGAAAA
ESTC130	49			GCCTGCTCACAAGGTAGACAAAAACATAAATCTTCAGGAAAATGAAACANGAGAAGCTGAAACAATCTACACCTGAATG

ESTC132	30	GGTAAAGTCTAAATTACTGCCTTAGCAAACNCTATGTGTGTCAGGTTTTCTGCTGCA
ESTC137	21	CCAGTTTGGCTTCTGTCCTCANAGTCTCTCCATGTGGCAAACA
ESTC139	45	AGGAGCACAGCCTAAGGACAATGAAGGTCAGAGAGTTCTCAGAGAGGNGGGGGCTGGGTCCCTGAGCTAG GAGGAGG
ESTC14	20	CCCATTGTGGTCACAGGAAGNAGAGGAGGCCACGTTCTTACTAGTTTCCCTTGCATGGTTTAGAAAGC TTGCCCTGGTG
ESTC142	72	CCTAGGCTCATAACAATACAGTCTCAATACAAAAGACGTAATAATCTATTTTATTCATTTTAAATC AAAGANACCATTCCATTTCCTAACAAACA
ESTC143	29	GTTTACGGAAAGTACTGAAAATGCTATTANTAGCTGAATTTGTGATTTCCTTTTG
ESTC144	26	AAATCCATATTTTCTTGACATGAGGTNGCTTTTAGCAGCATTTCGG
ESTC146	20	CATGTCCAGGATAAGGAGCANACACCAGGATTTATACACGGTGGCAGCG
ESTC148	42	TCTTTGGTTGTCTACACAGACACTTAAGTACTGTATCGCTGTNATGCAGCGGCCCTGTGGAGGCCCCTG GGGGTGGCTGGGCCTGGCCTGTGTCCTGAG
ESTC149	28	TCAGTTCATTTATTTGCTTAAGAGTTANATACCATGAGACACACAGTTCTGG
ESTC15	28	GGATTGTAATATTGCCAGCTTTGTAAAGNCATTAAAGCAGAAGTTTCTTCAGTGATCTT
ESTC150	20	CCAGGAAAACAAAGCACACANACTTATAGAATACTTTGGTTTAAAAATTATTCATAATATCAATATT AAACCTGATGTTTAAAGAAACCTAATGAGA
ESTC151	49	GAAGCTAAGGCCCCCATTTTTTTTCTTTAATACAAATCTACTGGTGCTNAAAACTCAGAGCTTAGGA AACACAGCC
ESTC155	37	TTTTTAATTGACAACTCAATCTCTACATACACATACAGTNTTGCACGAATTATAAGTGGATCAACAATT ATATTATTGATACAAACTCATGAGCATTTACA
ESTC156	32	GCAGCATTTGTGACAGGAGAGCGCAAAACAAANCCTGGCTGCGCCTCGGGATGGAGCGGGGCGGCCTCA CCACCACTGCAT
ESTC158	35	ACCAAGCACCCTGGGATTTACTGTCTTGATGACTACANGGCTTTGCACAGTCTGAGATGCTTCAGTGTGC AA
ESTC159	31	AGCTGGCAAGAGAGACTTCCTGAGGCACATCCAGNTACGTTGGTCAATTTAGGGCACGGTCGTGGTTCTGCA GCTTTGAAAGG

ESTC16	23	CACTGAATGTCTGCCATGAGCCNCAAGCAGCACAGTGATCATCACCCACAAGGACAGGTT
ESTC160	38	TTCTAGCATTGCTGGTGCAGTGGGGGCCTGAGCTGGGGNGCAGTCGGCAGTGTCACTGGGCCCGTTTG GGACTGGGTTGA
ESTC162	36	CTCTTCGTCCGTTTGCAAGTTGCTGTTTGTTTCCAGNTACACCAGTCAGAGCTCCACAG
ESTC164	31	TCATTCTCCATAGAATATATTGGTTTTGTAACANCGAATACAATCCAATATATAACATTAAAACAATCC GATACATACCA
ESTC169	22	GTCTCTGGGTGTGCAGGGAATCANTTTGCTGGATTAGAGGAAAGGTGCCGCCGTCTGTTTCCATGACTT
ESTC176	23	CACCTCCTCCCCTGAGCTACCCANGTAGTGTCTGGGAGCTGGCA
ESTC177	42	TGGGTGGCTCTTAAATACCTTCCATTATATTTCAAATTTNCTTTATTCTATTAAAATACCTTTTAT TCTCTTATTCCCATAAAAAGGCAACCAA
ESTC18	29	TCAGACACTGCCGACATCAGCATTGTCTCNTGTACAGCTCCCTTCCCTGCAGGGCGCCCCTGGGAGAC AACTGGACAAGA
ESTC181	21	TAGGGATTCCAAGTTGCCTGGNTTAATATAATACATATTCACAAAATTTACACAGCTCATGCGATAC CA
ESTC186	43	GCTTGACTAGCGAGGCTACATCACAATTTATAAAGTGCCAGATNAGTGCTAATTGTCATTCAGCTTG ATTTTCACCTCA
ESTC187	24	ACCATGATTGCCTCACACAAGCATNATCAATCGCCACGAGAGACTGGATGCCAAAGAGTATGGCTGG
ESTC188	25	TCTATTAACAGGGTTATGTCACACCNTGTCAACCTCAAAACAGATGATACTCATCACTTGTCTTCCAT CTTGC
ESTC189	27	AAAGTACAAATCCAGTATATGCAGAAAAGNTACTCAGCATCACACTCGTGATCA
ESTC196	42	TCCTCAAATACCACTTCCCCTAACTTATCCAGTCTAGTAAGCNTTTCAAAGGAGGAAAATGGGTTAC CTTTCAGGGG
ESTC197	26	ATCTCCAGTGTCTGCTGCCTCCTCCCNGCAAAGTCTCCCACAAGCACA
ESTC20	33	AAGATTAGGACAGACCGCGGTATAGTAAGCTCCAAGAATCTAGAGGGGGGCTGTGTGGGAA CGCTGCTTAGATC
ESTC200	44	TTTGGTGAAAATCCCAATATATGAGTTTAAAAAAAAATCATTANCATCATTAACAGTACTTTAAAT CAATTACTCCTTTGCCTGCAACAG

ESTC201	35	TCTTACTTGGGTAGTTTAGCAAACATTTTTAAAANCCACATCCAACAGATTGGTT
ESTC202	22	CTGCTGGAGGAGGAGGACGAGACGGGNCAGGCGGCCTGGGTGGCGCCCCAGAAGGCTGGCGTGGATGTTCGAGATGAGCC
ESTC203	27	ACACTTAACAGGTTAAAATATCCAAATNAAATTTACTGCAACTTTTGTAGAATTTTATTGTGCTACAAGACACGTTGCA
ESTC208	43	TATAGCCCCATCGCTCTCAGTTATTAGAATCTGAGAGGGATAANAGCAATAACTATTGTTTAAAAGCCTAAGAGTGAAAA
ESTC210	29	GATGAAGTGGCTTCCTTTGGCGAAAGGGATNAAGAAGTGAGTGACGGTGACCTGTG
ESTC212	27	GGGTAACCTGATGAGGAAGCTCTAGTGNAGAAATTCAGGACGCGGGTCTTCAGAGCAGAGGGCTTGGTTCAAGTC
ESTC214	21	CTCCAGAGTCCCTCCTCTCANACCAGGGGCAGGAGGGAGGTTAGGGAAT
ESTC216	49	TGGCAAGAAATTTATTTACACTAACACAAATTAATCACAGGTATTNTTAGATTGGTCAGAAAACAAAAGACCA
ESTC217	28	TTTTGTCAGTAAATGAGCAATACACTGANTGGAAATCTGCATGATTAAATAACATTAACAAGTTCATAAACACACCCCA
ESTC219	32	GTACACATCCTGGGGGGTGAGCACACAGCAAAANGGGGTGGGACGTGCAGAGAGGTATAGGGTAAAGGCAAAGGAAGC
ESTC22	41	TCATTGAAGAAAATTATGGGTTTATTTCTTATTTCTAATTGNAGAAATGCTTAATGTCACAGGCTACATAAGGGCC
ESTC223	27	CTTCTGAAGCCCAAGAGAGGGGCAGAANGTAGTTCTTGATTTAAAAAAACAGAAAGGGGAGGAGGA
ESTC224	37	CGAAGGTAGATTCCCTCACATATTACAAAATACANAAACACACACACACACACA
ESTC225	20	TGCACTGTTACTCCCCAGACNGAGAGCTTACATACCATATAGAAAGAGCATAAGTGCTTCAGAAGGAATGTGTAGGATCG
ESTC23	27	TTCTACTTTATTTCATATTCCCACCACNATAAGGACTCCTTTAATTTAAACTAAAAACCATACAGGGTTCCTGAAAGGG
ESTC230	43	GCTTCCTCCACGAATTTGAAAGACATATTGGCTGACCTGATACNTAAGGAGCAGGCCAGAATTAAGA
ESTC231	24	CAAAAGGGGTAGTCATATTCCCCANCAACAGCATGATAAAATAATTCAAC

ESTC28	23	GAAGAGCTGGGCACGCATCTGACNTTTCTTCCTCTATTCCTATAAAAATAAAAGGAAGGAGCAGAAATCTGC
ESTC3	20	CAGACATGACCTACCGTCCCNGGCCCTCAATTCATATTTATTCTTGAGCCGCTTGGTCAGGTTTGATTCGCACACTCC
ESTC31	32	ACAGCCCCACAGAACTATTGTAAAACAATATTNTCAGTCGGTGATCATTGTAATATACAATACAAAGCAATTTCCTCAGA
ESTC33	25	AGCACTTCAGCTCCTTGACGTTGTNGGACCAGGGAACTTCCGGAA
ESTC39	26	AAGGAAAGGGAACCCACCTGGGCTTNGGTCACAGAACTCAGAGCCTGGGCATTA
ESTC4	23	CCACTGAATCACACAACATGGACNAATCTCAAATCATTATGCTGATGGAAAGAAACCATT
ESTC40	22	GGCATGCTAGACAGAGGCATTANTTTGAAGATCTTTAAAAATATTTGACTTGTTCCCCCTTCAC
ESTC45	37	TTTGGAGGTTTGTGTCTGGAGTTTTGTTCTTGTAACNCTCTCATCATCGAGGCTATATATTAA
ESTC50	56	CTGTCCGTCGGTGGTGAGCCCCTGCCGCGTGTCCCATGGGCCCACTGGTGCGGANCCGGGCAGATGTTTACCCTGT
ESTC56	45	GTGCCCTGAAGATTAGCAGCAGCAGCAGCAGGTGGCAGGAAGGGAAGGGACACCAAGT
ESTC57	20	AAGTGGGCGCCCTCCCAGTCCCNTCTCTGGGCACAGATCCCACCAGTCTGCTC
ESTC59	38	GAAACACAAAGTGTTGAGAAAAAACTTCTCAAAATTNGTTCCAGACTTCAGGAAAATGATTTCCACATGGTAAGGCC
ESTC6	27	TCTGCAGCACTTCACTACCAAATGAGCNTTAGCTACTTTCAGAATTGAAGGAGAAAATGCATTATGTGGACTGAACCG
ESTC61	57	AGTGATTTTGGCTAGGCGTGGTTCTCATCTGTGAAATTCCACAGCGCAATGACAGCANCCTCTCTCCCACCCACTCAAG
ESTC63	20	ACAGACACAGCATCACACCANAGGGCCCACGGGGAGGGTCGGGGAGACGACACTTTTCCCTGGGAAAGGCAGCTCTAATC
ESTC69	20	GAGAGGCTAGTCAGGAGGGANACCCTCAAGTTTAAATCCCCACACTTACTTACTTACTGCTCATCCGTCACTTTGGCTAA
ESTC7	45	AGTTTCCCTAGAGCTGTGCGGCCAGATAGCTGTTCCTGAGTTGCANGCACGATGGAGATTTGGACACTG

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ESTC72	37		GGGCTTCCAAAATGGGTATTGGGGCCAGGAGGCTGGCNTTTGGCGTGACGCCTAAAAAGTGTGACC AACAATTCACAGCTACAGAGGAAATCTAGAACAAAATCAAATATTCATCACNTTGGGTTGAAAAGTTG GAAGA
ESTC74	49		
ESTC77	40		ATGACTTTCCTGTCCCATCGGAAACCAGAGTTTCCCAGGNGAGCCCTTCCTATCTGCGGTTA
ESTC81	20		GGCTCAGCACAGGGATAAGANCCCCACTCCGCATGTCCCAGAGGGCAGCACTCCAG
ESTC82	25		TTTCAGATGATGGGGTCTGAGATGTNTCCTCAGGCTGCATCAGCTGTCTTCAGTCTCCAGAACAGAAA GAGCCTGACCCA
ESTC83	53		CAAAATCAAATACACAGATCCAGATATGTGAACCATATACATATCTATACANCCATTATTTAGAC TTTCACAAACCT
ESTC85	28		TTTAGCTGCTATACCAAGTTTCCATAAANCTGTCTGCTGGTTGGGGGAGGCTACAGCCTGACCACATTC TTTGC
ESTC89	22		ATTGCAAAGGAAGTGGAACGTGNTCAAACAGAAATGGTGACAATGA
ESTC90	33		CTGGTTCTTCTTCGTCTTGGCATTCGTCCTCCTCNGGCCAGTGCTCCACCCAAGTGTCCTTCCCGATGAT
ESTC93	29		CTCCCCCTCCTCAGTTCACAGTGGAGACTANGGAGATTCAGGGCAGGATCC
ESTC95	32		GCACGTTCTTTGTTCTCCTCTTCCAGAAGTTGNAGACGTCTATTTAGTTTGATTATCTGTCG
DWU-100	127 C T		AAATGACTTGACGAAGCTCATAGAAGATTAGCAGGTAGTAGAATAATGACTGCTGACTCCTAATTCA GTGGATCTTCCCTGGCCACCGTTTGTATTGAGCTGCAATGCGTTCCTTGAGCTTCTTGACTGTTCTCCA[C/T]GCCAG AATTCTTATCAATGATCTTTCACCTAAGAAACAGCAAGATTCTGGCAAGCAACACGATCTAGAGATAC ATCTTATTGCGATTTTTCACAAAATCAAAGAAAATCAAAAGAAAAGAAAGAAGGCTTAGCTG
DWU-177	77 A G		TTCCATCCTAGATATCTACTCAAAATAATTGAGACAACAAGTGTTCAAACAGAAAGACGCTTGTGCTGAA TGTTCATGGC[A/G]GCCCTATTCACAGTAGCCAAACGATGAAAACAACCCAAGCTATATTACCA GATGAAAGGATAAAACAAAATGTGGTCCATCCATACAATGGAGTATTACACAGCCATAAAAAGGAAT GAAGCAGTGATCCCTACTACACTGTGGAT
DWU-286	213 A C		CAAATACCTGGACTATCAACCTTGTTGCTTAATCCCTGCAGCATTCAAGGTTAATCCATCTAAGTGTGAC ATTTTTGAAATTCCAGCGGTGCCACCCAATCATGCCCAGCTTCGTCGTATGAATGAGATATACATTT ATGTCTGACCTTCCCTCAAGACTGATTTTCATGTCTGGGGACTTACAATATCTCAAGGAACAGCAATG TCAACAGGG[A/C]TGGGAAACCAGCCCTATCTGAGTCTTCGGCTCCCTCC

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DWU-252	94	A	G	AGTATACAAACATTTAAGCTGTGGTCAAGGCTACAGATGTGTGCTGACAAGGCACTTCATGTGAAAGTGTCAGAAGGAGCTACAAAACCTACCCTCA[A/G]TGAGCATGGTACTTGGCCCTTGGAGGAACAATCGGCTGCATTGAAGATCCAGCTGCCTATTGATTTAAGCTTCCTGTGAATGACAAAGTATGTGGTTTTGTAAT
DWU-330	85	C	T	GAACATTCCTCTGCAGCACTTCACTCACTACCAAATGAGCATTAGCTACTTTTCAGAATTGAAGGAGAAAATGCATTATGTGGACTGAA[C/T]GACTTTCTAAAGCTCTGAACAAAAGCTTTTCCTTTGCAACAAGACAAAGCAAAGCCACATTTGCATTTTGAGAAAATTTACTGACAGAAATGCAATCTCCCT
DWU-370	231	A	G	GAAAATGTTAATTGGGCAGGTGAAAAGGGTACAGATGTGCTGTAGCAGACCTTTGTTTAAAAGAGAAGCATCATTTCCCAACAGGGCAACTGTAGAAGGCCAGCTGAAGAGTAAAGGAAAAGGTCTGAGGACTGAGCCTGTGGCTGGCTGAAAAAGGTGAATGTTGAAAAAGGTCCATCACAAGAAAGTCATTAGACGGTACCAATTCAGTGTCCT[A/G]GCATCTATTTCCTCTGTGC
DWU-1537b	89	A	G	CTCTTAACTTCAGTTCCCTCATCTATAAGAATAAGGGATTCAGTTGTGATCACATAGCTCAGGTAATCCAGGACCAGAAACCCAGGAGC[A/G]TGGGACCTGATCCACAGTGGGGACTCTGTAGCTACAGCATTTCCTGAACACACAAGAAATCCAAGAAATCCAGTAAGCAGCACACTGGCTGA
DWU-1537a	52	C	T	CTCTTAACTTCAGTTCCCTCATCTATAAGAATAAGGGATTCAGTTGTGATCA[C/T]TATAGCTCAGGTAATCCAGGACCAGAAACCCAGGAGCATGGGACCTGATCCACAGTGGGGACTCTGTAGCTACAGCATTTCCTGAACACACAAGAAATCCAGTAAGCAGCACACTGGCTGA
ESTD-ADAb	196	C	G	ACCATCTTATACTATGGCAGGTAAGTCCATACAGAAGAGCCCTCTCCCTGGGAATTCCATACAGAAGAGCCCTCTCCCTGGGAATTCCAGGGTCCCCAGCTCCACCCAGAGGCCCCTGGGAATTCCAGGGTCCCAGCTCCAGGCCAGCAGAAGTGGGACTGTGAGAAGTCCAAGCCAGTCCAGGCCAGAGAAGTGGGACTGTGAGGACATGGAGGCCTG[C/G]AGGCCACTGAGCTGTGGGTCCCGCGACCAACTCCTGAGCTTTCTGGCCCTCTGAGTCTGTCCTC
ESTD-ADAa	184	G	A	ACCATCTTATACTATGGCAGGTAAGTCCATACAGAAGAGCCCTCTCCCTGGGATTTGAGTGGGGTCCCCAGCTCCACCCAGAGGCCCCTGGGAATTCCAGGGTCACTGTTCCTGTCTCCCTGTGGGAATCAAGCCAGCTCCAGGCCAGCAGAAGTGGGACTGTGAGGACATGGAGGCCTG[G/A]GAGCTGAGCTGCAGACCCGCAGACCAACTCCTGAGCTTTCTGGCCCTCTGAGTCTGTCCTC
ESTD-ANT1	160	T	C	TCTCCTGTCATTCCTACTCCATTAGTTCAAGGTCAGTGAAGAACTGGGCAAATTACCAAGTAATTCATGGACTGCCCAACTGCGAAACAAGAAGGCGCAGTGGAGCAGGAGTATTAATGCTACGCGGTTACCTTTTTTATGGAGGACCGAACTGAGGC[T/C]GAGCTCAGATGATCCTGT
EST10398b	168	A	G	TGCCTGGGGTGGCAAGGCTGCAAACAAGGAGCAACCCAGGAGGCTTTATGAAGCGGGCCATGGTAAGATGCTGCCACCTCTTATCTACTTGATGATGTTCACATTTGGGGCTTGACTTTCCAACACGGAGAAGCATTGTTTCTTCGGGCCAAGAAGGTATCCTACC[A/G]GAGTAGTGTCTATTAGGCATTTG

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EST10398 2a	147	C	T	TGCCTGGGTGGCAAGGCTGCAAACAAGGAGGCAACCAGGAGGCTTTATGAAGGGGGCCATGGTA AGATGCTGCCACCTCTTATCTACTTGATGATGTTCAACTTGGGGCTGACTTCCAACACGGAGAAG CATTGTTTCTT[C/T]GGGCCAAGAAGTATCTACCAATAGTGTCTATTAGGCATTTG
ESTD-C7	14	G	C	--- ATATCGTGGCCTTA[G/C]TTACCTAGAGCTGGACAATCCTGCTGGA
ESTD-D4S95	90	T	C	--- CTTTCATGCACGATAGGCTTCTCTACTAATCACAGAATTTTGAGAGAGAGCAAAAACAACTTTCAAGG ATAATGGGGCAATCACTTTCTTTTCTT[T/C][T/C]TTAGAGTCTTACCGG
ESTD-GPPK2L	38	G	A	--- AGTCTTCATCTGCGGTGTCCAGGTAGATCCCTTTCACC[G/A]CCGAGAACTGCTCGATATC
ESTD-HRASb	82	A	G	--- CTGGGCTGCGCCCCAGCAGCTGCTGGCACCTGCTGCTGGCACGCGGCGCGCCCAGGCTCACCTCTATAGTGGGGTCG TATTCGTCCACAAA[A/G]TGCATCTGGATCAGCT
ESTD-HRASa	37	C	T	--- CTGGGCTGCGCCCCAGCAGCTGCTGGCACCTGCTGCACGG[C/T]GGCGCCCAGGCTCACCTCTATAGTGGGG TCGTATTCGTCCACAAAATGCATCTGGATCAGCT
ESTD-NRAMP	81	A	G	--- GGAGGCAGGAGGTGGGGAGGGGTCTGTCTGCTCCAGGTCCCACAGACCAGAGAAGCGGCCTCAGTG TATCCCACCCCCA[A/G]TGTGTGGGCGCTGGGAGATGAAGAGGAGTTGATGCAGGT
ESTD-OTC	18	A	G	--- GTGACCTTCTCACTTTAA[A/G]AACTTTACCGGAGAAGAAATTAAATATGCTATGGCTATCAGC AGATCTGAAATTTAGGATAAAACAGAAAAGGAGAGGTATGTAACA
EST36751 7	36	C	T	--- CCAAGTCGTTCAATTTTAGCTT[C/T]GCAGGTTTTAACT[C/T]GATTACTTTTCTATTCAAATCTCTGTA AAATTGAAATATGAACTTAGTTTTCTGATCTATGTTTCAAGTAAACAG
EST40562	109	A	G	CACGTGGAAGGAGCTATTTTTGGAGGCTTTAAGAGTAAAGAATCTGTCCCAAACTTGTGGCTGAC TTTATGGCTAAGAAGTTTCCACTGGATGCATTAATAACAAAT[A/G]TTTACCTTTTGAAAAATAA ATGAAGGATTTGACCTGCTCTGCGTCTGGAAAGAGTATCCGTACCGTCCTGACGTTTTGAAACAATACA --- GATGCCTTCCCTGTAGCCTGTTAGCAGTTTCAGCCTCCTCTACCCTA
EST18288 3	121	C	T	GCTCTCTATACCCCTGTGGTCCTCCCACGCTCTCTGGACTTCACAGAACTGGATGTTGCTGCTGAGAA GATTGACACAGGTTCATGCAGGTCGTGTGACAGGATGGGAGACTGGCTGCTCCCTGA[C/T]GGGAGCCAGT GTGGACAGCAGCACCCTGCTTTCAACACCTACGTCCCACTTCCAAGGTAAGGCAAACCTCTCTGCTGGCTC --- TGGCCCCTAGGACTTAGTATCC
ESTD-AK-168	31	C	T	GGGAGTGACAGCTAGAGCACCAAGGGGGGGCT[C/T]TACAGCTTGTGTTCCATGGAGGACAGGCTTCT --- GCTCATTCTGG
ESTD-ALB	180	A	G	AATCCCAGCACTTTAGGAGGCTGAGGCAGGCATATCACCAGAGGTCAGGAGTTTGAGACCAGTCTGA CCAACATGGTGAAACCCCATCTCTACTAAAAATACAAAATTAGCCAGGCATGGTGGTGCATGCCTGT AATCCCAGAGGCTGAGGCAGGAGGAATCGCTTGAACCTGGGAGGCGG[A/G]AGGTTGGTGGTGAGCCGGA --- GATGGCACCATTGCACTCCAGCCTGGGCAACAAGAGTAAAACTCTGTCTTC

ID	Pos.	Var.	Sequence
EST705233	182	G/T	TTCCCGCCAGCCCCCCATCCTTGGCACCCTGGTCCCCTCAGGGGCCACCCCGGGCCACTCACCGCTCT CGCTCTCGGTAACATCCGGCGGGGGCGGGCCGGTCCTTGGCACACATAGCTGGACGCGTTCCGTATAGGAGG ACCGGTGTAGGCCTTCCTGTCCGCGGCCTTGGCCAGGGGCCAGCCCCT[G/T]CAGAGAGGGGGTCCCTGT GGTTGAGCTGAACACAGCTGTGGAGTGTCTCCCACGTG
ESTD-APOA2	101	C/T	CCAGGTGTTGTGGCACGTGCCTGTAATCCCAGCTACTCGGGGAGGACTGAGGCATGAGAATCTTTGAAC CGGGGAGGCGGGAGGGGTTGCAGTGAGCTGAGATCG[C/T]GCCACTGCACTCCAGCCTAGGTGACAGAGC AAGACTCC
EST587077	112	C/T	CAGTGTATCTGGAAAGCCTACAGGACACCAAAATAACCTTAATCATCAATTGGTTACAGGAGGCTT AAGTTCAGCATCTTTGGCTCCACATGAAGGCCAAATTCCGAGAGAC[C/T]CTAGAAGATACACGAGAC GCACACTTGTCACCTACACATTCTGATTGGTGGACTCTTGCTGCTAAGAACCTT
EST741676	137	C	AGACCCATGAAGGAGTTGAAGGCCTACAAATGGAACTGGAGGAACAACTGACCCCGGTGGCGGAGG AGACGCGGGGCACGGCGCGCCTGTCCAAGGAGCTGCAGGCGGCGGGCGCCGGGACCATGGAGGA CGTGCGCGGCGGGCCGCCTGGTCAGGCGGGCGGAGGTGCAGGCCATGCGTCGCGGCACCGAGCGAGGC TGCGGGTGCGCCTCGCCTCGCGCAAGCTGCGGGCTCCTC
EST432118	132	C	CGCCTGGTGCAGTACGCGGCGGGGAGGTCGCAGGCGGCAACGCGGGCCAGAGCACCGAGCTGCGCGGGTGCG CCTTGCGCCTCCCACCTGCGCGAGGTCGCTGCGGGTGCGGTAACGCGGCTCCTCCGCGAGGGCGAGAAGCGCC TGGCGGGTGGGCCGGTGGGCGGGCGGCGCGGGGCGGCGGGGCGGGGCGGGCCCATCCGCGCGAGCGCGCCTG
ESTD-ARSB	126	A	GGAAGAAAATGGAGCCTGTGGGGAAGGAGGCGTCCGAGGGGTGGCTTTGTGGCAAGCCCCTTGCTGA AGCAGAAGGGCGTGAAGAACCGGGAGCTCATCCACCATCTCTGACTGGCTGCCAACACTCATGAAGCT GGCCAGGGGACACCCAATGGCACACGGCCCATCCCCAGAATTGAGCTGCCGACGTGTGGAAAACCATCAGTGAA
EST367704	144	C	TGTAGCCAAAGTCACCTGCATCATCATTTGGCTGCTGCCAGTTTGGCACGTTGGCAGGCTTGGCCAGCTATAATCC ATCGAAATGTATTTTCATTGAGAACACCAATATTACAGTTTGTGCTTTCCATTATGAGTCCCAAAAT TCAACCCTCCCGATAGGGTGGGCCTGACCAAAAATATACTGGGTTCCTGTTCCGTTTCCTTTCTGATCAT TCTTACAAGTTATACTCTTATTGGAAGGCCCTAAAGAAGGCTTATG
EST260211	137	A	TAATGTAAGCTCATCCACCAAGAAGCCTGCACCCATGTGTTTGAGGTTGAGTGACATGTTCGAAACCTGT CCATAAAGTAATTTTGTGAAAGAAGGAGGGCAAGAGAGAACATTCCTCTGCAGAAAACCTACCAAATGA GCATTAGCTACTTTTCAGAATTGAACAGAAAAATGCATTATATGTGGACTGAACCGACTTTTTCTAAAGC
ESTD-BA511	29	A/G	GGGCAACATAGTGAAACCCCATCTCTACA[A/G]AAAATACAAAAATTACAACAAAGCAAAGCC TGCCTGTAGTCCCAGCTACTTGGGAGGCTGAGGCAGGTGAATGGGGAGGATCCCTTGAAGGTGGGAGGTTGTAGCAAG CAGTGAGCCGCAAGATGGTGCCACTGCA

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Name	Pos			Sequence
ESTD-BCL2	116	A	G	AGCTGGATTATAACTCCTCTTCTTCTCTGGGGCCGTGGGGGTGGGGAGCTGGGGGTGGGGAGGGTGCCGTTGGGCCCCCGTTGCTTTCCTCCTGGAAGGATGGCGGCACGCTGGAGGAACA[A/G]GGGTACGCACAACCGGGAGATAGTGATGAAGTACATCCATTATAAGCTGTCGCAGAGGGGCTACGAGTGGGGGATGCGGGAGATGTGGGCGGCCGCGCCCCCCGGGGCGGGGCGGGGCGGGCCCATCTTCTCCTCCCA
ESTD-BCR	69	C	T	CAGTGGCTGAGTGGACGATGACATTCAGAAACCCGGAGACTCATCATCTGCGCAAGAGA[C/T]CAAAGAGGTCAGCTTCGTTGTCCCGGGAAAGGGAGGCAGGTGACAAGCTAACTCTGCTTCAAAATCAACCATCCGGTGGACACCTCCGGTGCCATCTGTGGCCATCTGCTGGCACA
ESTD-BRCA1aa	119	C	T	AAGAAGAGAAACTAGAAACAGTTAAGTGTCTAATAAATGTCAAAGATCTCATGTTAAGTGGAGAAAGGGTTTGCAAACTGAAAGATCTGTAGAGAGTAGCAGTATTTCA[C/T]TGGTACCTGGTACTGATTATGGCCACTCAGGAAAGTATCTCGTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAAACAGAACCAAATAAAT
ESTD-BRCA1bb	139	A	G	ACTAAATGTAAGAAAAATCTGCTAGAGGAAAAACTTTGAGGAACATTCAATGTCACCTGAAAGAGAAATGGGAAATGAGAACATTCCAGTACAGTGAGCACAATTAGCCGTAATAACATTAGAGAAAATGTTTTTAAAG[A/G]AGCCAGCTCAAGCTCAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGAGCTCCAGTATTAATGAAAGTATTAATGAAA
ESTD-BRCA1cc	126	A	G	ATGCATCTCAGGTTTGTTCTGAGACACCTGATGACCTGTTAGATGATGGTGAAATAAAGGAAGATACTAGTTTTGCTGAAAATGACATTAAGGAAAGTTCTGTCTGTTTTAGCAAAGCGTCCAGA[A/G]AGGAGAGCTTAGCAGGAGGTCCTAGCCCTTTCACCCATACACATTGGCTCAGGGTTACCGAAGAGGGGCCAAGAAAATTAGAGTCCTCAGAAGAGAACTATCTAGTGAGGATGAAGAGCTTCCC
EST512120	122	A	C	ATCCTGAGCTCGCCAATAAGCTTCTTGGTTCTACTTCTCTTCCACAGCCCCAATTTCACTTTCTCAGAGGAAATCCCAAGCTTAGGAGCCCTGGAGCTTAGGAGCCCTTTGTGCTCCCACTCAATACA[A/C]AAGGCCCCTCTCTACATCT
ESTD-C1R	40	A	G	ACACAGGTGCTGGCCACTGGGGGCTGGGGATCCTCCTCCCCCT[A/G]ATTTGCTCCGGGAAGCACATTCATCAA
ESTD-C1R	40	A	G	ACACAGGTGCTGGCCACTGGGGGCTGGGGATCCTCCTCCCCCT[A/G]ATTTGCTCCGGGAAGCACATTCATCAA
ESTD-C6	31	A	C	CCCAGTCAGTTTGGGGGACAGCAGCCATGCACTG[A/C]GCCTCTGGTAGCCTTTCAACCATGCATTCCATCTAAGCTCTGCAAAAT
EST201182	119	C		GTTCCGAATCCTCCTCCTGAAAGTGGCCGGGTTTAATCTGCTCATGACGCTGCGGCTGTGGTCCAGCTGAGGTGAGGGCCTTGAAGCTGTGGGAGTTTAGGGACGCGGGTGCGGGGTCTCTGCGTGCATCCTAAGCTCTGAGA
EST530186	67	A	G	ACAATCCAGGTCACACATTCCAGAAGAGGACGAGAGGGTGGTCAGTGAGCCTGAGCCTGGGTAGGTCCAGTAATCCA[A/G]GGATTCAGGAAGGAGGAGGCCACGAGGAGGATCGAAGTTAGTGAAGTC

ESTD-CB22	119	C/T	GGCAAGTTTTATTGATAGAGAGAGGAAATCAAATAATGGCAATGAGGAGAGACATCACCTGGAATGTTAG GCAGTGCCTAACTGGGGGATGGACAGACAATGGCAGTGCCAACCCATAGGG[C/T]GGATACAAAAG ACAGGCAAGGAAGGGGTAGAACCATCAAAGAGGAATAGGCTGGTGACCCAAAGCAAGGAGGACCT AGTAACATAATTGTGCTTCATTATGGTCCTTCCGGCCTTCTCTCTCACAC
ESTD-CB23	136	C/-	TAGAACCATCAAAGAGGAATAGGCTGGTGACCCAAAGCAAGGAGGACCTAGTAACATAATTGTGC TTCATTATGGTCCTTTCCCGGCCTTCCCATACCTCTTCCTTCCAGAGGACCTAGTAACATAATTGTGC CTCAGAGCAACCCTAGCCCATTACCTCTTCCCTTTCCAGAGGACCTGAA GGTCGCTGTGTTGTTGAGCCATCAGAAGCAGAGATCTCCCACACCCAAAA
ESTD-CB24	145	A/-	ACCAGGACCAGCAGCTCTCAGAGCAACCCTAGCCCATTACCTCTTCCCTTTCCAGAGGACCTGAA AAACGTGTTCCCACCTGAGGGTCGCTGTGTTGAGCCATCAGAAGCAGAGATCTCCCACACCCAAAAG GCCACACTGGTATGCCTGGCCACAGGCTTCTACCCCGACCACGTGGAGGTGAGCTGGGTGAATGG GAGGAGGTGCACAGTGGGGTCACAGTGCCAGCACCTTGTATGCCGTG
ESTD-CB25	146	A/G	GTTTCTTTCAGACTGTGGCTTCACCTCCGGTAAGTGAGTCTCTCTTTTTCTCTATCTTTCGCGGTC TCTGCTCTCGAACCAGGGCATGGAGAATCCACACGGGGCGTGAGGGAGGCCAGAGCCACCTG TGCACAGGT[A/G]CCTACACATGCTCTGTTCTTGTCAACAGAGTCTTACCAGCAAGGGGTCCTGTCTGCC ACCATCCTCTATGAGATCTTGCTAGGGAAGGCCACCTTGTATGCCGTG
ESTD-CB27	125	C/T	TTTTCTGTTTCCCTGAAGATTGAGCTCCCAACCCCCAGTACGAAATAGGCTAAACCAATAAAAAT TGTGTGTTGGGGCCTGGTTGCATTTCAGGAGTGTCTGTGAAGTGACAGTTGTCTGCTCATCACTGAC[C/T]ATCTTC GCTTTCTCCTGTTCATCCTGATGGAAGTCCTCAAACACCATTTCCATACC
ESTD-D4S338	59	A/T	TTTTCTGTTTACCTTGTTCAGATCCTTCAGAGGAATCCTTCAGAGGAATCCCTATATATGGCAGGTATATGA[A/T]ATGTA TTTCTTAAAACAATAAACTTGAAAGTCCAAAATTACTCCTTGATCCATGAACTGCAGAATAAATGTTA TTTAGCTGTCAGAAAAACAATACTAATCTTGCATATGTTCATCAGAGCCCTTGGGTGACCAGGTGTA
ESTD-CYP2D6	61	A/G	TTGCCAATAAGCAGTAATATTTGAGAGGAATCTTGTTTTCAATGCAGTAG CAGGCCAGCGTGTGTGAGGTGGTGTCACATTGGAGCTGTCTCCAGGGTTCCCCTTGGGGTCTCAG[A/G]CA GGTTCTCATCATTGAAGCTGTCTCCAGGGTCTCTCAGGGTTCCCCTTGGGCTGGCGAGAGCATACTCGG
ESTD-D11S1873	40	A/C	AAAAAAACATTTTAACACCTTTCAATCATCATACACCATA[A/C]ATTTCCATTTTCACATAAGTCA GTTTGAGCTGAGTTTCCCAATACTTGCAATCTAAAATGTCATAACTGATTAATGCAAGTTCAACAG ACAACTTTCCCAAGCATCTACGATCCAGAAGGTCAAAATATTACATATCTGGATTAAATTATGCCCA TATCTGCATGTC
ESTD-D17S33b	169	C/T	CATCCCCAAGCCACCATCCTCTTAGCCACTGGCATTTTTGCGGCCTCTGACAACTCAGGGCCGT CATGCTGCACACATCCAGGGGGCGGCCCTACCCTTGTAGTCCCATGGGAAAGGCTCCTCTGGGGCGGTG GGGTTGGTGTGGCTATGTGGTGGTCTTGTGTGTGTAGA[C/T]GGGGGCTTTCAGTTGCCACTATTGCGTT ATTGCAGATTGCTTTGTCTTTCCACCTGAGCGAGCCTC

ID	Pos			Sequence
STD-017S33a	75	C	T	CATCCCCAAGCCCATCCTCTTAGCCACTGGCCATTTTGCCGCCGCCTCTGACAGATACACTCAGGGCCGT CATGCTGC[C/T]ACACATCCAGGGGGCGCCCCTACCCTTGTAGTCCATGGAAGGCTCCTCTGGGGCG GTGGGGTTGGTGTGGCTATGTGGTCTTGTGTGTAGACGGGGCTTTGGTTCAGTTGCACTATTGCGTT
STD-018S8	133	A	G	ATTGCAGATTGCTTGTCTTTCCACCTGAGCGAGCCTC TTTGAGACCACCACCTGGCCAAACATGGCGAAATCACATCTCTACCAAAATTACAAAATTAGCTGGGGTGT GGTGGTACATGCCTATCGTAATCCCAGCTACACTCGGGAGGCTGAGGCAGGAGAATTGCTTGAACCC[A /G]GGAGGCAGAGCTTGCAGTGAGCCAAGATCACACCACTGCACTCCAGCCTGGGTGACACAGTGGA GACTCTGTCTCAA
STD-03S11	44	G	---	AACTGATTAGAACCTGAAAAATACATATTTATCTGAAAAGTCGAGTTATTGGCTCATCACATTGG AATTTTGCATCATCATTAAAAAAATCCAATAAAGTACACTGTAATAAAGAATTAACAGAATATCATTGT TTATTCAAACTATTTATCACTTATTTATTGGTAAGCCATACTAAATTCTAAAGCATGTTTCTGAAAG TTTA
STD-03S12	37	A	G	AGGTTCCACATTATTGCTGATGTTTGCTGATGTTTCC[A/G]GGAGCCTTGATGTCTGTATCTCCT CAGGTATCCCACCTTGAGACGTACTTTCAAAAACTCTCTACAGCCGTTGTTGTTATTAATTCAAGGT TGAACATAAAGTA
STD-03S2b	247	C	T	GATCATGTGGCCCAAGTGGCCAGAGCTACTATACCATGACCCAGACTGCTAGCAGAACATTCCTGC TGAGTCTTATTCAAAACTGACAGCCATTATGCCACCTGAAATATGGTCAGGTTACAGCTGTATTCCC AGAAGTGAAACATACTGCTCCTAGAGCCAGAGTCATACTGGATGTTCTGTTTCGGTCTTCACGATGG CAGGTATGAAATAATATCTGTCCTTATTGGAAGGATGC[C/T]GGT
STD-03S2a	248	G	---	GATCATGTGGCCCAAGTGGCCAGAGCTACTATACCATGACCCAGACTGCTAGCAGAACATTCCTGC TGAGTCTTATTCAAAACTGACAGCCATTATGCCACCTGAAATATGGTCAGGTTACAGCTGTATTCCC AGAAGTGAAACATACTGCTCCTAGAGCCAGAGTCATACTGGATGTTCTGTTTCGGTCTTCACGATGG CAGGTATGAAATAATATCTGTCCTTATTGGAAGGATGC[A/G]GGT
STD-07S399	83	A	G	TGAATCTTAATTGCTATCTCTACAAAAATGTATAAATCCTTTCACAAACATTTCATCCATCGACTCTAGAGAT AACTGCTAGACCC[A/G]GTCTCCTACACTCCTTTATTGGAAGAAATGACAAACATGACAAACATTTC TAGAATATTTGAAGAAACAAACAATGACAAACATTTC
STD-DMb	146	A	C	GTGGGGACACCGAGGGCTCCAGGCTGTGGGCGCTTGCAAGCAGCTGCTCGGGCCTCCACT TCCATGGTGGTGTGGGCCTGGGGACCTGATT[A/C]TCTGGTGGAGGGGGAGGGGAGGGGAGGAGGAGACA ACCTCCTGATTTGAGGAAGGGGAGCAGAGCAGAGAGGAGAACACAGAGT
STD-DMa	66	C	G	GTGGGGACACCGAGGGCTCCAGGCTGTGGGCGCTTGCACGTGTGGCTCAAGGAGGAGGAGACCTCGGCCTCCA[C /G]TTCCATGGTGGTGTGGGCCTGATTATCTGGTGAGGGGAGGGGTAGGGGCAGCTGCTTCCAAGA CAGAATGCGATTATCTGGTGAGGGGAGGGGTAGGGGCAGCTGCTTCCAAGA CCTCCTGATTTGAGGAAGGGGAGCAGAGCAGAGGAGGAGAACAGAGT

Name	Pos.			Sequence
ESTD-DRD1	154	C	T	TCCCCAGCCCTATCGGTCATATTGGACTATGACACTGACGTCTCTCTGGAGAAGATCCAACCCATCAC ACAAAACGGTCAGCACCACCAACCTGAACTCGCCAGATGAATCCTGCCACACATGCTCATCCCAAAGCT AGAGGAGATTGCTCTGGGG[C/T]TCGCTATTAAGAAAACTAAGGTAC
ESTD-DRD2	144	C		TCTGCCTTTGGTGCAGGAGGCTGCCCCGGAGCCAGGAGCTGGAGATGCTCTCCAGCACCA GCCCACCCGAGAGGACCGGTACAGCCCCATCCCACCACCACCCGCCAACAGCTCTCCCCGACCCG TCCCCACCACGGTCTCCACAGCACTCCCAGCACCCGCCAAACCAGAGAAGAATGGGCATGCCAAAG ACCACCCCAAGATTGCCAAGATCTTTGCCAAGATCTTTCAGACCATGCCCAATG
ESTD-DRD3	109	C	T	AAGAACGATGGCCAGGATGAGCGCCAGTAGGAGAGGCATAGTAGGCCATGTGGGCGGGCCTGGCTGG CACCTGTGGAGTTCTCTGCCCCACAGGTGTAGTTCAGGTGGC[C/T]ACTCAGCTGGCTCAGAGATGCC ATAGCCCAGAGAGGAGGTGCGTGATGCCAAGGGGCTTCCTGTGTGAGGAGA
ESTD-ERBB2	93	C	T	TCTTTCAGGATCCGCATCTCGCCTGGTTGGGCATGGCCATCTGCGCTCTAGGTGTGTCAGCGGCTGG GGTGAGGGGGTTGGTGGGTCAGTGC[C/T]GGGGCGCCGGTGCAGACCCCACGCGGCGGCTGGGAGGACTTCA CCCCGCCTCACCTCCGTTCCTCCGACGCAGTCTCCGCATCGTGTCACT
ESTD-ETS2	43	A	G	ACTCACAGTCGCTTTAAGTGAAAATGGTCGAGAAAGAGGCACC[A/G]GGAAGCCGTCCTGGCGCCTG CACAGACTATTTTAGATTTTCTTTGCCTTTTGCAACCAGGAACAGCAAATGCAAAACTCTTTGAG AGGGTAGGAGGGTGGGAAGGAAGCAACAACCATGTCATTCAGAGAGTTAGTTTG
ESTD-F9	111	A	G	AGATCCTGATGATTTTTTTCCTATTTTTTTCTAAATGTTTTCTAAAGTAAGTTTGAAGTTTACAGTTTAGATTTATGCCCA TGCTCCATTTGAGTAATATTGTGTAAAGTATGATGTTTA[A/G]GTCAAACTTCATTTTTTTTCC ATAGGTATGTCCAATTATCCAGCACAATTGTTAAACAAAAC
EST68787 5	144	A		CTTCCTATGGGATTTGACTTTTATTTTCTCCATTGTCTTATTTTTCTCCATTGTCTTACCTTTACAGGTGTTAATATAGTGAAAAG GAAGCTTGCAGCTCATGCAGCTCAAATTTGAAGCTTACAGCACTTTCGAACATTGAAGTTGTTTTTGAACTGGTGTCACCTTTAATTACAACCTAG AGAATCAAGCACTTTCGAAACATTGAAGTTGTTTTTGAACTGGTGTCACCTTTAATTACAACCTAG CAGACGGAACTGAACTCAGGGTAAGAAT
ESTD-GCDH	200	C	G	CGCAGACCGGTCAGTGTGGGGGTCGGGGAGTGTGGAGGGGGAGGAGGAGGAACTGGGGGTTTAGGGACT TTCCGGGGGTGACTTTCCCGTTCGTCTGCTTGTGCCTGTGTTCTGCTGCCCCGTTCTGCTGCCCCGTTTCTGCTGCCCCGTGTTCTGCTGCCCCGTGTTCTGCTGCCCCGTTCTGCTGCCCCGTCTCAGCTGTCGTGTCTGCCGAGAGCT G[G/A]GACTCTGTCCCGGAAATTCCGGGAGAGCT
ESTD-GCK	88	A	G	GTTTTATGCATGGCAGCTCTAATGACAGGATGGTCAGCCCTGCTGAGCCCACCACTCCTGGTCACCATGAC AACCACAGCGCCCTCTCAGGA[A/G]CACAGTAAGCCTGCGCAGGAGAATCCCCACCACCTGGC ACCTGCGAGCCTAATTACTCAAAAGCTGTCCCGAGACAGTC

				Sequence
EST34088 2	62	A	T	GTGGGGGCAACAGTGGGAGAGAAGGGGCCAGGGTATAAAGGGGCCCAAGAGAGACCGGCTC[A/T]AGGATCCCAAGGCCCAACCACTCCCGAACCACTCAGGGTCCTGTGGACAGCTCACCTAGCTGCAATGGCTACAGGTAAG
ESTD-GNAT2	56	A	G	GACCCTGAGTACCTCCCTAGTGAGCAAGACTTTCCGTCAAAGACTTGAATTTCAGGTAAGTGCATGGTTCCCTAGG TTGAAACCAAGTTTCCGTCAAAGATGTGCTCCGATCCAGGGTCAAAACCAC[A/G]GGCATCA
ESTD-HT2	154	G	---	GGGCTAAAAATTTCCGAGCAACTTTGCATAGACTGTTTATTTGACTTGACAGAGTTGCTAGAGATAGG CAGGGAGGAGAAGATGTGTTACAGTTTGTCAGAGAATAAAAAGGATAAACTGGGGTTTTCTGTGC TTTGCTTCTTCACATCCCTGGGGAGTTAATAGCTGCAATTTTCAAAGAAACGGTATACAGGGACAGCA AAGCGCAGTCGTGAAGTTTCAAACAAGACACCTT
ESTD-HT5	149	C	---	AACACACAAGCCCCAGCGAGAATTGAACTCGCGACCCTGGTTTACAAGACCAGTGCTCTAACCCT GAGCTATGGAGCCCTCGTCTGCTGTTGGTTTTCTTCCTTCATCTTATAGATTGATCGTTATGCTCCTA ACATTTTCGTGCTCTGTAAATCCCTCGAAAAGGTTCT
EST37382 5	124	A	G	CTGAGAAACAATTGGCAAAATAAAGGAATTTGGCACTCCCCACCCCCTCTTTCTTCTTCTCCCTTGGA CTTTGAGTCAAATTGGCCTGGACTTGAGTCCCTGAACCAGCAAAGAGAAAGAAAGG[A/G]CCCCAGA AATCACAGGTGGGCACGTTCGGCGTCGCCGTCTACCGCCATCTCCCTTCACGGGAATTTTCAGGGTAAACT ACCCAGTGGAGCCCGCTCATTGCACGGTCTTGGCAGGAGGTGC[C/T]CTGGGGAGGAAGGAAGATG
ESTD-IGFBP1	43	C	T	TTCCAGGGCACACATAGCTTAGTGGAGACTC
ESTD-IGHV4-6	120	C	---	TTTACTATTTCAATGGATACAGAATTGTGGGGAGTCACTATATTCCTATGAACAAAAATTCAGATTT CAGTGTTAAGTAAGTTGCCTACATTGTGTGTGACGGGCAGTGGTGGATCCGAGTGGTGTGGTGGG TGCACGGACATAATGATTCAGAAAGCAATATGGAAAGTAATAAACGGAGTATCTATGGATACGAACTGAAAGT ATGTAAATACTTCACAAAATACTAATAAAACGGAGTTGAATATAAAACCCA
STD-IL1A	110	A	G	CAAAGTAAGCACCCAATAAATGTTAGCTATTACTATCATCATTATTATTATTTTTTTG AGATGGAGTCTCGGCTCTGTCACCCAGGCTGGAGTGCAGTGGC[A/G]CAATCTCGGCTCACTGCAAGCT CTGCCTCCCGGGTTCATGCCATTCTCGCCTCAGCCTCCCGAGTAGCTGGGAATACAGGCACCCGCC
STD-IL1B	99	A	G	CCACTTACAGATGAAATGGGTACAAATGAAGGCCAATAGCCCTCCCGAGTTCACCGT GGGTCTCTACCTTGGGTGCTGTTCTCTGCCTC[A/G]GGAGCTCTCGTCTGTATTGAGGGTGT
EST740082	134	A	T	TCCAGGGTGGCTGGACCCCAGGCCCCAGGGGGCCCAAGGCAGGGAGGACGTGGCTGCGGGCTCGTGAAGCATG TGGGGGTGAGCCCAGGCACTGTCCTTCGCCATGTCGGCCGGATGCGGCCTCCGTGGCGCTGCCTCAGCCCTGCGTC[A/?] CTCTGGGGACCTGACCAGCCAGGCGCAGCCCTTGTTGAACCAACACCTGTGCG

Clone	Pos.	Allele 1	Allele 2	Sequence
EST45311 0	151	C	T	GCCCTCCTCTCTCCAATTCTGTCTCCCTATAGTTTCCTCTATTAAGTGAACTACATGCATTCTTTAGT GGATAGATGCACACAAACACACAGCCATTATGGGGAAGGATCCACGTGTTGGCCATATTGTAACA CATTTTCTGCAAAT[C/T]ACCTCTTCATTTAACAGCCCTTATTCAATGGCCTTTCTTTTTTCAGTA GTACATACACATCTGTGTCATTTGTTGAAT
EST65258 8	80	A	G	TGCCCCATCACGGCGGCCGAGACATGGCTTGCCACCAGTCTCTTGAGGATGTCACCAATTAACCAGAAAT CCAGTTATTTCC[A/G]CCCTCAAAATGACAGCCATGGCCGGCCGGGTGCTTCTGGGGCGTCGTCGGG GAGGTTAGGTGCGTGTTTCCTGTGCATGGAGACTTGAGGAGGGAGGGCTTGAGGTTGGT
EST38216 3	26	A	T	ATGCAGGATGAAGGTGGACAGGGAGG[A/T]GAGGGCCAACCTGTCATCCCAGGGCCTGCAGATGTCG CTGGACTATGGGTTTGTGACCCACTGACCTCCATGAGCATCAGGG
EST62782	149	G	T	ATACTAGTACAAGTGGTAATTTTGTACATTACAACTAAATTATTAGCATTTGTTTAGCATTACCTAA TTTTTTCCTGTCCATGCAGACTGTTAGCTTTACCTTAAATGCTTATTTAAAATGACAGTGGAAG TTTTTTTCCTC[G/T]AAGTGCCAGTATTCCCAGAGTTTTGGTTTTTGAACTAGCAATGCCTGTGAA AAGAAACTGAATACCTAAGATTTCTGTCTTGGGGTTTTTGGTGCATGCA
ESTD- KRT10b	183	C	T	CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTCCATGTCAGTGTTACCTTTTGGCAATATT AAAGGAAGAAGAAAATGCATTTAAAGTAACTGCTAAGGTTTTTCCATTAAACCACTATTACTTCTAAG AGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAG[C/T]TGCTTTTAAATAGT CTCTGCCCAGATACATCTCCCCTATATAAGTTATAACCAGTATTGATA
ESTD- KRT10a	133	A	G	CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTCCATGTCAGTGTTACCTTTTGGCAATATT AAAGGAAGAAGAAAATGCATTTAAAGTAACTGCTAAGGTTTTTCCATTAAACCACTATTACTTCTA[A/ G]GAGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGCTGCTTTTAAATAGTC TCTGCCCAGATACATCTCCCCTATATAAGTTATAACCAGTATTGATA
STD- RT8b	231	C	T	ACCCTCACCCCTCCCTTAGCCCGTGGGAAGCAGGAAATCTCTCTCCAAATCCATGAATACACATCGG ATTGGACACCTTGAGAGTCTTAACAGCAGGCCTGAAGACCTTCAGACGCCTCAGAACAGAAGTT TGCTAGAGGTCAAGGGTCAAGACTAAAGAGGGGCCAGAATGTTAAGTACAAAAGTGAGGCCCATAG GCTGCCTATCTCTCCGTCTCAGGTTTACCA[C/T]GTCAACATTGACACA
STD- RT8a	21	C	T	ACCCTCACCCCTCCCTTAGCC[C/T]GTGGGAAGCAGGAAATCTCTCTCCAAATCCATGAATACATC GGATTGGACACCTTGAGAGTCTTAACAGCAGGCCTGAAGACCTTCAGACGCCTCAGAACAGAAG TTTGCTAGAGGTCAAGGGTCAAGACTAAAGAGGGGCCAGAATGTTAAGTACAAAAGTGAGGCCCATA GGCTGCCTATCTCTCCGTCTCAGGTTTACCACGTCAACATTGACACA
ST75099	82	C	T	CACTTGTGTGTCTAGATCTCGTGTCAGTGGCCGCCTCTACTGGGTGCGGGGCAACCGGAAGACCATCTTGGAGGATGAAAGAGGCTGGCCCACC AGCATCGATGTCAA[C/T]TGGGGCGTCTTTGGCCGGTCTTTGAGGTGTGG

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ESTD-LF79	142	A	G	GGGTGATTTGAGGCTCAGTTAATATTTCAAAATTGTAACCGTAGCAAAACTGCATTGGTGTATTAGA AAATAAAAAATTTCCAATATGTAGTGCTTCCCTTACCACCAGA GGGAACC[A/G]GGGAGGGCTTCCCTTACCACCAGA
EST358799	142	A	C	GAGATCGGTGGTGTGAGTTATTAGGCATGGTTACCTGTGATTCTCCCAATCTTGTGCGTTCCACCGATG GAACTGCCGGCAAATCCTGACACGTGTGCACCAGGCTGTACCCAATTAGGTGAACATGGCTTCGAG
ESTD-LMP2	35	C	G	AGAGTTG[A/C]ACAGATTCCTGGAAGAGCAGCGGGAGTGGGGGCAGGAGAGAGCTGCCTGGATGA A
ESTD-LPL	113	C	T	TACACACTTCCTTACCCATTCACTGAAACGACT[C/G]GCAAACTGGAGCCTTGTGAGGAATGGAGT TGACCTTCCCAAAGCCACTATGATAAGCTATTGGTG
ESTD-MCC	45	C	T	TGTCAGTGTCCCCTAGGGGCACCTCACCACTCCCAGCTTCTTCAGCTCTGCCTGTCCTGCTGCCTGCA AGGGTTTGCTTAATTCTCAATTCAATGTCTTCTTAG[C/T]AGCTGTGGGGTTTTGTTGTTG AGATTGTTATCAGAAGTTCACAACATTTATTAAAAATTTTTCACCTG
ESTD-METH	118	C	T	TTGTCAGGAGTGTGCTGATGCTGCCCCCAGCTCTGTCCCCAGC[C/T]GAACTTCAGGACAACGTGC AG
ESTD-NF1	25	A	G	CATCCATGTAGGAGAGCCTTAGTCAAGTGAATGCTGAGGAAGCAGTAAAACAGCATCCCGAA TCTCAGGAAGTCTCTGTCTTCCAAGGGTTGGTCTCAAGTGCATGCTAAGGTGCTGATTACC[C/T]GGATTTTCTGACG ATCTTTCAACTGCTAGAAGCATCTGGTTCCTGTTTAGCATGG
				ATTATCCAGATGAATTACAAAACT[A/G]TACCAGATCCCACAGACTGATATGGCTGGT
ESTD-NFKB1	107	A	G	AACATGGACTTGTATATTGTACAAAAAAAGTTTATTTTTCTAAAAAAGAAAAAAGAAGAAA AAATTTAAAGGGTGTACTTATATCCACACTGCCT[A/G]CCCAAAACGTCTTATTGTGGT AGGATCAGCCCTCATTGTCTTTTGTGAACTTTTTGTAGGGGACGAGAAAGATCATTGAAATTCT
ESTD-NPPA	45	A	G	GAGAAAACTTCTTTTAAACCTCACCTTTGTGGGTTTTGGAGAAGGTTATCA TGTCCCTAGGCCCAGCCCCTGCTGTCCCTGCTGTTTATCTTC[A/G]TACTGCAAAGAGAACACA GACAT
ESTD-NRAS	202	C	T	GTGTTTCTTAATCTTTCCAGGAACACAGTGACCATATTCTTTCTGCAGGCATATAGAATTGGT GGGTTTTCTTTATGTGGGTTAGGGTGATATTGGATACTTTTGTTTGTGATTATATTAGCAATTTGAGGG ACAAACCAGATAGGCAGAAATGGGCTGAATAGTTAGATGCTTATTTAACCTTGGCAATAGCATTG[C/T]ATTCCCTGTGGTTTTTAATAAAAT
STD-PAI1	100	A	G	GCCACCACCACCCCACCCCAGCACACCTCCAACCTCACACGTGGG[A/G]GTCAGCCGTGTATCATCGGAGCGGCGGGCC TCAGGTGGCACAGGAGAGATGAGGGAAAGACCAAGAGTCCTCTGTTGGGCCCAAGTCCTAGACAGACAAACC TAGACAATCACGTGGCTGGCT

ID	Pos			Sequence
ESTD-PAR	120	A	G	CTCTTCAGGAACCACCAGTCTTCTTACCAAACACGACTTATTGCTGTCCGAGAGGTACAACCCGTGAGAACTTCTTCCTAACTGTAATTTAGTTAAAGGAATGAAACTGGCTCTGAAGAACATGGAGATACTGCCTAATGACTGGCTTTCATTAGCTCTGTGAGTGTTTCTTTCACTTTCTGTGTTCTAGAACGTTTTCTAGGACTGGCAGTTAAGCTTTCACTTAGGCTTTCTGTATACCCATGCCC
ESTD-Per/RDS	74	A	G	ACCTACAGACGTGCGCTGGATGTGTGTCCAACCCGAGGAATCTGAGAGCGAGAGGGCGCTGGCTGCTGGGAGGA[A/G]GAGCGGTGCCGGAGACCTGGAAGGCCT
EST68308 5	29	C	T	GGAAAGAGATTTAAGGAAGCTTGATTGGA[C/T]AATTCTGGTTCTTTTGGAGTGTGGAAGAGTTCATGTCTCTGCCTGAGTTACAACAGAATCCTTTAGTACAGCGAGTAATAGATATATTCGACACAGATGGGAATGGAGAAGTAGAGACTTTAAAGGTAAGAAAGTAGTTATTTTTA
EST54045 6	39	A	G	GGAATATTAAAAAATATTTTAAAATACCTCCATTTGCTT[A/G]TCCTTTAGTGAAGATGATACCTGCAAAAGACATGGCTAAAGTTATGATTGTCATGTTGGCAATTTGTTTTTCTACAAAATCGGATGGGAAATCTGTTAAGTAAGTACTGTTTTGCCTTGGAATTGGATTTTTAATGTTGACTTTATCAT
ESTD-PXMP1	88	A	G	ATGAAAACATGGTTCTTTAATTTTATGATATGTTTGTATAGCTATCTTAAAAGGGCTTCTTTTTTTAATGCAGACAGAAGAGGGGGAAAAA[A/G]GAGCGAGCTGTGTGGTGGACAAGGTGTTTTCTCAAGGCTCATACAGATTCTGAAAATCATGGTCCCTAGAACATTTGTAAAGAGGTAAGTCTTATGAAATTATAATCTTCCCGAGGAATCTGAGAGCGAGAGGGCGCTGGCTGCTGGAGAGTGTGAAGAAGCGGTGCCGGAGACCTGGAAGGCCTTTCTGGAGAGTGTGAAGAAGCTGGGCAACCAGGTGGAAGCCGAGGGCGCAGACGCAGGCCAAGAAACGTGGATCTCCCCCTCATCCAACTCCGAAAGTCTGAA
ESTD-RDS	127	A		TTGGGAAGTTAGAGCCTATATTAAATTACGGAATTACTAAGGCAGGACACAGAGGCTTAATTGAAAATATCCCAAAGTTGAAATGTCTCAGTTC[G/T]CTGTGTGTGGGTTAGATGCAGGATTTATATGATCCGTTAACCTCT
ESTD-s14544	94	G	T	ATCACAGGTCTCTGGTCTCTGGCCATCATTCCTGGGAGAGATGG[A/C]TGGTGGTCTCGCAAGCCCTTTGGCAATGTGAGATTTGATG
EST529080	45	A	C	AGGAGAAGTCTGAGGGGGAAGAGAGACAAGAATGACATTGATGAGTGAAGATGT[C/T]GGCTCAGGATGCGGGAAAATGAC
EST19590	55	C	T	TGAAGCTTCTGCCCAGCTTGCATTGTTTCTAGGAGAACC[C/T]GCGTCATACCTTTATCTATAGCCTTCCCCTAGGTCTT
EST76136	39	C	T	
ESTD-SPTB	176	C	T	TGAAACACCCTGTGGTCCGGAGCCAGGTTGTTTCTCTGGGAGCCTGAGGAGTTTGTTGTCTGTGTGCAGTCCCCGCGCCACCTGGCCATGTCCCTGCCTGGTTGAGCCTGGACATACACCTTCACCTCCTTTGGCCGGGAGAAGACATTTACCCCACCTGGCCCATGTCCCTGGCCTGTCGTGTGCACA[C/T]CCTCTGTGGTGTCTGGAAGACCCCAACCCCTGCCTCCCCCACCCACCCAGTTTCCTCTAGCAAGGGCAGGAC

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Name			Sequence
ESTD-TAT	224	C	AAATGGTCAGGAGACCCTGATCCACAAGAAGTGGTACCATTTCATCAGGGCCATCAGTTCATTCAGCTC CCATGACTGGGGATGCTAAGTCAGCAACTGAGTTCATTCATCTTAAAATGACTTGTGGGACAGGATCA ATTTCCTCTCACCTAGAACGTTGTTTACAACTTTCTTCCCAGTATGGATGGGATTATGATGGGGGG GAGAAGCAAATTTAAATAGGACCCATGAGACACATCA
ESTD-THRB	125	A C	TGCGGCCTTTCCTCCGGCAGGGTAGACTTCTTACTTGGCTGTTGATTTCCAAGAGAAAGAGAGTCCCAAG CACACGAAAACAGAAGTTGCAGATCCCAGTGCCCAAACAAGTCTGAGTGCCAGGCAGGACTCAACGGTCCCCCTGTAGATGGG CCACACTGGATTGGCCCAAACAAGTCTGAGTGCAGGCAGGACTCAACGGTCCCCCTGTAGATGGG_underlined... [A/C]CTTCAT
ESTD-TYR	122	G T	TAGTGAAGTTTCATCTCCTGTCAGCTTCTGTTGATTTCTTGTTCCCACCGCAACAAGAAGAGTCTATGC GCAGTGCATCCATTGACACATAATAATGCATCCAGACAAAGAGGTCATAAATATTGATGTCGTTAAA[G/T]ATCCCCCAA CATGGGTGTTGTTGATCCATTTTCATTGGCCATAGTCCCTATGGGGATGACA
ESTD-TYRP1	222	A C	AGTAGTGGATGAAGCTAACCAGCCTCTCCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AAACTCCAGAATCCTAATCAGTCTGTGTGTCTAACAAATGCCCTACTCTCTTATGCATTAGTATCACAA AATACAAGCATATGTTAG[A/C]ATTAAAGTTCTAGGCATACTT
ESTD-TYRP1	222	A C	AGTAGTGGATGAAGCTAACCAGCCTCTCCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AAACTCCAGAATCCTAATCAGTCTGTGGTCTAACAAATGAGTTATTAACTGTATTTTCTTCACTTTATTACCTTCTTTCT AATACAAGCATATGTTAG[A/C]ATTAAAGTTCTAGGCATACTT
ESTD-VB12	148	C T	TTCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTGTTTCTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCCAAGACACAAGGTCACAGAGACAGGAACACCAGTG ACTCTGAGATGTCA[C/T]CAGACTGAGAACCACCGTTATATGTACTGGTATCGACAAGACCCGGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD-VB12b	148	C T	TTCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTGTTTCTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCCAAGACACAAGGTCACAGAGACAGGAACACCAGTG ACTCTGAGATGTCA[C/T]CAGACTGAGAACCACCGTTATATGTACTGGTATCGACAAGACCCGGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD-VB12a	74	A G	TTCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTGTTTCTATTACA GGACAC[A/G]GTGGATGCTGGAATCACCCAGAGCCCAAGACACACAAGGTCACAGAGAGACAGGAACACCA GTGACTCTGAGATGTCACCAGACTGAGAACCACCGTTATATGTACTGGTATCGACAAGACCCGGGGC ATGGGCTGAGGCTGATCCATTACTCATAT

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EST586070	105	A G	CTCTGGATGGGTTCACAGGTGGCAGGCACAAGCCAGTCCATCCTGTAGTCATCATAGTGTTGTTGGCTCC CAAGTTGCTCTCCTCACTGGAGAGAACACAAGGACAGCCAC[A/G]TGGCGCGGGGGATGGCGGGGGGAGTTC TGGTTGCGGCCCACGGCCTGTGGCCCTCGTTGTGAACGGTAGCCTTTGCGGTTGCCGGATGCCTAAACCTTTGT TTCTTGGCCAAGGAGGGGCGGGGGTGCCATGCCTGAGATGTAGATGCGGCC
ESTD-VWF	36	G	AGGTAGGAAAAGCAAAGAGTTGATTAGTGAAGGAGGAATGGACCTACCTTCCACACTGTCCTTTGG TCCCCTAGAGTCTG
EST717706	189	C G	AGCACCACCTCTCACGTCAAGCCTCAGCACCAGATGCTGTTCTATAAGGATGACGTGCTGTTTTACAA CATCTCCTCCATGAAGAGCACCAGAGAGTTATTTTATTCCTGAAGTCCGGATCTATGACTCAGGGACAT ATAAATGTACTGTGATTGTGAACAACAAAGAGAAAACCACTGCAGAGTACCAG[C/G]TGTTGGTGGA AGGAGTGCCCAGTCCCAGGGTGACACTGGACAAGAAAGAGGGCCATCCAAGG
ESTD-TNFAb	152	A G	TTCCTGCATCCTGTCTGGAAGTTAGAAGGAAAACAGACCACACAGACCTGGTCCCCAAAAGAAATGGAGG CAATAGGTTTTGAGGGGCATGGAGGACGGGGTTCAGCCTCCAGGGTCCTACACACAAATCAGTCAGTG GCCCAGAAGACCCCCCTC[A/G]GAATCGGAGCAGGAGGATGGGGAGTGTGAGGGGTATCCTTGATG CTTGTGTGTCCCCAACTTTCCAAATCCCCGCGATGG
ESTD-TNFAa	88	A	TTCCTGCATCCTGTCTGGAAGTTAGAAGGAAAACAGACCACAGACCTGTCCCCAAAAGAAATGGAGG CAATAGGTTTTGAGGGGCATGGAGGACGGGGTTCAGCCTCCAGGGTCCTACACACAAATCAGTCAGTG GCCCAGAAGACCCCCCTCAGAATCGGAGCAGGAGGATGGGGAGTGTGAGGGGGTATCCTTGATGCTT GTGTGTCCCCAACTTTCCAAATCCCCGCGATGG
EST524186	113	A G	CAAATTACAGGGTCAACTGCTATGATGTGTTTGGAGCCCAGTCACCCTTTGGTGGCTACAAGATGTCG GGGAGTGGCCGGGGAGTTGGGGCGGGAGGTGCCGAGGCGCATACACTTA[A/G]AAGTGAAAACTGTGAGTG TGG
EST135863	89	A G	CCCACTCTATTTGCCCAGCCCCAGGGACAGAGCTGATCCTTGAACTCTTAAGTTCCACATTGCCAGGA CCAGTGAGCAGCAACAGGGCC[A/G]GGGCTGGCTTATCAGCCTCCCAGACCCTGGCTGCAGA CATAAATAGGCCCTGCAAGAGCTGGCTGCTTAGAGACTGCGGAGAAGGAGGTGCGTCGCTGCCTGCC CCGGTCACTC
EST519767	123	A T	AGGCAGAAACTGGGCCCCATGCGGGGGACGTGGAAGGCCACTTGAGCTTCCTGGAGAAGGACCTGA GGGACACAAGGTCAACTCCTTCTTCAGCACCTTCAAGGAGGAAAGAGAGCCAGGACAAG[A/T]CTCTCTC CCTCCCGTGAGCTGGAGCAACAGCAGGAACAGCAGGAGCAGGAGCAGCAGGTGCAGATGCTG GCCCCTTGGAGAGCTGAGCTGCCCCTGGTGC
EST114586	140	A G	CCACTTTGGTAGTGCCAGTGTGACTCACGTCATCCACAATGATTTCTCCAGTGCTGCTCATCTTGTTCTCGAGTTTT CTCTGCCATGTTGCTATTGCGAGGACGGACCTGTCCCAAGCCAGATGATTTACCATTTTCCACAGTGGT CCC[A/G]TTAAAAACATTCTATGAGCCAGGAGAAGTTTATCTGCCCTCTCACAGGACTGTGGCC TCCCGAGGAGGGATGAGAAGTTTATCTGCCCTCTCACAGGACTGTGTGCC

Name	Pos	V1	V2	Sequence
ESTD-AT3aa	60	C	T	AGACCTCAGTTCCTCTTCTGTGTAAAAGGGGAAGTTTGTTCTTGGATCTCCAATGGGCCCAGC[C/T]AGCACTGGTGCCCTGTGAGTCGTGTATCAGGTAGAGGAGGATGGGACCAGGTGGAGAGGAATTTGAAAGGGCATTGGAATTCAGAGCAAAGAGACAAAGACAGATATTAAGAGCTGGGAAATGTGG
EST398528	106	C	G	CGGTCTTCCTTCCAGGTATTGTTGCAGAAGGCCGAGATGACCTCTATGTCTCAGATGCATTCCATAAGGCATTTCTTGAGGTGAGTACACCTTCCCCACTCTCTTA[C/G]GGTACAGAAAGGAGATGCATGAACAGCAGGAACACGTGGAAAAGGCCTGTTCCAGTGTTAAGGCATGCAAAAGGCCTCCACAGGCTGCTATAATACAGCCCT
EST624480	112	A	G	ACCTGGTGTTGCTGCTGCTGTGGGTGAACCTGGTGTCCTCTTGGCATTGCCGGCCCTCCTGGGGCCCGTGGTCCTCCTGGTGCTGTGGGTAGTCCTGGAGTCAAGGGTCCTTA[A/G]GTGAAGCTGGTCGTGATGGCAACCCTGGGAACGATGGTGTCCCCCAGGTCGCGGATGGTCAACCCGGACACAAGGGGAGGAGCGCGGTTACCCTGGCAATAT
EST360272	120	A	C	AGTGACTTCCAAGGAAATGGCTACCAACTTGCCTTCATGCGCCTGCTGGCCAACTATGCCTCTCAGAACATCACCTACCACCTGCAAGAACAGCATTGCATACATGATGAGGAGACTGG[A/C]AACCTGAAAAAGGCTGTCATTCTACAGGGGCTCTAACGATGTTGAACTTGTTGCTGAGGGCAACAGCAGGTTCACTTACACTGTTCTTGTAGATGGCTGCTGCTCTAAAAAGAACACAAATGAATGGGGAAAGACAA
ESTD-COL2A1cc	112	A	G	AGAATGTATATAGTCCTGGCCATCTCCATTTTCAGTCCAAAAGTTATACAGCTAGACAACAGTGGTGGACATAGCGTTGCTATTTATGCTCTTCCTGTCACTTTC[A/G]GGGTGTTCAAGGTGGAAAGGTGAACAGGGTCCGCGCTGGTCCCTCCGTCCAGGTAAGTCAACTCAAGCATATACAATACTGCCTTTGGTCAGCCTATTGAGCTGTAAATCACCATACGGTACCT
ESTD-COL2A1dd	97	C	T	TGAGAGAACACCTAGTCCTCCTCATCCTTCTCTCAATGGCAAGAAAGTTAAGTGACCTATCTAGGGCAATAGACTGAGTTGCTGGGAACTTCTTCTACTGCAGCAGAAGACTTA[C/T]TGGACTTCTTTCATTTTATTTGACCAAACACTATCATGGAACACCCAAGAGAGATTAATGGCAAAGATATACAATACAATTTTATGCATT
ESTD-CPT2	150	A	G	GCCGCAATGCCCGGGAGTTTCTCCAATGTGTGGAGAAGAGGCCTTAGAAGAGACATGTTTGATGCCTTAGAAGGCAAATCCATCAAAAGTTAACTTCTGGGCAGAGAAAAGCTACCATCACTTCCTCATCATGAAAACTGGGAGGCCGGCCAGCAT[A/G]GTGCTCATGCCTGTAATCCCAGCATTTTGAGAGGCCGGGGATCACTTGAGGTCAGGAGTTTGAGACCAACCTGGCCAACAT
EST122740	135	A	G	CCCCAGTTGACAGCCACTGCTCTAGACTAAGTTCTTGCTTCCAAATAGAGCCTTACCAAAGTGTATTACATAAAGAAGTCAAGTGGTTTACTCCTCATGACCAAATATCTTCCCTCCTTAGGATGAGGTG[A/G]TAGTAAATGACCGATGGGGTCAGAACTGTTCCTGTCCATGGACGATACTATAACTGTGAAGATAAATTCAAGCCACAGAGCTTGCCCAGATC
EST76807	91	G		ATGCTAAGGGGGATCGGACGACATGAAAGGACCCTGTGAGCCGATTGTCCTATCTCCAGCGCCGCCCTGTCATCCAGCTCACTCATCAATGGGCACCAGTCAGGCCCAGCCCGAGGCACTGGCCTCCGGAGGACTCACCACCTGCGCCCCCTGCTGCCATGTGGACTGGTGGTGCAAGTTGCAAGTTGGAGGACTTCTTG

ID	Pos			Sequence
ESTD-SSA1	111	C	T	TTCACTTTGTGGATTGTTTCTTTGCTGTGTGCAGCACCTTTCAACATGATGATCCCATTGTTGTCCAAG TTTGCTTTGGCTGCCTGTGCTTGTTGTGGGATATTTGAAAGAGAT[C/T]TTTGCCAGTCCAATGTCCTAGA GAGTTTCCCAATGTTTTCTTTGTAATAGTTTCATAGTTTGAGGCCTTAGATTTAAGTCTTTAATCCATT TTGATTTGATTTCTGTA
ESTD-RYR1	109	A	G	CTTCGTGACGGGAGGTCACGTCCTCCGCCTCTTTCATGGACACATATGGATGAGTGTCTGACCATTTCCC CTGCTGACAGTGATGACCAGCCAGACTTGTCTACTATGAG[A/G]GGGGAGCTGTGTGCACTCATGCC CGCTCCCCTCTGGAGCCCACTGGAGCCAATCAGCTGAGAATCACGGGAGGCCACCTGCGCTGGGGCAGCC ACTCCGAGTCCGGCATGTCACTCACGGGCAGTACCTAGCCGCTCACCGAGG
ESTD-WT1	70	A	G	AAGACCTACGTGAATGTTCACATGTGCTTAAAGCCTCCCTTCCTCTCTTACTCTCTGCCTCTGCAGGATGTG CG[A/G]CGTGTGCCTGGAGTAGCCCCGACTCTTGTACGGTCGGCATCTGAGACCAGTGAGAAACGCCC CTTCATGTGTGCTTACCCAGGCTGCAA
ESTD-F2	100	C		GATAAGTACACTGAGGCCCCAGGAGGTTATTGCCTAGTAGCCAACTGTGCATGCACGCTTAACCTCT GCACCAAATGGCCTCCAAGGCCCGTAGGGGAACTGGGGGGATCTAGGGGTGGGTGAGGATGGCCC AGCCCAGTCCCGGCGGTGCCTGGGTCCCAACAGAGGAGGCCGTGGAGGAGGAGCAGGAGGATGGGC TGGGATGAG
EST4443877	62	C	T	GCAGCCAGGAGCCGCTGCACCATGCCCCGCATAGATGCGGGACCTCAAGCTCGACTTCAAGGA[C/T]G TCCTGCTCCGACCTAAGCGGAGCAGCCTCAAGAGCGAGCCGAGGTGGG
ESTD-PBDA	103	A	G	CCTTCTCATGCCCAGATGGAAATTCCAGTCCCTTCAGGATCTGCCTAACCTGTGACAGTCTAAAGAGT CTGAGCCGGTGGCTGGGAAGGGCAGGACTAATCCAA[A/G]TCTCTACCCGCCAGCTTGCTCGCATACAG ACGGACAGTGTGTGGTGGCAACATTGAAAGCCTCGTACC
EST128393	122	A	G	TGCAAAACACACAAAATCTTCTCCAGATGCCCTATGGCTGTGTGGAGAGCAGAATATGGTCCTCTTGCT CCTAACATCTATGTACTGGATTATCTAAATGAAACACAGCAGCTTACTCCAGAG[A/G]TCAAGTCCA AGGCCATTGAATGCTATCTCAACACTGGTGAGTGATTACTTGAGTAAGGGAAACTTGAATGTTATTCAAC TGGATTTCCAGTAGGTTCAGTTACTTATGAATATTATGATACTTAGCTTAG
ESTD-CTLA-4	48	A	G	ATGGCCTTGCCTTGGATTTCAGCGGCACAAGGCTCAGCTGAACCTGCCT[A/G]CCAGGACCTGGCCCTG CACTCTCCTGTTTTTCTCTCTTCATCCGTCTTCTGCAAAGCAATGCACGTGGCCCAGCCTGCTGT GGTACTGGCCAGCAGCCGAGGCATCGCCAGCTTTGTGTGTGAAGCCAC
ESTD-ACE	96	C	T	GATCAAGCAGTGCACACGGGTCACGATGGACCAGCTCTCCACAGTGACCGTCCACCATGAGATGGGCCATATA CAGTACTACCTGCAGTACAAGGATCTGCC[C/T]GTCTCCCGGCGGGGCCCAACCCCGGCTTCCA TGAGGCCATTGGGGACGTGCTGGCGACCTGCTCTCGGTCTCCTGAACATCTGCACAAATGACTCACTA
EST5441988	88	A	G	CTTCTGCCTAATTGAATTGAATGATATGTTGCTGTGTGGGAGGATGTATTTGGGTTAGCGTGGTCGTATGTTGTCTA TTTTCTTGACCCCTACTTAC[A/G]ATCCTGGGAGAGTGATTTGGGGGTTCGGGGAGAGAT CTATAGTCCAAGTGAA

				Sequence
ESTD-PS-1	99	A	G	GGGGAGTAAAACTTGGATTGGGAGATTTCATTTCTACACAGTGTTCTGTTGGTTGGTAAAGCCTCAGCAACAGCCAGTGGAGACTGGAACACAACCATAGCCT[A/G]TTTCGTAGCCATATTAATTGGTTTGTGCCTTACATTATTACTCCTTGCCATTTCAAGAAAGCATTGCCAGCTCTTCCAATCTCCATCACCTTTGGGCTTGTTTTCTACTTTGCCACAGATTATCTTGTA
ESTD-B3AR	104	C	T	GGCTGCCAGGGGTTCGGTGGGAGGGGCCCTAGCCGGGGCCCTGCTGCGGGCGGTGCTGGCCACCGTGGGGAGGCAACCTGCTGGTCATCGTGGCCATCGCC[C/T]GGACTCCGAGACTCCAGACCATGACCAACGTGTTCGTTGGACTTCGCGTCGGCGGCGCGGACCTGGTGATGGGACCTGGTGCCGCGGCGGGGCCACCTTGGCGC
WI-567b	48	A	G	TCTCACACTGACCCCTTACCTTCATCCTCGCTGCCTGGTTC[A/G]AGCCCTCCATCTCTTTACAGGGATCCGCCACAGCATCCCAACTGATCTGGCCTTAGGTCTTCTTCTCCAATCCATTCATTCTTCAAAAGGCTGCCACTGTGATCTCTCCCAAAGGTCTTGATGCTACCATCTTGCTTCAAGCC
WI-801c	58	G	T	ATGGAACATTTCTTCCATATGAATGAGGTTCTCAATCCATTCACACATCCCCTTTCT[G/T]AGATGGTATTGGAGAAGTAGACAGAGAAGAAATTAAGTAGGCAATGCATGTTTGCAGGGGGTGGGGGCTGTGCATCTGTGTATGTTAGTTACATGGGCACATATACGCTCATGTTTGTCCTCAGCCCACCAGAGAGTTAACATTTCTGCCACCCTC
WI-801b	58	G	T	GAAATTCACCTATACAAGAACTATTTCTCTAATTATTTACATTAGTTCATTATTCTGAAATATTATTTTTTACA[A/G]TACCCTTTGATTATTTTTGATTCATTTGTAACGAGAGATTACAATATCAGTAACGCTGTTCATTGATAGTGCTATCACAAATGTCTAAAATACTTTGGGTCAACATCAAAATTAGAAGAAAACTTACAAAGTTTTATTTGCTTTATGGTTTA
WI-1099b	76	A	G	AGGAAATGGCTGATACTCCTGGTGGCTTCATTATAGTAAAAGGAGATGTAATTGCTTGATGAGCCTCTCAA[C/T]TTCTTAACTGCTGCCTCAGTCAGTGAACATTTAATGAAGTCTACACAAATTAATTAGTGTAAGTTGTAAATGCTGAATAAGCTTGAAATAAGTTGAAGAGGAGACAACTGTGCTTTTTAAGAAAATAGAAGAGAGTCACTTTCATTAGAAATGGCTTTGGGGATGACAAGTA
WI-2529	71	C	T	TAAGGGCCTGTCTGTCTTCCCCCAGAGGCCCCACGGGACAGAGAAAGCATCTTGATACCCAGGGCCACAAATGAGCAATCCATAGATACTACATATAAGAGAGACCTGTACCCTATGAGGTAACCTGAGGTGAGGATGAAGGAGTGAGTCATATTGGGTGGCAATTAAATGACCCAGCCTCCTCTCTCCCTCCTCAAGAAGACTTTTACATTTAGACAGG[C/G]AGCAGAGCAAGCAGCAAAGGAGAAGGAAGT
WI-10088	205	C	G	

Name	#	A1	A2	5′ flank	3′ flank	Sequence
WI-2625	98	G	A	---		GGGCAGTCCTGGCCTGTGAGTGGTAGACAGCACTGAAGGATGAAGGAGGAGAGAGAAGAAACAGGCAGAA GCACTGGTGAGTTAACAAGGCTTATTAGGA[G/A]CAAATTGATGATACTCCCTGAGGACTCGCAG AAATTACCAGCAGTGGACAGGGTTATCTGTGGTGAATTCAGTTATTCCACTTGCAGGAGGAAAGCCA GCCAGCAAAG
WI-2924	54	G	A	TGACCTTCCTA GTCTTCTCTTA TAGG	GCCCTAAGTGT AATCACAGGG	TCTGTTGTCATATTCCCTCTTTGACCTCTGACCTTCCTAGTCTTCTCTTCTTATAGG[G/A]CCCTGTGATT ACACTTAGGGCCTACCTGGATTATTTAGAACAATC
WI-2939	72	G	T	GGCTTGTCTCA GTGCCTTT	CTTGTTGAGGG AAGGTCTTG	CCATTGTTGAGGTGGGTGGGGGTCACTTGTCATTCCCTCGCACTCAACAAAGTGGCTTGTGTCTCAGTGC CTT[G/T]CAAGAACCTTCCTCAACAGAATGTCTTTCCATGCTCCCGTGTTCTTGAAAATTCGACT TTATCCTGAAAAACTCAGCTGCAGTGTTATCTCGGTATAAAGCCACTCCTG
WI-3203	99	G	A	GGTTATGCCGC AGACGAG	TCAAGTATTGC CTTGTGTGG	CTTGCTACCATGCATTCACAGCATACAACCCTCAGTGAAATGCCGTAAACCCCATTATAAAACAT CTTGCCATCGAAGGGGTTATGCCGCAGCGAG[G/A]CCACACAAGGCAATACTTGAAGTGACTTGGA GAATAAAGATTTGGATGATGAAAGCACAGAGAAGGAGATGCTAAAAGTGA
WI-3473	101	A	G	AAGCATTTTA GCCCTAGGGA	CCTGATGTCAC CAACATTTTCT	GGAAAAAGAAACCTGAAGGATGAGTAGAAGTTAATTGGGAAGTAGTTGGTGATAGGCCCTGTTTGGA GATTGCAGAGAAGGAAGCATTTTAGCCCTAGGGA[A/G]TGCAGGCGTCATTTCTGCACATGGTGATATTTAAG
WI-1796b	29	A	G	---		ACACACTTTTCTGTATGCTCTTCATCAAA[A/G]TGCAGGCGTCATTTCTGCACATGGTGATATTTAAG CAGGAGAGCCATTGTCTTGGGCTCCCC
WI-1796	29	A	G	---		ACACACTTTTCTGTATGCTCTTCATCAAA[A/G]TGCAGGCGTCATTTCTGCACATGGTGATATTTAAG CAGGAGAGCCATTGTCTTGGGCTCCCC
WI-4360	93	C	T	GTAGTCACATT AGGTATTTCC AAATAA	GAGAGATATT TTCAGAGGCAT TTT	AGTCGTCCATCTTCAGGGTCTAACTCTGGATCTGGCCTGCAGAGTAGGAAAGAAAGATGGGGTGAGT AGTCACATTAGGTATTTCCAAATAA[C/T]AAAATGCCTCTGAAAAATATCTCCCATGTCCCTGTC TAAATATAACATTTTCCC
WI-1959b	87	C	T	---		GCTGAGCTTTGTGGCAGAGCCAGGAGACAATTCAGCTGCCGGATTTAATAGATTCTGCAGCACTGCAA CAGGAACCAAAAATCAGTC[C/T]GGGTAACTGAGAGTGGTTTTCACACCCAAA
WI-1973b	28	A	G	---		GTTGTGCCTGTAGCAGACACAGAGGCA[A/G]AGAGGAAAAAGCCTTTTGGTCCAGGGGCTTACAC TGAATCCCTCAAACAATGCAAGATGAGCTAATGCTTAGAGGTATAATCTAAGTGTGTGAGAAAAACA AAGGTATAGGGTTTG
WI-1980b	140	C	T	---		CTTGAGTATGCGTGGATTTTGGTATACACAGAAAATGGGAGAGAGCTGGAACTAATCCCCCATATACCA AGGGACAAATTGTATCTGTTCTACAATTATACAGTGAAATTATGTTCCATGACAATGGTAAT TTTTAA[C/T]TGACAGTTTTAATTGAGTGAAATTACCATAAAAATAATAATAGTAGCAGCTAATATT TACTGAGCTGTTACTAGGTGCCTATAAATAGC

Name	Pos				Sequence
WI-2015b	190	A	G	---	TGTCAGATAGTCCGTCTCTACCTAGGTGCAGTAGCATGCTAGGAGCTATTAAAGTACACAATTATGCT ATATATTTATACACAATACAATTACTTGCAGATAGCATGCTAGTGAACCCACAAGACTAT GTGTGAATCGTCGTTATTAGGGTTGCTATAAACTCTACAGTGGTGCTTTTTCCAACT[A/G]CATATACTT CTAATACCATAGAG
WI-754b	49	C	T	---	GAAGGCACAGGGAGGAAGATGGCTGTCATCTACCAGCCAGGGAGGAGAAGC[C/T]ACATTTATTGGTAA TCCTATAAAGTGCATTCTTAAAATTTGTATTTACTTTAGA
WI-754	22	T	C	---	GAAGGCACAGGGAGGAGAATGGCT[T/C]GTCATCTACCAGCCAGGGAGGAGAAGCCACATTTATTGGTAA TCCTATAAAGTGCATTCTTAAAATTTGTATTTACTTTAGA
WIR-1b	56	A	G	---	AGGCAATCAGACCTACAGAAGGAAACCCAATAAAAACTCTGATGATCGTACATCC[A/G]TGCGCTG GAGGGGTGATGCCCTCCTGAGGACATGGGAGCTTCATGTTTGGAGCCCTCCTG
WIR-1	56	A	G	---	AGGCAATCAGACCTACAGAAGGAAACCCAATAAAAACTCTGATGATCGTACATCC[A/G]TGCGCTG GAGGGGTGATGCCCTCCTGAGGACATGGGAGCTTCATGTTTGGAGCCCTCCTG
WIR-3b	72	A	G	---	TAATTTAAAATGGGGCCAATAACACAGTACTTATCTCACAGCATTCTCTAAAGGCTAAATAAGAA GAAGT[A/G]TCTAAAAGTTATTAGCTCAGAGCCTCACACATTCTCAGTGACTGATAAACAATAAGCA AAGCTGGGGTGCTGAGATAAGA
WIR-3a	69	A	T	---	TAATTTAAAATGGGGCCAATAACACAGTACTTATCTCACAGCATTCTCTAAAGGCTAAATAAGAA GA[A/T]TGTATCTAAAAGTTATTAGCTCAGAGCCTCACACATTCTCAGTGACTGATAAACAATAAGCA AAGCTGGGGTGCTGAGATAAGA
WIR-4	47	T		---	GAGCCTTTCTAAAAATAAGGATTGTGACTAGCAACCTCCTGCTACAGATTCCCTGCTCACATGTCA AGGCAGCAGCAAATTTGCCCAGCTGCC
WIR-5g	209	C		---	CGGGACAGAGAGAGACAGAGAGAGAGAGTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCCAGACCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACAGG TTTTACGTCCAG
WIR-5f	196	C		---	CGGGACAGAGAGAGACAGAGAGAGAGAGTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCCAGACCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACAGG TTTTACGTCCAG
WIR-5e	194	C		---	CGGGACAGAGAGAGACAGAGAGAGAGAGTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCCAGACCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACAGG TTTTACGTCCAG

Marker	Position	Allele		Sequence
WIR-5d	191	A	---	CGGGACAGAGAGAGACAGAGAGAGAGAGTTCTGCGAGCATTCACAGAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCCAGAGCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACAGG TTTTACGTCCAG
WIR-5c	177	C	---	CGGGACAGAGAGACAGAGAGAGTTCTGCGAGCATTCACAGAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCCAGAGCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACAGG TTTTACGTCCAG
WIR-5b	159	A	---	CGGGACAGAGAGACAGAGAGAGAGAGTTCTGCGAGCATTC[A/G]CAAGAGGTTATTAGGACTCAGTTCTG CTGTGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCCAGAGCCTGTGGTCCCACTGTT AGGTTTTGAAGGGAAGGCAAGGGTTAAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACAC AGGTTTTACGTCCAG
WIR-5a	37	A	G ---	TAACCCTGAAACTTTGTCTTCCTCATCTCAGGGAGAACACAGACTTCATGTTAAGACCCAGAA[A/C] CGCAGTCTTGGGGTTGGGGCAG
WIR-6	63	A	C ---	TTCGTGACTATT[C/T]AAGCATCTGTAGAATATTGAATACATAGTCTTGAGATTGATC
WIR-7	12	C	T ---	GGCGTCCTATGACATCCTGGTCATCCTGATTGCTACTAATGATTCCTG[C/T]GCCCTG
WIR-8	46	C	T ---	AAACAGAAAAATAGAGGTTATAAGGATGGAACTAAAAGTTGTCAGAGAGGTATGA[C/G]CTGAAG AAAGAATTACTCTCTTTGACCAATAAATACAATTGGGAAACACTGGAAAACCATGGCTTGATTACT GACAAC
WIR-2	56	C	G ---	TGTCCTTGCTTATGCCTGCCTCTTTCGCTTGGCCAGGATGATGCGTCATTAGTATTTCACAGAGAAGTA GCTTCAGAGGGTAACTTAACAGAGT[G/A]TCAGATCTATCTTGTCAATCCCAAGCGTTTACATAAAA TAAGAGATCCTTAGTGCACCCAGTGACTGACATCTTAACACAGCCGTGTGTTCAAAT GTACAGTGGTCCTTTCAGAGTTGGACTTCTAGACTCACCTGTTCTCACTC
WI-7069	93	G	A ---	GGTCATTTCCTTTTTATCTGTCAGGCAGCCAGCTCTGACTT[A/T]CTCTCTGTTTCTGTCATCTCTCCC CCACATACCAACTTCTTCACCATGATGATTACCAATAATACACAGTTCCTTATATGAGGGGCTCTGGA AAATTAGACAGTGAAG
WI-18694	41	A	T ---	CACACTGTTCACACCTATATTTCAAGTTGGAAATGC[A/G]TATTGCAAGCAGCAATACAAAGTA
WI-18612	37	A:G TGC	CCTATATTTCA AGTTTGGAAAA	TTGTATTGCTG CTTGCAAAT	TTCATGAAGAATGCATAATCTCTGAAAATTATGAAAACATCCT

ID	No.					Sequence
WI-18517	87	C	T	CAGGAATCAG CAGCCTGA	TGTTTGGACAA GTGCAACA	TTAAAAAATCAACTAGGGCTCACCCTCCAACACCCCCTCCATTTGTCAACCTCTACAGCCTGCATGCC ACAGGAATCAGCAGCCTGA[C/T]TGTTGCACTTGTCCAAACACAACTGACTGC
WI-18668	76	C	T	GGCGAAAAAC TAGGCAAAAA	GCTAAAATTAAA CTGCACTTTT	CGATTGACAACCTTTATTTTCAACTAGGTAACAGTCCAAAATCAGTGTAGATTGGCGAAAAACT AGGCAAAAA[C/T]AGCAAAAAGTGCAGTTTAATTTAGCAAAGGCTCAAGACAGTATGTGGAAGGAA GC
WI-18680	75	T	C	GCTGTCACTCT AGCATCTGGA A	CCTCCTGAATA TACAACGGAGC	TAAAACATACGAGTACTGTACACGCAAGCATGCATCCCCTGAGTCTGAGTGAGGCTGTCACTCTAGC ATCTGGAA TCTGGAA[T/C]GCTCCGTTGTATATTCAGGAGGGGA
WI-18704	99	A	C	GGGTTCTCCGA GGGGTAC	TGAAGGCCCTG CTGG	CACCCAGGCTGTACCCAGGCTTTCTTGTGCGAGCACCACCAAGGGCAGGTTGGGCTTGAAGGAGCC CTTGAGGAAACACGGGTCTCCGAGGGGTAC[A/C]CCAGGCCTTCAGCTTAAGTCG
WI-18673	29	A	G	---	---	TGTGGGCAAACCTTGTTTAATTGCAAAC[A/G]ACTTAATTTACAGCACATTCAATAATGAACCAAC AGGAGAGTTGCTGACTTGTAACATATGAATATATAAAAAATCCCTTGCAATTCAGGTAGTCAAGGTA AAAAGCGCATACAAGGAAG
WI-18640	121	T	C	GTCGTGGGGTG GGGG	GCAAATACCAC TGAAGAGGAC A	ACCAGTCATGTTTATTGGAGGTTAATTCCTATTAGGGATATGAAAGGATTCAGCAACGATTGAGATT GTGTTCCTCACGGAGGGGCTCGGGCCAAGGTCGTGGGGGGTGCAGAG[T/C]GTGTCCTCTTC AGTGGTATTTGCGGACC
WI-18533b	91	A	C	---	---	GGGGAGAGAGGAGGTAGATTGCCAAATTGAGGCATTTTTTAAACTCCCGAGATTTTCTTCTTTATTT TATATTTTTCATTTTCATCCTAA[T/C]TTACTGAAGCCATTTCTTGGTTAACTTTAGA
WI-18533a	59	T	G	---	---	GGGGAGAGAGGAGGTAGATTGCCAAATTGAGGCATTTTTTAAACTCCCGAGATTTTCTT[T/G]CTTTA TTTTATATTTTCATTTTCATCCTAATTTACTGAAGCCATTTCTTGGTTAACTTTAGA
D11734	83	A	C	TCATCTGATAC AACCAGGATA CTTGTTCAGAT AGGCTACAACT TTC ATTT		GAGCATATGCTGCATGAGGACCTTTCTATCTTACATTATGGCTGGGAATCTTACTCTTTCATCTGATA CCTTGTTCAGATTTC[A/C]AAATAGTTGTAGCCTTATCCTGGTTTTACAGATGTGAAACTTT
D49493	159	A	T	CCTGAAGGAA TCTGGGAATT	ACTTTCAGGCC AGGGC	CAGGACTTGTGGTGCAGCTGCAGACACAGAGCACAGCTCATGGGCAACATCACTGGGCGCCCAGAGAG AGCTGTCCGCCAGTGCATCATTAGGGGGTCTTCATTGCTAGTGACTAGCCCCTTAAATGCCAGCCTG AGTACCTGAAGGAATCTGGGAATT[A/T]GCCCTGGCCTGAAAGTGCCCATCATTCATACCCACTGTT CT
EST100307	98	T	C	CATTTTTGTTC TCTCAAGTCCC	GCAGTGGTGGT ATGGATGA	TATTTCATAGAGGAGGACCTAGGAGGAGGTTGACACAGCACACTGCTCAGCAGATGACTTAAAATTTT CCCTTAGCCATTTTTGTTCTCTCAAGTCCCTT[T/C]TCATCCATACCACCACTGCTGATTG
EST100522	24	G	A	GCTCACTTCTG GAGGCTG	TGTGGAACCTC AATCTTAGACT TC	TATTTGGCTCACTTCTGGAGGCTG[G/A]AGAGTCTAAGATCTAAGATTGAGGTTCCACATCTTGTGAGGGCCTTC CTGTTGAGTCATAACCTGGTGGAAGTCATCATGTGGAAGAGCAAGAGGAGAGGGCTACAGAGAGCAAGAGGAA A

ID	Position			Flanking	Sequence
EST10605 2	118	C	G	---	CTTGCGTAAATCACAGTTCTCGTGTATTCATACAAAAACTTTGTTTTCTCTGACAAACTGTACACATAGAAACAAATTTCCAAATGGACAGGAACTTAAATTTGTGGAGATGCCCCATGT[C/G]TTGTGGAGACTTAAAAAAAGAAAAAGATCCC
EST11048 0	61	T	G	CTCTCAAGTAG ATAAGAGGCA TAATCT / GCTAAATTTC AGAAAGAATT TTGTTT	CATGTGTCAATCCCATGATTGAAAAGACATGTTGCTCTCAAGTAGATAAGAGGCATAATCT[T/G]AA ACAAATTCTTCTGAAAATTTAGCTTATGAACTCATTACACTGCAAACCAGAGAAGGAGCAC
EST11260 8	101	G	T	---	TATGGAGGCCAGAGGAAGTGACACTATATGTGGAAGTGCTGAAAGAAATGAAGTGTCAACACAAAA TTCTATATCCAGCTAAATATCATTTAAGAATGAAG[G/T]GGAAATGAAGGCAATATCAGATAAA
EST11349 9	109	C	T	---	TTTGATGGAGAAATCCGAGGCCTGCCAGCATCCCACCAGTAGATTTCTTTGGACGAAGAAAATCCT TCTGTGGATTCAGCTTACCGCGCCTTTCCTCATCTGCTGGTGT[C/T]TTCCTCAGAGCTTTAATGTCCGT CCTGCTCTCCGAGTCAG
WI-16632a	71	A	G	CCAACCTACTT TGGAGCCCT / CTAAAAACTCC T	GAATTCTGGGTATTAAATAGCGGGGTGCCACAGGAGCACATAGGAAGAAGCATCCAACCTACTTTGGAG CCCT[A/G]AGGAGTTTTTAGAGAAGCTGGAGCCCGAGAACCAGTAGTAGGAGGTAGCCAGACCAA AGGGGAGGAAGGAGTGGGAA
EST11772 6	74	A	G	---	CCAGGAATAAAAGAAAAAGAAGTCAGAGGAAACAGTCTTTGATGTTATGAGGCTGAGACACTACTC TTCCTTCA[A/G]GACTATTTCATTCTGACTATAAGTGAATAAATACATTGAAGACTTCAGGAGCTCA
EST11795 3	82	G	A	---	CTTGTCCATTTATTTGTGCATGTTGTTCTTAAAAGGCTTGTGAAAGATAACTTGGAATGTGGGAAAC ACATAGATCCCAGA[G/A]TATTTAAAAGGGGCTGGAAAAGTAGCCTTAAGAC
WI-16644	42	G	A	CAATAAGCAG CTCATTTTGAT TATAC / ACTTCATGAAT TTTACTTCATG TATACC	AGAGCAATGGTGCGATCTCAATAAGCAGCTCATTTTGATTAC[G/A]GGTATACATGAAGTAAAATTC ATGAAGTAAAATTCATTATACCAAAAGCCTCCCACAGAACTTTCATGCACCCTGAGCTATGTGAAC TGAAAAGTAACAGTGGGAT
EST12005 9	56	A	G	GGCTGGTCACT TCCTGGAT	GCCTAGTAATTCCAAAAGGAACATGTTGTATAATAACACTCAGTACAAAGTCTGT[A/G]ATCCAGG AAGTGACCAGCCCGACGTGTGCTATGACCCCTCGAACCTCCATTCCATAGTTTTTGAAATC
EST12055 9	32	T	C	---	GTGGAAAATTTTTTTATCTGTATACGTCTTTCC[T/C]ATTATTTATCTTGTCCTTGATTTCAGCACCC CACCCGATTTGCAGGCAGTGCTTTCTAAACTGTGCCCTGTGAGCTGTTAAAAGTCTCT
EST12492 1b	95	A	G	---	CCCCTAGCAAATGACTTGGAGTTGTGTCCAATTACCAAGTTACATGTTGCCAAAATTAAGCTCTC TTCCCCAGAGGCATTAACTGACGATTAT[A/G]GGAAACGACACAGCAAAATTGACGATGCAGCGTTTTA CCTTTTTA
EST12492 4	25	A	G	---	ATCTTGAGGTTTCTGGGCCTGTCAG[A/G]AAGTGACATCTTTTACTTACCACAGGTCAGGAACCCTAT AAAGAAACTGTGTAGAAAAGATATCAGGTCAGACTTTTCTTATCAGCTCAATAA

EST	No.			Fragment	Sequence
EST12502 2	52	C	G	---	ATAACTAGGGAGGAGAAAACCAAACTGGAGGCAAGTCCACAGGTCACACTTGTCA[C/G]CAGCAAGTAT AACAAAGTGGGTTTCGATGAAGAGAAAAATGCTCACGGGGGAAATGACCATTTTAAGGGCCATGTG GTCGTCGAGGCAGGTTAGAGG
EST12619 8	105	T	C	---	CCAGAGAAAAATTAGAATGTATCGGTAAAAGAAATAGGAATGCATATTCAACTCACTGTCACAAA CAGGTGTTTATTATCCCAAATGACAGTGTTGCCTGAGA[T/C]GATGCATGTGGCAGAGAG
EST12620 0	67	A	G	---	TTTTCTCTCCTTCATTTATTCATTGTTCAAAACACTGTCTAGTACCACATTGTCCACCGGGC[A /G]TTGAGAATACAATATTGAAGAAGAGTCACTGCCCTCTGGAAAAATCAGAGTATTTGA
EST12817 9a	22	C	A	---	TTGGGGTTCTCCAGGATTCCAG[C/A]CTCGTAGCTGATGTGCAGTCGTGTGCATGTGTCTCATCCATGCTCCACGG GTTCTTGGGGAGTGACCGGGATGGGAATCCATGTTGCTTGCGTACTCCATCCAGGTCATTGCG
EST12941 8	23	T	A	---	TCTCAGCTTCCACCTGACCTGCA[T/A]CAACAGCCCAGTTATTTCACCAGAATTTGTTTGCGTTTCA ATGTAGTGTTTAGCTTTAATACACTGCACTGTTTG
EST12949 2a	52	A	G	GGCTTTAATCA TAACCTAATA ATACTGTT	TGTGTCCCTGT GGGTCTC	AGGATTTCATGAGGCTTTAATCATAACCTAATATACTGTTAAAAACAACAC[A/G]TCTGTCACTTG CAGAGACCCACAGGGACACACATTCTCTCCTCTCACATAGACTCTGAGGTAGGAGGTACACTGGCT AAGGAATAA
EST13067 4	104	C	T	---	ATTTTTGTTTTCTTAAATGAAGCATAATAAACAGTAAAATTCTCAGAAAAATCATCTATAGTTGA GTGTAAAACTCCCCTAAATCAGTCAGTTCTTAGGGCCACA[C/T]GGAGCGAGAAGCAGCTTCCCACCCAAG CACCTCTGAACT
EST13117 6	66	A	G	---	TGCTGTCTGCATCAGTCCTTTAAAAATTTAATCGCTTTATACAATTGACACCAAATAAAATGCAC[A /G]TATTTAAAGTTTACAAATTGAGAAGCTGACACGTGTCCATACAGACACCTCATTTTACTGTGC TTTACTG
EST13121 6	44	C	T	---	TCTGCTTTAAAGATTCTTCATAGCTGCTTAGGTTGTTGTTCTCC[C/T]AGCATATTCAGCTATAATCA CCTACATTCCCTCCACAAATATTTCCTGTGTGTGCCAGGCCAGTCTCCTCCACTGTCCCATGAATAGCC AGTCTTATTTCCACTCT
EST13226 6	74	T	G	---	AACTGTTTACTAACAACAAGGTGCTTAATTTGAAAAGCATTTGAGGAATAAATTAATGAAATAGTCT GGCCATTT[T/G]GACTAACCAGTTCTACAAATTTCACATATCCGTCACTCAGATGAGCATATCCACCAAG TCAGAGGAAACAAAACATG
EST13230 6	72	G	A	GCTCAGATGTG AGAGACGC	CCGGCTCCTGT ACAGAGA	GCATCATCAGCGGCTTTACTGAACTTACACAACCAACTTGCCGCTCAATATGCGCTCAGATGTGAGAG ACGC[G/A]TCTCTGTACAGGAGCCGGGTACTGTTCAATCCTTTGCATGCAGGTGTTACCACAGGCA AACAGTTTACTCCACAT
EST13236 9a	70	T	C	AACCAGATTT TCTCTCAGGCCT	ACAAGAGGGTT TGACAAAAGA G	AAAGATATAAAAACAACTCCCATCAGTAGCAATACAAGGTTATACATTTAACCAGATTTCTCAGG CCT[T/C]TTTGGATACCTTTAGTAGTTAACTCTCTTTTGTCAAACCCTCTTGTATATAACCA

EST	Pos	N1	N2	5' flank	center	Sequence
EST13278 2a	51	A	G	CTTCACCGAA CAATATTTTAG G	CATATTCTTGG GTGGTGAGAA	TTCGCGAGAACGTTTACAAGCTCCAAACCTTTCACCGGAACAATATTTTAGG[A/G]ATTGAAAATTAT
EST13282 0	99	A	T	CCACACATTC AGTCCAAGA	GATGGAAAATT TGAGGAAGGTT GG	TTCTGTAGTTCTCACCACCCAAGAATATGACAGCTTG / GCTCACTAGATGAGCATTGACCAAATATTTAGATAATACCTGTTGGGAAGTGCTGAATTACTAGCC / TGCCTGAGAATCCCACACATTTCAGTCCAAGA[A/T]AACCTTCCTCAAATTTCCATCTCCCATCAGA
EST13290 9	-39	A	G	CAATTTTTAGA AGTTGGGGTT CTT	AAATCACTTCA TGGAAATTTCA G	AGCTCATCTGCAAGCAATTTTTAGAAGAGTTTGGGTTTCTT[A/G]CTGAAATTTCCATGAAGTGATTTTT / TTTTCTGTGCTTAACTTCAGTTACTTAAAGACCTAAAAGACAAAGTGGTATCACATCACATATTTGT / ATGTGTGGGCTTTTTG
EST13518 2	45	C	G	---		GAAACATCCTCCAGTAGTAGTATTGAGGTTAAAATGATTCAGCATTTA[C/G]ACTTTAAAAATTACCTCA / ATGTTCCTCGGAGTCGTCCATAGTTTAAAATGACTTCTGCACCTTCCTTATAAACCTGATTG
EST13522 8a	66	A	G	---		CAGGTTGGTGATTCTCAACTAGGAGCTATTTTGCCCCCATCCCCACCCGGCAGTGTCTGGAGAC[A/ G][GTTTTGATTGTCACAACTGCGAGAGGTGGGTGCTACTGGAATCACTGGGTAGAGGCCA
EST13568 6	69	T	C	---		CTTAAGGAAGTGAGCCAGATGAATCCAATGACCAACCTGGTTGAGAGCCATTGGTCTAGGAGTAGA / AA[T/C]GCACACAAGGAATAAAGGGAGAAGGAGGTTCGGTTAGTTGAGGGAGAGAAAGTTGGAAGCA / TTTCAAGCTAAGTAAATGGT
EST13785 0	101	C	G	---		AAGATTACGGACCATAAGAAACTGCCCCCGACCCATACACACAATTTATAGCAGGTAAAACCAA / CTGAAAGGAACAAAGTAATGACTTCTTGAACAAA[C/G]TGATTACGAAGTGAAAGGCTACAGGG / TGATTACTA
EST14038 1	25	A	G	---		CCTCAACCATCTGTAACCCGAGCCC[A/G]CAGTGACCGGGACTTGCTGCTTCCCCATCCCAGCCCTCT / CCTATCAGCATCCGCTAAGCGTCAGTGCAGCAGGTG
EST14083 7	23	A	G	--- GGAACAAGTC		CAATGGTGTCCATGTGAACACATAT[A/G]ACCTATTCATAAAGTTCATAAAGTTAAAAATAATCCCTTCTTGCAATCA / CAGTGCAAAAGGCATGAGGGTGAAAGTCATCTGCTAAAATGACCGAACAGGAGGGTAGGAGG
EST14221 5	42	T	C	GCATGCTAGA CAGAGGCATT	AAAATATTTTT AAAAGA	AATATCAATGCATTCTTGTTGGCATGCTAGACAGAGAGGCATTA[T/C]TTTGAAGATCTTTAAAAAT / ATTTGACTTGTTCCCCCTTCACACTCATTTTAAATTGT
EST14812 2	50	A	G	CAAGTCAGCTT CTACATTCTGA ATA	TAAAGATTTAC TTAAATCCCAT TATGTACT	TTCACTTAGTACCAAGGATGCCTTCAGTCAGCTTCTACATTCTGAATA[A/G]AGTACATAATGGG / ATTTAAGTAAATCTTTAGAAGTCCCGGAGTTTGCCTTTTCATATCAGGTGAAAACAAT / TTTTTCATATGGGTGATT
EST14815 3	128	A/T	A/T	CATCACCCACC ATACTGGTT	CGGGAAAACA GTACCGGAA	TTTGCTTCGGCAATACATAGTGGCAATGCAGCGTGAGTTCGGCCGTCTCCCCACTGAACCAGTAAT / TCACCAGACAATGGGCACCACTTAAATAAACTTGCCCGTCATCACCCACCATACTGGTT[A/T]TTCC / GGTACTGTTTTCCCGTA

EST	Pos			Flanking		Sequence
EST15420 6	109	C	A	---	...	TTTTAACCCCAAGAGACTTGTAGAGTGTCAGGACTCCGATCACATTTCTCTGCCTATAGCTTGGATATCTTAATCTCTCCCCTTTGTCATCATAATCATATAGCCAAGGGACT[C/A]GGAATTTTGGCTGCTTCAAGTCATTCCAAAACCTCTCAGG
EST15700 6	48	G	C	GAAAAGACAAAGACAACAGAGGA		GTCACCAGCACTTTATTAAGACGTGAAAAGACAAAGACAACAGAGGA[G/C]AGCAGAGAATAATATCTCTGTTTCAGCTATTCCAGGATGTTATGCCAATTATCCAGAGTCCTTGATCTGATGTAGTA
WI-16739 57		G	A	GGTTTTGCCATCACAAGC / GATAGTTGATGTTCATTATTCCCTATAA		AAGGATTGAAAAACATACCTAGATCATATAAATTTGTGAAGGTTTGCCATCACAAGC[G/A]TTATAGGGAATAATGAACATCAACTATCCTACAGCTAAACCTAATGAAGACCAAATTGCCTCCAAGGT
WI-16782 96		C	T	GGTGGGAGTCTCACTGTAAGGTC / CTTCTATCTTTCTGTTCCTCCATC		CTTCTTCCTTCCTAGACGTGGAATACACACGGATACAGTATCTGGAGATGTAGCAGCTGGCTCTTGACCATAATGGTGGGAGTCTCACTGTAAGGA[C/T]GATGGAGGAACAGAAAGATAGAGAAGAGTTTGGGGTGCTGATGAAATTGTGGGG
WI-16783 64		A	G	TCCTGAGATGTCTTTTACCTGACTGCTTGGTTCAATCCTTATTAG		AAAAATGTAAAACTTAGAGGTTGCCTCTTTGTGTCACTTTCCTGAGATGTCTTTTACCTGAG[A/G]CTAATAAGGATTGAACCAAGCAGTATTTTTTAATGGCAAAAGTCCAGATGTAACTCGAGT
EST15948 2	58					CAGGACTTAAGGTCATTTGCCTGGAAGACTTTAACTAAAGGTCAGGGCAACATAGGA[T/C]TGTGACAGCACCACTCGGACCAGGAAGTGCTGAAAATCGTCACACTAGCGTGCCCAGCCCCTTTTTCCTGGCTGCTCTGCCTCCCAGAGC
EST16088 8	89	G	C	---		GGTTTTGAAGACGCAGCAGCTTATCTCCACCTGCCACTGGGATTCTCATTTGAGAGCTGTGTTTGTCAGCCTTTTCAGAGAAAAGGCCGCTC[G/C]GGGTTTCTGAACCCTCTATGGGCATTTTAGAAT
EST16089 9	96	C	T	---		CGTCTGAAGTTTTCTTTTATCACAAGTCACATCAATCCCTGGGCCCCTGCTCAAATGCCACCTCTTCCTGAAAGCCATCCTAAGTAGTCTCTC[C/T]AAAGAGCCATCCTGCCCCTTTCTTGCT
EST16100 1	24	C	G	---		ATCCCAGCTGTGAAGGGACCAGGAGAG[C/G]GTAAACACAGTCCATTTATAAGGGGTGTGCACATTCCCAGGGGCTCCAAATAATGCAACATTGTTTCACTGTCCATGCCATGCTGATAGTTTCATAGTAAAAAGTCACTCCAGACACAGGTTGGCTC
EST16104 9a	83	A	G	---		TTCTTTTAAATAACCCACAGACACACCATGACACTTCCAAATTTACAGAGCACAAAAAGTGATTTGCAGCTGGTTCCTCCAGGGA[A/G]TTTGGCCCCCGAAGCTGGCTCAGTTCACCTCCAGGACCTCAGTC
EST16118 0b	119	T	C	---		ATGGTATAACAAAATCAGTTCAGTTCCAGGTTTTTCTGAACAAATGATCCTTTGGTCTTTCCCGTGGCATGCTCCTAAAAACTAAAAACAACCCTCTACGTCTAATCAGTCACCTAAGATA[T/C]CGAGTGGCAAGTCTTTCACA
EST16118 0a	32	C	G	---		ATGGTATAACAAAATCAGTTCCAGGTTTTTTTT[C/G]TGAACAAATGATCCTTTGGTCTTTCCCGTGGCATGCTCCTAAAAACAACAACCCTCTACGTCTAATCAGTCACCTAAGATATCGAGTGGCAAGTCTTTCACA

Name	Pos	A1	A2			Sequence
EST16151 2	53	C	T		---	AGCCAATTCAAACGAACTCTATCAAAACACACAAAGGCCTAGAGAGGAGAGATTA[C/T]AATGAACGT AAATAATTCAAGGCAATTTTGATCTAAAGCATTTTGCTTAGCTCTACAAAGGCATGAATGAGGTGT GGTCACGTTTTTGTATAGGA
EST16182 6	54	G	A		---	CATTGGTTGGGTAGGGAAAGATAGTAGTGTGCAAATAAAATGGTAAAACAGCAG[G/A]AAATGGAA TTATAGCTTTCTTTCATATAGGGAATTGAAATTTATTACTGAGGGTGATAGGCAGAAGTAGTA
EST16183 2b	59	A	G		---	GCAGGTAAACTGTGGTTCACAACGTATTGTCTTTCATAAAGAAAGAAATATCTAGTTG[A/G]GTAG AGGAAGGCACTGTCTTCCTGGCCCTTCTTCGTTCATATTTTATGTCACTGTCCTAACGTGGGCCGTGT GCAAGAGATCTTTGAGA
EST16198 4a	28	G	A		---	AATCTTAGGCTCTTGGCTTTCAAAATCA[G/A]TACAGACACAGATAAGAGCTTTAAGTATTCGCATTT CCCCAGGAGGAAAAAGTCAGCATCATAAACCACATGGGTCACACTGCTCACGCACATGGTGTC
EST16229 2c	52	T	C		---	TGTGAACTCGAATTCGCTTGTCCAGTCCTGAGTCACAGTTTCATTGGGAG[T/C]CCCTGTGCAGCC CTTGCCAGTTTCCACGAGGCAGGATACTCCACTAGCTGATTCAGACAGGCAGAGGCTGCA
EST16229 2b	45	T	C		---	TGTGAACTCGAATTCGCTTGTCCAGTCCTGAGTCACAGTTTCATT[T/C]TGGGAGTCCCTGTGCAGCC CTTGCCAGTTTCCACGAGGCAGGATACTCCACTAGCTGATTCAGACAGGCAGAGGCTGCA
WI-16816	124	A	G	GGAGCCATTGT GTGGGGTTA	GCCTAGATTT GTTCAGGACAG	CAGACTTTTCCTCACACCTCATTGGCTGGGTCACATGCAAACTCCTTGAACTATCATTGGCAA AGGGAAATGGGTCATCAAAATTGCTTAAGCCAAGCAGGAGCCATTGTTGTGGGGTTA[A/G]ACTGTCC TGAACAAAATCTAGGCTC
EST16269 5b	49	G	A		---	GCCACTCTCCTGTGTGGCTTGCTCCTGTCCCAGTGCCACA[G/A]TGGTCTAGCCTCATGG CAGAAGCATTTTAGCCAACTCCTGGTCTCCTCCCACTCTCTCCTCCGCCGCTGGGCCTCCACCACC TCTTCCTCCAATC
WI-16824b	83	G	A		---	GTCACCCCAGCCAATGCTTCAGGAATAAATGATGGTGCTGCAGCTGTTGTTCTTATGAAGAAGTCAG AAGCTGATAAACGTGG[G/A]CTTACACCTTTAGCACGGATAGTTTCCTGGTCCCAAGTGGGTGTGGA GCCTTCCATTATGGGAATA
WI-16824a	47	T	C	TGATGGTGCTG CAGCTGT	CAGCTTCTGAC TTCTTCATAAG AA	GTCACCCCAGCCAATGCTTCAGGAATAAATGATGGTGCTGCAGCTGT[T/C]GTTCTTATGAAGAAGTC AGAAGCTGATAAACGTGGGCTTACACCTTTAGCACGGATAGTTTCCTGGTCCCAAGTGGGTGTGGAGC CTTCCATTATGGGAATA
EST16445 3	96	T	C		---	TTGCTTTATTAATCCAGAACGGACATGCTACAGATACTGTACAGCATGAACATTTATTCATTACAAA AATGGCTTCCAAACCATTAAAAAATGAACT[T/C]GGAATAAGAGCATAAAACGGAACAGTAACATCA
WI-16857	47	G	A	CAAATAAGCA GCTAATGGCA A	TGTGAATTGGG AAGACCACT	TATAATCCATCCTCCAACACACACACACAAATAAGCAGCTAATGGCAAT[G/A]CTAGTGGTC:TCCCAA TTCACAAGACCTGTCCTCAAATTGTTTCCGTGATAAGTGTGGAGAAATCTGCTCTTTATGTA

ID	No.			Sequence
VI-16879	79	C	T	GATACAGGCC ATATTTCCCA / CAAGGCTTTCT AGAACTAGAGT CC / AGACAGGTCAAACAAACTCCTAGGGATAAAGATATAAATCCAGCACAGCATTATTTCCAGATACAG
VI-16882	99	A	G	GAAAATGCCA CGTCTCTGAC / GACACATGTCA GGTAAATCGC / GCCATATTTCCCA[C/T]ATAGGACTCTAGTT[C/T]AGAAAGCCTTGGGGAGAACAGGCACCCAG
				ACATGAATGGCAACCTCTTAGGTGGGAGAAGACAATTCTCCCCCTTTCACCCAAAGGTTACTCTGAC
/I-16888	70	G	A	GCTAACTTTGG GCAGGTTC / AATGTTCTGAA TTGACCAAATT TAA / AAGGCTATGAAATGCCACGTCTCTGAC[A/G]GCGATTTACCTGACATGTGTCATCTCCCT
				GTAGTAAATGTTCATCACTACCCGGGGAGAGCAAAGAACCATGAACGGTAGCTAACTTTGGGCAGG
/I-16905	75	C	T	ACTTGGCCTGT GTTGTTCA / GTCTATACTCT TCTAGGCAGTG GG / TTC[G/A]TTAAATTTGGTCAATTCAGAACATTCCAAAT
				TTTGTTGTTTGTTATTTGCCTCCCAACATCAGAACATAAGTTCCATGAAAACAGGAACTTGGCCTGTG
/I-16910	74	G	A	AAGAGTAAAG ATGGCGCTAG AA / CAAAATGAAG TATCGTTTCTA TAACAGA / TTGTTCA[C/T]CCCACTGCCTAGAAGAGTATAGACA
				AGTTTTCAGTATGTGCTTAAGGAGGTTATATTCGCTATGACTTTCATCTCAGAAGAGTAAAGATGGCG
/I-16918	93	C	T	CAGCCATTAA CACCAGCAC / TCCTGATACAG AAGTGGCATC / CTAGAA[G/A][G/A]TATCTGTTATAGAAACGATACTTCATTTGGGCCTGAACCAGTGAAGGT
				GGAAAGAAAAATAAACTACCACCATTCTCTCTGCTACCAGAGCACTAAATCTAGGAATTTGAC
				TTTACTGCAGCCATTAACACCAGCAC[C/T]GATGCCCACTTCTGTATCAGGAACTTAACGTGACAACC
				ATGAAAGGTCCTCTGAAAG
?-3947b	127	A	C	GGAAAGCAGA CCCTGGGG / ATGTGATTGCC CGTGG / TGAGTCAAAACGATCTTGACGGGAAGCTGTTAGAGGTCTCATGAAATAGGCCTGGAGCACAGGATT
				TGGCTGAGGCTTTCAACTGACATCAGACAAGAACTGCAATCAAGGGAAAGCAGAACCTGGG[A/C]CCA
				CGGGCAATCACATGAGATG
?-3947a	58	C	G	CATGGAAATA GGGCCTGGAG / GCCTCAGCCAA ATCCTGT / TGAGTCAAAACGATCTTGACGGGAAGCTGTTGAGGTCTCATGGAAATAGGCCTGGAG[C/G]ACAGG
				ATTTGGCTGAGGCTTCAACTGACATCAGACAACTGCAATCAAAGGGAAAGCAGAACCTGGGGACCA
				CGGGCAATCACATGAGATG
/I-16966	43	T	C	AAATGCACAC TACATAACAA CCTAA / TGCAAGTTATC AGTATAAAAA CTCATATT / CATTTGTTTTACTTTAAAAATGCACACTACATAACAACCTAATA[T/C]CTTAACTTGGTCCAACTATTT
				AGTATAACTAAATATGAGTTTTTATACTGATAACTTGCAATGCCATTAAA
?-16995	55	T	C	GAGCAGTAGA GACTGAGGTA AATAGTATT / CATGTTGATTT CCAGCCGT / TTGAGTGCCAGACATCAAGCATAGAAGAGCAGTAGAGACTGAGGTAAATAGTATT[T/C]ACGGCTGG
				AAATCAACACATGCCTCTTCTTCTGTGAAGTTGTCAGCATGGAGCTGAGAAGGCTGAGTCAATCT
?-3992b	60	T	G	---	CACATTCCCTT	AAATACATGGTGTCAACCTCAGCTAAGTGTTTGGGGGTTTAGGAA
				TAGGACTGTAAGGGAATGTGTTTGGGGGTTTAGGAA
?-3992a	46	G	A	AAGCACCCAG AAGTACACTG ATC	CACATTCCCTT ACAGTCCTACA C	AAATACATGGTGTCAACCTCAGCTAAGTACACTGTC[G/A]CCCTCATCTGAGATGTG
				TAGGACTGTAAGGGAATGTGTTTGGGGGTTTAGGAA

VI-17010	23	T	C	TTCAACAGGA AAAGCCATG	AATAATACGGT GTTTGAATGT CA	ATGTTTCAACAGGAAAAGCCATG[T/C]ATGACACATTCAAAAACACCGTATTATTAGAGAGCTCATTAAT TGTTTAATGCAGACAAAAATCAAGGCTAACTAAAAGCAGATCCAATGACCCAGTGATCAACCTAGA GGTTCCCACG
ST17127 'b	74	C	T	CACTCGGCAC AGACAGAGT	GGGAGGCGCAGG GGTG	ATTCCGTCTCCAAACAGCATCCCAGGCCGGGCATCTCCCCCACGATTTATAATCACACTCGGCACAGA CAGAGT[C/T]TGGGAGGCGCAGGGGTG
VI-17040	94	T	C	AATTCTCTTAT CATCTCAAGCC A	GGACTATGGCT TATTCAGTGAT G	CACGCGTTCATTAAATTTGGTACAAAGCATGAAACACTCAGGACACAGATTGGCACAATACATGCAGTTC GAGAATTCTCTTATCATCTCAAGCCAGT[T/C]CATCACTGAGTAAGCCATAGTCCCAGTCTCGTTTTCC AAATCTTTCTCATATTGT
II-17044	47	G	T	GCCAGGGGAT TAACGTATAG G	GGGGATCCCT TGTTTAAGA	TTGTTTGTTTGTTTTCTCCTCCTGCCAAGGGATTAAACGTATAGG[G/T]TCTTAAACAAGGGGATC CCCACTTATAGCTGACAGCAGCAGCTGCAACCACTGACTCTCCTGCAGAATGGCAGGGAATCGAAT CAAAAGAAAAGCAAGTG
II-17021	62	T	A	TGGACTTGTCA GCCTATAACT ACTC	TGTAGAGTTAG TGGCAGCTGC	GCATGTGTTGGAGCAGATCTCCATGGTAAGCCAAAAGTGGACTTGTCAGCCTATAACTACTC[T/A]G CAGCTGCCGACTAACTCTACAGGCACAGTAACTAACTACACTTATACAGGAGCACATGCCAAGTGCCTGG GAGGTGCCAATAAAATCAA
II-17065	90	T	C	CCAGAAAGGA AAAGCATAAA CTT	CCCAAGAGAC AATGAAATCCT	TGTAAAAAATGTAGACATGGGGGAAAAACATTCGTAATCAACATGTGCTGTTTCTCACTTCCGGTA CCAGAAAGGAAAAGCATAAACTT[T/C]AGGATTTCATTGTCTCTGGGT
I-17066	32	A	C	TGTACAGCCA ACATCACTGTT T	GAGATGTTGAA AATGTTCTGA A	TTCATAAGGTTGTACAGCCAACATCACTGTTT[A/C]ATTCCAGAACATTTCAACATCTCAAAAAGA AACTCTGCACCCATTAGCAGTGTCCCTGTAGCTTCCCTCATAGCAATGGCAACTGCTAATC
I-17074	86	T	G	---	---	TGCTGACTGTCATGACTTAGTAAGGCCATCACAGGTTGCCAGAACATCTACTCAACTGTTCCAAGCAT AACCTCCTACACAGGCCTT[T/G]CTACATAGGAGTATATTGGCCAAGACTCACCACTAGAAGTGATT
7104b	108	T	C	---	---	CAGATGAGAACTCATGCTGGCTCATCTGCAAGCTTCCTGATGCTTTGCGAGCTTTCCCATTCATTCCA AATCAGAGCAGTCAGTGGCCCGTGGTTCCAGACGGCTT[T/C]CTCTCTTTGTTAAGAAATTA
7114a	37	T	C	TTTCCATCAAG GACTTTGTTTT T	TTGTATTATAA ATAGCAGAGTG AAGAGAC	AGCGTCCAACAGATGTTTCCATCAAGGACTTTGTTTT[T/C]GTCTCTTCACTCGTCATTTATAATAC AAGCTACCTCCCAAAGGCCTCTAAGTGCTAAAAGAAGACTGCAGCCACAATCAGAGTTACAT GGGA
I-17150	76	T	G	GATGAAATTC AGATAGTCTTC CTCTT	TTCTCAGAATC CTGGAAGATAT G	CGTGGCTGGACTAAGTGCTCTTTCCATGTGGACACATCTCCACTGAACAGGATGAAATTCAGATAGTC TTCTCTT[T/G]CATATCTTCCAGGATTCTGAGAAGGGCCTCTTTGTCTGCTCTAATT
I-17163	43	A	G	CATTCTTCTTGT AAAATAACAA TAACGTT	CAGAATCTTGC TTTTGCCTT	GAAATCGAATACGTCCATTTCTTTGTAAAATAACAATAACGTT[A/G]AAGGCAAAGCAAGATTCTG TAAACCAACATTGGAAAAGGGGACACAGGGGAAAGGGCCAGATTTTCAACGGTTT CCTCCACATCTGCAGACAAA

ID	#					Sequence
VI-17178	127	T	C	GGACTCCCTCA TGAGGAGC	CCCTCAATTT CAACTGCTTC	AGCAAATGTCCCCTCCAATTTCATTAGCTATGATGGAGTTATCAGTTCATTTCGAGAGCGGAATTACTGG GGCGAGGGGGTTTAATATCCTGATGGGTTAATTCAGTGAGGACTCCCTCATGAGGAGC[T/C]AGAA GCAGTTGAAAATTGAGGG
NI-7180b	81	C	G	---	---	TCATGGACATCCTGAAGCAGCAGACACAAAAATATAGAGAATCCTGCACTTCCCAAGTCTCGTCGCACAG GCTTCAACACAATTAC[C/G]AACATCTTGCCCATTTGTTCATTATCCGCACCCACACTGACAGATGAG GGAGTC
NI-7180a	47	T	C	CACAAAAATA TAGAGAATCC TGCA	TGCGACGAGAC TTGGG	TCATGGACATCCTGAAGCAGCAGACACAAAAATATAGAGAATCCTGCACTT[T/C]CCCAAGTCTCGTCGCA CAGGCCTTCAACAATTACCACCAACATCTTGCCCATTTGTTCATTATCCGCACCCACACTGACAGATGAG GGAGTC
NI-17156	54	G	C	TGTTCTCTAAA CTTTAGATATC TGTGGAA	CAAGAAATAT ATATTTGATTC	TGAGGTAGCAGGGCATTCTTAAGAAATGTTCTCTAAACTTAGATATCTCCCAT[G/C]TTCCACAGA ATCAAATATATATTTCTTGGTTGGAAATTTAAATGTTCTTAACTGTCTTAACCATCCTACCACCTCAAT TAATATTCTTG
NI-17149b	79	T	C	...	...	CAGGCAGTTAATGTGCTGACATAGTAACAAGGTTGAAGGAGGAACATCTCATGCACGTGCGTGGAA ACCCAATTGTCA[T/C]TGTGTATGAACTACAAAAGGATGGGAAAAGAACACATTTCCTCACA
NI-17149a	48	C	G	CAAGGTTTGA AGGAGGAACA	CCACGCACGTG CATGA	CAGGCAGTTAATGTGCTGACATAGTAACAAGGTTGAAGGAGGAACATC[G/T]CATGCACGTGCGTG GAAACCCAATTGTCATGTGTGTATGAACTACAAAAGGATGGGAAAAGAACACATTTCCTCACA
NI-17197	67	G	A	GCAGAAGTAG CTGGGGCTAC	GGTGAGGTGGT GCATACC	ATTTGCTATGTGTGCTGGGCTGGACTCCTCGCCTCCTGCCTCAGCAGCAATCCTCCTGCCTCAGCCAGAAGTAGCTGGGGCTAC[G /A]GGTATGCACCACCTCACCCTGCTTATCAGTTTCGTTAATAGAATATTTGACTTTAGATGCGCA
NI-17198	38	A	C	TCCCCCTTGTC CCTAGTTT	TCCATTTGTCC ACTGAGAAATT	TGTATTTCAGTACTTTTCTCCTCCCCCTAGTTT[A/C]TAATTTCTCAGTGGACAAATGGACAA ACCATCTCTGTTGAATTTGAATACACAGATACATCAAGATATCTTACAAGAAAACAATGCACATCC TTC
EST18753	27	C	T	CTACCCAGGCT GGTCTCAT	GGATCGGCATGA GCCTGA	TCGCTATGCTACCCAGGCTGGTCTCAT[C/T]TCAGGCTCATGCGATCCTCCTGCCTCTGCCTCCCAGTGGCTGG GATAAGACACAACTGCCACCACGCCCTAGGAGTAGTCTTAATGCCTGATGGGTGGG
VI-7108b	74	C	T	GCCATTCAGTC TCAAAGTAAA CA	AACTACGATTT ATCATATGCTC CC	TTATTTAAAACATAACCAGATGCACCTTGGTTTTTACATTCTCTGGTTGCCATTCAGTCTCAAAGT AAACAC[C/T]GGGAGCATATGATAAATGTGTAGTTTAAGGAAGCCATAGCACTTACAGAGT
EST19067	41	A	G	---	---	ACACAAAATTTACCATCGTGACCATTTAAGGGTATAGTTCA[A/G]TGGCATTAAGTACATTCAACT TTTTGAGCAACCGCCATCACCATTCATCCATCTCGTT
EST19067a	40	A	C	CGTGACCATTT AAGGGTATAG TTC	AAAAGTTGAA TGTACTTAATG CCA	ACACAAAAATTTACCATCGTGACCATTTAAGGGTATAGTTC[A/C]AGTGGCATTAAGTACATTCAACT TTTTGAGCAACCGCCATCACCATTCATCCATCTCGTT
EST19125	28	A	G	---	---	CTGTTTCTCAGAGATGACACTGCCAACA[A/G]TCACAGATTTGCATACAATACAGTTATGTATTGGC TATTCACAATTTACAGTAGTGTTTTTCCTCTGAAAAA

ID						Sequence
EST20824 3	115	T	G	AGTCGGGGAGT GCTGATTG	AAGATTTATC TTGGACCCGA ATCTTAGG	GTGTGGAAGCCGGGAGTTTATTATTATTCAAATCAGTCTCTCTGAAAACTCAGGGATTGAGGTTTTA AGGATAACTTGGTGAGTAGAGGGCCAGTAAGTCGGGAGTGCTGATTGT[T/G]TCGGGTCCAAGATAAA ATCTTAGG
NI-17347	50	A	G	ATCCTCAGAA CTTCTCAGCCT	TCAAGCATCCA CTTGTGCTA	TTGGTTAAATGATGCCCAGATGGGGTCACATCCTCAGAACTTCTCAGCCT[A/G]GTAGCACAAGTGG ATGCTTGAAGAAACTCAGTCTTGGAACTCAGACAGCAATGGCGGGATGTGAGTGGGACCA
EST21904 2	128	G	A	TTCATATGGCC ATTTTAATAA GTG	GGCAGGTGTTC AGAAAGCAT	TGATTGTGGGTCTCTGGGAGCAGGTGGGGCCAGTTCAGTGGAGGAGCAGAGGGAAAGTAGACGCAGTAGAAAT GAGACTGGAATCAATAGAACAGAAAATGTACTAGGCTTCATATGGCCATTTAATAAGTG[G/A]TA TGCTTTCTGAACACCTGCC
EST22111 3	82	T	C	GAAGATCTGT CTGGCCATTCTT T	TGGAAAAACA GCCCCAC	CAAACAATGTAGAACATAAGGGAACAAATTCAGAGAGCTCAAGTCACCATGTTTGCTAAGAGAAGAT CTGTCTGGCCATTCTT[T/C]GTGGGGCGTGTTTTCCAAGGCACA
EST22197 2	78	T	C	AATTATTCTGC TATTCCTGCCA	ACCATGAAGG ATGCGGT	GTTAATGATCACTCACCAAAATCCACAGGAGAATCTTAAATGTTTACAAGCACCAATTATTCTGCT ATTCCTGCCAT[T/C]ACCGGCATCCTTCATGGTAGAGTATCACAAGTAAAAGTTTCTGGTTGTTTCATC TACTTAAAACCA
EST22311 9c	92	T	C	...	...	TTTTTCCATGGATTAGATCATCTTTTTTATTGGAGTTATAATATACATAAAAATCCACCACTGTAAACAG TAGCATTCAATGGTTTTTACTCTA[T/C]GTCAAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACTTTCATCATTCCAG
EST22311 9b	54	A	G	...	...	TTTTTCCATGGATTAGATCATCTTTTTATTGGAGTTATAATATACATAAAAATCC[A/G]CCACTGTAAA CAGTAGCATTCAATGGTTTTTACTCTATTGTCAAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACTTTCATCATTCCAG
EST22311 9a	41	T	C	GGATTAGATC ATCTTTTTATT GGAGTTATAA	TTGAATGCTAC TGTTTACAGTG G	TTTTTCCATGGATTAGATCATCTTTTTATTGGAGTTATAATA[T/C]ACATAAAAATCCACCACTGTAAA CAGTAGCATTCAATGGTTTTTACTCTATTGTCAAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACTTTCATCATTCCAG
EST22319	19	A	C	...	...	TCGAGGAGCTCTGAGGAGC[A/C]CACCAAGGGACGTGTCCCAGGGCCACCGTGCAGGCAAGTGTG GTCCAACTCCTTCCTCCCTTTACAAACTCCAGCCTTACAAACACTGGCTGACAGGCCTTCT TAAGCCTTTTTAACTGT
EST22433	103	A	G	AAGACATGTT CACCAAGTGA AA	CAGCTTCAGCT TAACTGACAGA	GATGTTAATGACTTTCCTTTGAGATATGATGGAAAAATATTCCAGGTACACATGGAAAAGACATGTT CACCAAGTGAAACCAATCTAACCAGAAAGCTTTACC[A/G]TCTGTCAGTTAAGCTGAAGCTGAAATT CTGGGGAGCTTGACATGCTG
EST22657	71	A	G	AAATGGATCC TTATCTGCACA T	AGTTTCAGTT	TATCCATTTCAAGAAAAAAAAAGACTTAAAAAATACAATTCTATCCCAGAAATGGATCCTTATCTG CACA[A/G]CCATTGAAGAAAAAAAAAAAAAAATTCATGCAAACTGAAACTATGCTT

ID	Pos	1	2					Sequence
EST22993 b	71	T	C	TCTACCCCC	ATCCTTTGTT	TTTGACTGTAA TTGCCTGTTAA	TG	GCCTTTTATGTCTCCTTTAACATCAAATGTTTATAACACACTGATCCTTTGTTCTACCCCCA AT[T/C]CATTACAGTCAAATTAACAGGCAATATAATAGGTCTAACAGAATGCTTGCATT
EST23021	108	T	A	---	---	---		TTATTTCTCAGCTTACCATTGTGTACTTATATCTCTGTACAAGGTGTTTTTCTCCATGGAGAAATG TTAAATCTTTGTGAGGTTAATTTATTAATCTTTGCCTT[T/A]ATGGTTTGACAGTTTGTGTCTTTCT T
VI-17387	55	C	G	TGAAGAAAAA	CCTTTGCAGAT	GCTTTTGCCTA AGATTAATAGT AACTACT		ACAGAATTTAACATGCAAGTTCATTACATTACCTTTGCAGATTGAAGAAAAA[C/G]AATATTAG TAGTTACTATTAATCTTAGGCAAAAGCCATTCTTTG
EST23669	101	A	C	CCAGAGGCAG	AATGTAAGCT	CCTTCCCCTCC TGTAAGC		TTTTTGGCTTGTCTGCAGAATAGATGAAAAAGAGAAAATATACCCAGATACTTTGCTCACTCTCCA AGTGCACACTAGGCAATGTAAGCTCCAGAGGCCAG[A/C]GCTTACAGGAGGGGAAGGGACGCCTGAGGC CAAGAGTGCTGGCTCACTG
EST23733	31	T	G	TTGTTTTGTT TT	GGCTGTTAGTT	TGCACTTTAAA TCCCATCAAT		AAAGGCTGTTAGTTTTGTTTGTTTTTTCCT[T/G]TATTGATGGGATTAAAGTGCATATAACTGAAG GCAAAGTCCAAGGCCTAGAGAAAGATATGAGGCCCGAGAGAGAGAGGCTCAGAGATTCTAGAGGCGGC TGAAGAATACCCACCTAAA
VI-17470	83	A	G	GTCCGGTCCCG CCAG	CCAGTGACGAG GCCGA			CTGACACGTCCCCTGTGTGCGGGGGGTGTCCATGTGGCGGTGTGTGAGGAGTCCC GTCCCGCCAGCCCTA[A/G]TCGGCCCTCGTCACTGGCCTTGTATTTCTGTCTTGGTTGGAAA TACCATCAGCCTTCC
VI-17519	55	T	C	A	GTTGTCCTAGC TAATGAATGC	AATTATTATTT TGCAGGCAATA CTC		TTTTAACGAAATCTCACTACTGCAAATGCATTGTTGTCCTAGCTAATGAATGCA[T/C]AGAGTATTG CCTGCAAAATAATAATTGAGATTCTATTTTAAGAAGCTTAGAACAGTACACATGGTCATAG
EST25356 b	95	C	G	---	---	---		TCTTTGATACAGGTAACCAGTTTGTAACATTATTCAGAACTTCACTGTATCTTCAAGTTTTTGATAT CAGCATCTCTGTGGAGAAAGCAGTGTG[C/G]TATAAGTCAACATCAGGATTTCTTTT
EST25356 a	26	A	C	---	---	---		TCTTTGATACAGGTAACCAGTTTGT[A/C]ACATTATTCAGAACTTCACTGTATCTTCAAGTTTTTGA TATCAGCATCTCTGTGGAGAAAGCAGTGTGCTATAAGTCAACATCAGGATTTCTTTT
VI-7581c	99	C	T	---	---	---		GGGTGACGCTCCAGAATGGGAGACAAGCCAATTGGGAGCAGATTGGATCCAGCTTCATTCAACATT ACTACCAGTTATTTGATAATGATAGAACCCAAA[C/T]TAGGCGCAATTACATTGACGCGTCATGC
VI-7581b	86	T	C	ATTCAACATT ACTACCAGTT ATTTGATAA	CGTCAATGTAA ATTGCGCCT			GGGTGACGCTCCAGAATGGGAGACAAGCCAATTGGGAGCAGATTGGATCCAGCTTCATTCAACATT ACTACCAGTTATTTGATAA[T/C]GATAGAACCCAACTAGGCGCAATTACATTGACGCGTCATGC
VI-17596	86	A	G/C	ACTTCCTTGTG TAAACACTCC	CATTCTTATAG CTAGAAATCGA CAATAT			GTGTGCTGGTAAATGGATAATAGCAGTCTCTCATCTCTGAAGGGGTGGGAAGTAGGAGAAGGCCTACT TCCTTGTGTAAACACTCCC[A/G]ATATTGTCGATTTCTAGCTATAAGAATGGGCCACTAAGTGGTC

ID	No.	A1	A2	Flank	Sequence
NI-17623	46	T	C	---	TGTGGTTTAATTTAATTTCCCATATAATTAATGGTGGGCACATT[T/C]GCATGTGCTTACTGGGTC ATTCATATATCTTTGTGAAGCATCTGCTCCAATCTTTGCCTGACTTTGGAGTTTTTGGT
EST26419 1b	46	T	C	---	ATTTCATACAGAGATACAAAGGCAACTATGTGCAACAATCTGA[T/C]GGGCAGTCCAAACTTCT TGGGAGGAAGTAAATTCATGTGAAATGTCATGGCTGGTTCGAGGAGAAGGTTCAAAGGAGGTAG AGAGGAGGAGACAGAGAATG
EST26419 1a	35	C	A	AG / CAAGAAGTTTG GACTGCCC AG / ATACAAAGGC AACTATGTGC	ATTTCATACAGAGATACAAAGGCAACTATGTGCAACAATCTGATGGGCAGTCCAAACTTCT TGGGAGGAAGTAAATTCATGTGAAATGTCATGGCTGGTTCGAGGAGAAGGTTCAAAGGAGGTAG AGAGGAGGAGACAGAGAATG
EST26780 5	69	G	C	---	TCAGCTTTAATTTAAGGGACATGTAAATAAAAAGATGCATTTGACAGAGGACAGCAGACTAGTTCAAGC AG[G/C]AGGTTAGACCAGTAACAACAACCAGAAAGCAAAGTGCTCGTTCCATCTGGCTTTACCA CACTTACAAACTGATACCC
EST26900 7	39	A	G	---	TACTTCAGTTTAAGGCAAATTCCACACAGAGACTGTCTC[A/G]GAGACGGGCACAGAACCAGACACC GTAGAAACACCACCATGCATGACGGGGAAGCAGAG
EST27152 1	101	C	T	---	CAAAGGATTTTATTTGTTCCCTAAAAAGTAAAATCTAGAAAATAGCAACCCACTGCAAGAAGAGTT CTATACTAAAACATTTCAATCATTCTCTCTCT[C/T]TTCACATGGTACTCTTCATGTCACACAT CATCGGAAAACAGACTGA
EST27504 0a	33	G	A	GCACTTTGCAA CAATTTAATA ATTT / GCTGGTGTGAT GCTACTGTAAT G	TTTTTGCACTTGCAACAATTAATAATTTATC[G/A]CATTACAGTAGCATCACCAGCAGTCAAT AATGCCACTTAGGCAAAGTCTTTCAGTATTTCTGTTACACATTCTGTTAACAAGAACCCATACATT GGTAAAATTCATTCT
EST27662 4	51	C	T	CACATTCTGTT CTCCAGTCTTG / TTATGGAAATG GCTTATGTAAC C	ATCTTAAAGGACCATTAGAAAAGGCCAGTCACATTCTGTTCTCCAGTCTTG[C/T]AGGTTACATAAG CCATTCCATAAATTCTATAGCCTTCTCTTAGAGTAACACACTCTTGTTAGGAATGTTC
EST27788 3	100	A	G	---	ATTTTATTAGGCGGTACAATTCCAAGGTGGTAAGGGTGAAAGGAGGAAGGCAGGCAAATACAT TATTGAGCTGAAAACAACTTACATTCAAGGAC[A/G]GCTTCCAGACAAGCCATGTAGAACCAGCAT GCCCTTGGGACTGTGTGGAT
EST27828 4	58	G	A	GGAAGTCATC AGAACCCCAC C / GTGCAGAGAGG TACTCCAAGTA C	TCTTCTAAAACTTTCCTTCTGTTGGATCCCAGTGACGTGGAAGTCATCAGAAACCCAC[G/A]GTACTT GGAGTACCTCTCTGCACCAAGATAGCTGGCTGATTTCTGCTCAGTCACAATTTACTTGAA
NI-18369	58	G	A	AATAAAATTTC AATCTGTCAC ACAATC / TCAAGAAGGCC TTATCCATTT	TAAAAATTTGAGATACATTCCCAATGTAAACAATAAATTTCAATCTGTCACACAATC[G/A]AAATG GATAAGGCCTTCTTGACAAATTTCTGCCACTCGTTAACGCATCAGAACTCAATCTTATCTC
EST28036 4	37	T	C	---	TCCCGCTTCCAAAGCTTTATTGGCAAATATGCTCTA[T/C]AAAAGAATGATCAATCCTTGTTGCCTCT AAGTCAATGAATGAAGAGCTGTGTCCAGGGACACCACCACGCCGTGCTGAAGGAGACTGTTGTG TCCACCTCTTATTCATAG

ID	Pos			Seq A	Seq B	Sequence
EST28483 7	31	T	A	GGAGTAAAAG GTGTTTCTTCT TTAAA	TTTCTCTGCATT TATTTTTATAC CA	CATTTGGAGTAAAAGGTGTTTTCTTCTTTTAAA[T/A]ATGGTATAAAAATAAATGCGAGAAACATTAAC GGAGAAGTGTACAGACAACAGACGAAGACATGAGTTTGTTTCTGACTGTGACACATTGGTGAAA
WI-17724	50	T	C	TGGGCCCTCCC TGTC	TGGGTTGGCAG TGTCC	AGAATTGGTCTAGTAATCGTTCAGGATTCGGTGATGGGCCCTCCTCCTGT[C/T]GGACACTGCCAACC CACAGCTGGAGGGGCCACTTAAGGCACGTCATTTGTGATTAGA
WI-17730b	68	T	C	...	...	TGAGCCTGGGGGAGAAAGACCACAGAAGTGAAGTGCTATTAGTTACATCATCACCAAGTGTACATACTG TTT/C]CACATGATTTATGGCTGTTGATGTTGACCTCAATAACCTGGCTCAATGTCTGATGTAGTATGTGTCA
WI-17730a	39	A	C	GACCACAGAA GTGAAGTGCT ATT	TCAACAGCCAT AAATCATGTG	TGAGCCTGGGGGAGAAAGACCACAGAAGTGAAGTGCTATT[A/C]GTTACATCATCACCAAGTGTACATA CTGTTCACATGATTTATGGCTGTTGATGTTGACCTCAATAACCTGGCTCAATGTCTGATGTAGTGTCA
EST29041 5b	53	G	A	GGAACAAACA CATTAAGCAT CA	GGTATTGTTGA TTTGAGGAGTT AGC	TACTCAGAAATGTGAGTTCATGAGGAACAAACACATTAAGCATCATTGTCACT[G/A]GTAACTCCT CAAATCAACAATACCCTTATTTTATTTTAGCCATGAAAAC
EST29128 4	58	A	G	...		CTTTAGAAGGACCACCAGTCTTGTTGGACTTAGGGCCTACCCTATTCCAGCAGGTGCC[A/G]TTATTT TCACTTGGTTACGTCGTTGTAAGGACCGTTTCCAAATGAGGTTACAGTCACAGGTTCTGAGCAGACATGA GTTTTGCTGGGGACACT
EST29912 3	103	C	T	TCTGCCAGCTT ACAGGCT	GCGTAAGTGTC TCATTCTTCTG T	ATTTATTAGGTATCTGCTGTTGGGGGTGGGGTGGGGGGAGATTGTTGAGATACTGCAACAGACACAAA AGCAAAGAAAGAAACATTCTGCCAGCTT[C/T]ACAGAAGAATGAGACACTTACGCATG GCCATGATACACAGCAGTGA
EST29936 3	121	G	C	...		TATTGGTATGCTTAGGGAAGATTCTGATTTAGAGAGTATTAAATCTTAAAGTTAACTCACCATGAAA TTAACCTTCTGTACTGCCTTCACTGATGAGGCAGTAAAACTACATAGGGATAAA[G/C]AGCTCAGTA TCTGGAATCATGCTTCCTG
EST30223 2	99	A	G	...		AAATAAATACATCACTCATGGGGGAATGGGATATCCATCCCCTCAAGCATTATTCTTGAGTTACAAGCAA TCCAATTACACTCTCAAGTTATTTAATATTCC[A/G]GGATTTAATTCTTCCTAGTTCAATCTTGGGA GG
WI-16260b	86	G	A	...		CTTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTGTGAGGTGGATTCAAGAGAAAAAGACCCAGA GTTTCACAATAGGTAGC[G/A]ATAACCAGGTCTCACTTCCCCTTCCGGTGAGAACTTCGTGGGAC
WI-16260a	59	G	T	TGAGGTGGATT CAAGAAGAAA A	CTACCTATATT GTGAAACTCTG GGT	CTTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTGTGAGGTGGATTCAAGAAGAAAA[G/T]ACCC AGAGTTTCACAATAGGTAGCGATAACCAGGTCTCACTTCCCCTTCCGGTGAGAACTTCGTGGGAC
WI-17835	30	G	A	ACAGGAAATA TTGTGCTTTCT TG	TGGGGTATAGG AAACAGGC	AAGAGAAACAGGAAATATTGTGCTTTCTTG[G/A]GCCTGTTCCTATACCCAATATCATAAGAATT GTTGTTGCTTCTATAATGTTCAGCTTCAAATTCTTTGCTTAATCAATCCAAATGAATTACCTGAATT TTCTCCTCTGTTCAAA

ID	Pos	Alleles	Flank 1	Flank 2	Sequence
EST31951 4	87	C T	GGGTGTCCAG CCAACA	CCCACCAAAAT CACCTCC	ACAGCCATTTATATGTTTACTTGGTAATATCAGAGACTGAAACATTTCACTCTTTAGCAATGACA TCGGGTTGTCCAGCCAACA[C/T]GGAGGTGATTTGGTGGGGAATTCTTATCACAATATTCT
EST31968 8b	95	T G	---	---	CGAATTGTCTCTCTTATTTGTGATTCTAGTAATCCTAAAAGATTTGGGGGGCGGGTTACTATAAGT GCATTTTATAATGGGGATTTTCTGCT[T/G]AACTGCCCACTGATTCTTACATGGGAAAGGTGCAAAG ACAGTGGTACTGCTCCC
EST31968 8a	75	T C T	GCGGGTTACTA TAAGTGCATTT T	TGTAAGAATCA GTGGGCAGTT	CGAATTTGTCTCTCTTATTTGTGATTCTAGTAATCCTAAAAGATTTGGGGGGCGGGTTACTATAAGT GCATTT[T/C]ATAATGGGGATTTTCTGCTTAACTGCCCACTGATTCTTACATGGGAAAGGTGCAAAG ACAGTGGTACTGCTCCC
EST32063 2	103	C T	---	---	TCCATGGATGAACAGACGCTACCATGCCACATCCCCTCCGACCAGATCGTGCTGGCCAGAGC TGGCTTCCCCCTCCAGACCTAGCTGGCTTTGTAGT[C/T]GTTCAGGCGCCCATTGAAATAGCAAACGCAC AGTCATGTAGCACTCGG
WI-16303	65	A G	---	---	AAGGCTTTCCAAGCATTCAAAGGCACTGGGTGTTGTGCTCTAAGTTCTGGTCACTGCAGCCCC[A/G] TTCTGTATTAGGGAGCACCCCAAGCCCAGTAACAAATATGGTTCTTGCAG
WI-17800	29	C G	GGGAGCACAA GAGAAACTCA	TTTCCTACAAT TAATCCCAGTC TT	TGGACATGGGAGCACAAGAGAAACTCACTC[C/G]AAGACTGGGATTAATTGTAGGAAATATTTCACAG TTTCCACAAGTCAGAGAGCTAATCCCACCCCTCTGTATCTGGAACATACACTGCTGCCATTTTCTGC CCATGAAGGGAAATACCC
WI-17857	34	T G C	CCTAAAGTCTG GGATGACTTTC C	TTGGCTTAGGT TCTACTTGATG T	AAACTGTCATTCCTAAAGTCTGGGATGACTTTCC[T/G]ATTCTACATCAAGTAGAACCTAAGCCAAT TCAGAATCAGAATCCTTTTGTCCATCAAATTCCAGCTAACTCCAAGCTGAATTAAATGTTCATTCT
WI-17860	121	T A	TTTGCCAGCAA AGCAAATA	ACTAAGGAGC AGTCAGTCGG	GTATCTGATGTAGTAACCATGGCCTGTCATGATTAATTCTTGGTTTAAATCTTTA[T/A]CCGACTGAC TAGTGTCCAAAGATAATTAATTCTTGGTTTAAATCTTTGCCAGCAAAGCAAATA[T/A]CCGACTGAC TGCTCCCTTAGTCTGTGATC
WI-17866	43	A T	TTTTATAGCCT ACTTCTCAAA ATTGTT	CCGTTGTCACT AATCACACAA A	CAGCAACCTTTTTGTTTTATAGCCTACTTCTCAAAATTGTT[A/T]TTGTGTGATTAGTGACAACG GGGGAATCTACACAATGCTCACACTCACAGTAAACTACCA
EST33301 4c	80	G A	---	---	GAAAAAAAGTCAAATGTGTTCCCTTTATGGGTGATGCCACCATGATCATTGCCTCACACAAGCATGATC AATCGCCACGAGA[G/A]ACTGGATGCCAAAGAGTATGG
EST33301 4b	63	G A	---	---	GAAAAAAAGTCAAATGTGTTCCCTTTATGGGTGATGCCACCATGATCATTGCCTCACACAAGCAT[G/A] ATCAATCGCCACGAGAGACTGGATGCCAAAGAGTATGG
EST33460 1	44	G A	AGCGTGGTTTT CAATACTAAA CA	CTGTATTTATT GTAAATATTT GCATTGTT	CTATCCAAAGATATTTATTGCAGCGTGGTTTCAATACTAAACA[G/A]TGTAAACAATGCAAATATT TAACAATAAATACAGTGATTAAATAGCCATGGCATATCCAGTTGATGTAATACTTTGCAA

Marker	Pos	Allele 1	Allele 2	Flank A	Flank B	Sequence
WI-17904	50	A	G	AAAGCATGAC AATAAAATGA ACAC	CGCTTATGTTA ATAGTAATTCC CG	CAAGTGAATATTGATACATGGCTGACAAAGCATGACAATAAAATGAACAC[A/G]TACGGGAATTACTATTAACATAAGCGGATAACATCAAAACATCTGGTAAAATGCAGTTAAAACAACAACACAAATGA
EST34149 5	69	A	G	TGCCAAATAC TCAAGTGTGA AT	AACTACTAGCG AGAACAACTA ATAAAATC	GTTTTTCTTGAGTGACACAAGCTTGTTCATTTTGAGAAAATGTGTGCCAAATACTCAAGTGTGAA TT[A/G]GATTTTATTAGTTGTTCTCGCTAGTAGTTTTGGTATTCTCATGAAAAAAAGCAGCTAGTTCAGC TTACAAATCACACAAGT
EST34343 8	95	C	A	---	---	TGGGAAAACATAGTAACTCAAGAATATATTCCAGTCTTTATGTTACTAAAACATTGTAATAGTGT TTTTATCAATGATGCCGAGGTCACTGCT[C/A]TACAAAGATTAAAGAAACTTACCATCAAACACTTC CAGTGCATCAA
WI-17982	98	C	T	GGACCATATG ATATATAACT CCTAAAAGC	CAGAAAATTATG TGATAATAACT CCTTCC	GGTACACAATTTAATGGAAGGAACCACAGGTATGTTGAAGAAGAACATCAGTACAGCTGGAGACAGG GAGGGACCATATGATATATAACTCCTAAAAGC[C/T]TGGAAGGAGGTTATTATCACATAATTCTGGGC GCTACAGAAGTTTTTCATCA
WI-17993	118	A	C	---	---	CTCAGTAACTCCGGTGTATAATCTGCCATTTATTGATTTATTTATGATAAAAAACAACCTCTCATTGA AAAACAGCTAAGGGGTGACATCTCCAGACCCAACCACTGTCCCTGTAATGT[A/C]CTGCTGAGAGTCC ACATTTTGGAAATCCAAT
WI-17996	84	A	G	GTAGAGGCGA AGGGAACAG CAGC	AGGCACATGGG CAGC	CCCATCCAGAAACCCCAGTGTGATGGTGGAAGCAGCATGCTCTCCCCAGGCCTCGCAGT AGAGGCGAAGGGAACAG[A/G]GCTGCCCATGTGCCTGTCTCTAAAGACGCCACCCTCAGGTTGATGT CACCTGTGGGAGGACCGGGGT
WI-17136	33	C	G	---	---	ATTCTTTATAAAAACACCATGTCCCTAAAATGT[C/G]ATTCAACATATATGCACACCTTCGATGTAT AGGACACTGATCAAAAAGACAGAGAAAATGTGTCCCT
WI-18041	24	A	C	---	---	GCCACTGAAAAAGGTGCTCTTCC[A/C]GTTTCTAACTCCCTGGACTCCCTCATTGGAACTGAAGCTC ACAGATGTTCAGCTGGACTAGTTTAGACTTGCTGTATTTAAAAGGCAGTGTTGATGCTCCAGGAT TCAAATACTTAATCA
EST35164 8a	57	A	G	CACAGCCCTGC CCCC	CCCTCTGGATT CTGAATCTCAA	TTGAACCAAGGCCCTAACAGATGACTCAGCAGGCCTTCAAGCACAGCCCTGCCCCC[A/G]TCTTGA GATTCAGAATCCAGAGGGTGCTCAGTCCTTGGTTAGGTGCTTCTGTGACATTCCTCTG
WI-18052b	67	A	G	---	---	AGCGAATGAAAATGCTACATAGGCTCCCTGAGTCTTCATGTACGAATCTTGGTTACACATCTTAG[A/G]ACAGCAGAGCTGCCTGAGGTTGTGTTAATGTCGTATGCATGCTCAGCACAGTGCTGGCATGGCCCATCCATGCTTT
WI-18052a	50	T	C	CCTGAGTTCTT TCATGTACGA ATC	CTCAGGCAGCT CTGCTGT	AGCGAATGAAAATGCTACATAGGCTCCCTGAGTTCTTTCATGTACGAATC[T/C]TGGTTACACATCTT AGAACAGCAGAGCTGCCTGAGGTTGTGTTAATGTCGTATGCATGCTCAGCACAGTGCTGGC ATGGCCCATCCATGCTTT
WI-18054	46	G	A	GGGAGGTGGGG GAGTAAAA	CGTCACCCTGC TTCCA	CTGTTGTGCTGAGAACAGAAGAGGGGTCAAGGGAGTGGGGGAGTAAAA[G/A]TGGAAGCAGGGTGACG CATGCAGGAGGTCCAGACAACAAAAGACGGGTGATTTTGCTCAGGTTGGTAGCAACAGAGGTAATG

Name	No.	Flank A	Allele 1	Allele 2	Flank B	Sequence
WI-18064	54	GTAGCTGCTAAGCTGTATTTCAGA	G	A	CCAGTGGTATGATTGTGACATTC	CAGCTGCCAATCATCTCTCAAACCCTGTGGTAGTGAGCTGCTAAGCTGTATTTCAGA[G/A]GAATGTCACAATCATACCACTGGGGAGAAAGAGTAAGCACAGTGCCAAACTGGGGTACCTGGGAGGCAGAAA
EST35347 2	97	GCATAAAATTTTCCAGTTGGTAA	T	C	CCCTCGGCACCTGCT	TTTAGCACCATTCTTAGTGGAGCAGGATTCTTGATCATGGGGGTGGAATTTTGTGTATCTGGGCTTCATGGGATGCATAAAATTTTCCAGTTGGTAAG[T/C]AGCAGGTGCCGAGGGTCTGGATCAGAAAAAAGGCAGGCA
WI-18070	28	AACCCACTACTTACTCAGAGTGTGTAT	A	C	AAAACTAATAAGAAACTGGAGGTTTTT	AAACCCACTACTCAGAGTGTGTAT[A/C]ATATTAACACATGAAAGATATAATCTTAGAAAAAACCTCCAGTTCTTATTAGTTTTGATATTTCTGTACTCAGAGAGCATTTAGGTTGCAAAGGATATAA
WI-18080c	80	---	C	T	---	TGGCATAAAGTTTGCAAATATCAAATATCAAACTAGTCTCTCTTGTAATTAAAATCTACTATGCCGTGTTTGACTTTATC[C/T]TCTTATGTAAATGAAGCCAAATGCATGTTAATCCTTCTCCTTGGTGTAT
WI-18080b	65	---	G	A	---	TGGCATAAAGTTTGCAAATATCAAATATCAAACTAGTCTCTCTTGTAATTAAAATCTACTATGCC[G/A]TGTTTGACTTTATCTTCTTATGTAAATGAAGCCAAATGCATGTTAATCCTTCTCCTTGGTGTAT
WI-18080a	41	GCAAATATCAATATCAAACTAGTCTCTC	T	C	CAATTTACATAAGAGATAAAAGTCAAACA	TGGCATAAAGTTTGCAAATATCAATATCAAACTAGTCTCT[T/C]TTGTAATTAAAATCTACTATGCCGTGTTGTTGACTTTATCTCTTATGTAAATGAAGCCAAAATGCATGTTAATCCTTCTCTTGGTGTAT
WI-18086	63	---	G	A	---	GTGGGCATCCTATAAAAGCAGCCATGGTGTTGAAACAAATGATATGCACAGAAAGCATACTTCT[G/A]TGGCTTTGGTTACACGGGGTTTCTTTCAAGAGGAAGATGACTCAGCCCCTCCCAGCTCTGCAGTCTAGCTTAGGAGAGGTGTTTGAA
WI-18115b	71	---	C	T	---	AACTACATAGTAGTATGGTGCCTGGCTTAGAATCAATGGGTAAAGCCTTTAGTGTACCTTTGGTATTCCCTTC[C/T]TTTTGGGTATGAAAGACAGACCTCTGCTGGAGGACTCATTACAATGTAAAGAAAGGGGTGAGTCAGT
WI-18115a	70	TTAGTGTACCTTTGGGTATTCCCTT	C	T	AGAGGTCTGTCTTTCATACCAAA	AACTACATAGTAGTATGGTGCCTGGCTTAGAATCAATGGGTAAAGCCTTTAGTGTACCTTTGGTATTCCCTTC[C/T]TTTTGGGTATGAAAGACAGACCTCTGCTGGAGGACTCATTACAATGTAAAGAAAGGGGTGAGTCAGT
WI-18136	78	---	A	G	---	TTTTGAGAAGCACTCTGTAAGGCAAGGATGCATTCAAAAAATGGCTTTGAGGATTAATCTTCTCTTTAGGTAATTTGC[A/G]TAAGAACAATAAAAGCATTTAAAAGTCCACTGCCGCCTTAGAAACT
WI-18169	115	CCATCTTTCCGGAAGCTC	A	G	GAGTTCTGCTTGTGCTCCA	GGCAAAATATTTTTACATCACACCTGGAATCGCCCAAGTCTTTCCACTACTGAAGGCAATCGTAGAGTGTGCAGGAGGAAAGGTGTTATCCAAGCAGCCATCTTCCGGAAGCTC[A/G]TGGAGCACAAGCAGA
WI-18190b	26	---	G	A	---	TGAAAGAAGCTCCCTGGAGAGACGGGACACAGGGACAAAATCAAGAATCAAGAATGAGCTGGAGACATTAATCCTGGCGA

ID	Pos	Allele	Fragment	Sequence
WI-18190	62	G/A	---	TGAAAGAAGTCGACACAGCGGACACTGTCATAAGTGGAACAAAGATGAAGCTAATCATGGA[G/A]GCAAGCTCCCTGGAGAGACAGAGGACAAAATCAAGAATGAGCTGGAGACATTAATCCTGGCGA
WI-18181	100	A/C	AAATATATAC AACACTCCCTT CAGATC TTG	GACAGTGAAAACATTGAAAACACAAATACAACAAACATTAGGAACAAGAAATGTGTAAATCCAA TGTGTGAAAAATATATACAACACTCCCTTCAGATC[A/C]CAAAAGCTTAACAAATGGTAAAACGTA TGTGTTCTTGAAC
WI-18215	78	G/A	AGCAGAGTTC CTGCCCTC	ATTCATACAAGCATTCCTGAGTACAAACTAGGGGACAGGTATTTCACAAAACAAATAGAGCAGA GTTCCTGCCCTC[G/A]GTGTGCGGGGGAGAGAGGAGGGATTCAGCATTTGGTGGAGTATGTTAATT CCCTCAAGTTAATTCCTTC
WI-18232	60	T/A	TGGTGTTGATT GTGATACACTT AA	CATTCCGAAAATCTGATAGTTAAAATATCCCGTCTGGTGTTGATTGTGATACACTTAAG[T/A]GAA CCCCTGAAAAACCTTTATTTGAAATTGAAGTTTTGCTCAGAAACTGGGCAGAACTTTCACATTCTG AC
WI-17892	76	T/C	GGAAAACTTG AGTTTGAGATC ACA	TTTAAAAATGCTTAGATTTTCCTCAGTATTTTATCAATAGTGTGTAAGCTGGAAAACTTGAGTTTGAG ATCACAT[T/C]CTGTCTCACTAGTCTATTCACTTCTGTGGGCATTTCGGCAGAAGTGGC
WI-18242	30	G/A	CCCCCAAATGTT AATCGTAACA	AATATCCCAAATGTTAATCGTAACATACT[G/A]GAAAGCTGTTACAGTAGAAGTGTTAGCAAAAT TGGATGCCACAACTATCTCACCATTCCTTCAAGCAAGTGAGGGTCAGAATGTTTCTTGCCTATATC TGCAAAAGATCGAACAAG
WI-18266c	119	C/T	---	GCATCAGACACATCACCACTCCTGAAAAAAACCTTCTACAAGAATTGAAAAGTGTTGCAGGACCTAATA CTGAAAATAGGAAAATATGGACTATCTTCAAACTGCACAAATGATGCATGAATC[C/T]ACATTGAGAC CCGCAACTCCGAGGTACCT
WI-18266b	124	T/C	---	GCATCAGACACATCACCACTCCTGAAAAAAACCTTCTACAAGAATTGAAAAGTGTTGCAGGACCTAATA CTGAAAATAGGAAAATATGGACTATCTTCAAACTGCACAAATGATGCATGAATCCACATT[T/C]TGAGAC CCGCAACTCCGAGGTACCT
WI-18266a	97	C/T	AAATAGGAAA TATGGACTATC TTCAAA	GCATCAGACACATCACCACTCCTGAAAAAAACCTTCTACAAGAATTGAAAAGTGTTGCAGGACCTAATA CTGAAAATAGGAAAATATGGACTATCTTCAAA[C/T]TGCACAAATGATGAATCCACATTGAGAC CCGCAACTCCGAGGTACCT
WI-18312	73	A/G	GCTGTGTCAGCTA TTGTTATTTCA AA	CTGAGCCTCTTGGATATGTGGTTTAGTGTCTATCATTAATTTTGGAAAGCTGTCTGTCAGCTATTGTTATTTC AAAT[A/G]TATCTTCTGCTCCTTTTCTCCTTTTCTGGGATTCCATTCTCATTCTGCATGTGTTATA
WI-18330b	66	A/G	---	AAACATCTACAGCTGTGTCTTAGGCATCCGTGTAAGAAATCGGGATAAGAGCTGAGGAACAAGAGGG[A/G]TATGTAGGCAGTGAGTCAGGACTATGCAAAACCATAAAATAAAGAACATAATTTTTTGTTGAT TCACA

Marker	Pos						Sequence
WI-18330a	49	G	A	TCCTGTGTAAGAATCAGGGATAAGA	AGTCCTGACTCACTGCCTACA		AAACATCTACAGCTGTCTTAGGCCATCCTGTGTAAGAAATCAGGGATAAGA[G/A]CTGAGGAGAACAAGAGGGATATGTAGGCAGTGAGTCAGGACTATGCAAAACCATAAAATAAAGAACATAATTTTGTTGATTCACA
EST37564 5	85	T	C	AAATTCAAGCCATCTACACAAAGA	CTATGGAGGCCTCAATGAGA		AAATTAGTTAGCCATAACAGGCTGGAATTGCTGGTTAGAATACTGCATGTTATTTAAGCTAAATTCAAGCCATCTACAAAGAT[T/C]TCTCATTGAGGCCTCCATAGGCTGCAAACACATCAAAGGCATTACTGTACTGGAGAGGACTGAG
WI-18327	104	G	A	AAACAGCTTTCGTTAGGCTAGTT	CGCATACAATGGCTCAGCGT		CAAAGGGATTTTATTACCTACAACAAGTAAGGAGGACAGCTGGGCAGTTCCCAAAGCAGTACCTCCCAAACAATGGTGAAAACAGCTTTCGTTAGGCTAGTT[G/A]CTGAGCCATTGTATGCGGAGGCAGAGCTCAGCGT
EST37624 6b	102	G	A	---	---		GTGGCAAGAGCAGCTAAAACACACTCATTTGCATGAACTCCAAATACGAACAGTGCACGCTGATGGCCTGCAGTCCTCTGCCGTGCCTTGGCTCTCTGGACG[G/A]TTCATTCTACATGGCTGCTGCTTTGCGTCCTCTGACCTCCCCATTCC
EST37624 6a	58	C	T	---	---		GTGGCAAGAGCAGCTAAAACACACTCATTTGCATGAACTCCAAATACGAACAGTGCA[C/T]GCTGATGGCCTGCAGTCCTCTGCCGTGCCTTGGCTCTCTGGACGGTCATTCTACATGGCTGCTGCTTTGCGTCCTCTGACCTCCCCATTCC
WI-18357	89	C	G	CCCAGCCCTTAGCATCAA	AAGGACTCAAAGACTGAAGATGA		AATGTTTTAAAAGTCTACCGTGCTGAGGTGGCCATGAAGCCAAGCCCATGGAGAGACATTTCAGATAATCCCAGCCCTTAGCATCAA[C/G]TCATCTTCAGTCTTGAGTCCTTCCAGCCCAGGTCCAAGCTTGTGGACCAGAGACAAGCC
WI-18012g	117	A	G	---	---		TTTTATCTGGGTCAGCTCCTCCTTCTTAATGGCCTGAAGGTCATCTCCTTCAACTTCCAGACTTGGAAGATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTGCCCCTTCGTGA[A/G]GTGTTTCCTGATACACGGCTGACGTTTCGAGGG
WI-18012f	113	G	A	---	---		TTTTATCTGGGTCAGCTCCTCCTTCTTAATGGCCTGAAGGTCATCTCCTTCAACTTCCAGACTTGGAAGATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTGCCCCTTC[G/A]TGAAGTGTTTCCTGATACACGGCTGACGTTTCGAGGG
WI-18012e	112	C	T	GCCACTTTTGCCCCTT	TCAGCGTGTATCAGGAAACA		TTTTATCTGGGTCAGCTCCTCCTTCTTAATGGCCTGAAGGTCATCTCCTTCAACTTCCAGACTTGGAAGATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTGCCCCTT[C/T]GTGAAGTGTTTCCTGATACACGGCTGACGTTTCGAGGG
WI-18012b	46	T	C	---	---		TTTTATCTGGGTCAGCTCCTCCTTCTTAATGGCCTGAAGGTCATCTCCTT[T/C]TCAACTTTCCAGACTTGGAAGATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTGCCCCTTCGTGAAGTGTTTCCTGATACACGGCTGACGTTTCGAGGG
EST38390 4	75	A	G	GCAAAAAGGAGCTCTGCATTG	GCTAAGTCAGCTGATTAATAAACTTAA		CATATCATAGCCAGATCTACAACCCCAGAGTAATTCCCATGGTTATGTTACATGGCAAAAAGGACTCTGCATTGT[A/G]ATTAAGTTTATTAATCAGCTGACTTAGCATTGGGAGATTATTCTGGAT

ID	pos			seq a	seq b	sequence
ST38512	91	T	G	TGACGATGCC AATACTTCG	CACTGCACTCT GGGAAGC	TAATAAAAACTGACCCAATTGGTAAACTGTGTCTGGACTGAGAGAGAAACAATGAAAAATCTGTAAAT ACCTGATGACGATGCCAATACTTCG[T/G]GCTTCCCCAGAGTCCTAACAGAATGGTATATTCCTCTGAAAA
ST38519	24	C	T	CCTGCACCTCC TAAAAGATCT T	TCTGTTAGGAC TTGGGGGA	CCTGCACCTCCTAAAAGATCTTTT[C/T]TCCCCCAAGTCTCAACAGAATGGTATATTCCTCTGAAAA AGATGAACGTCATCAATGGATTGTGCTCTCGTTCAGCTTTGATTTTTTGTCCTTGAGAACCTTG
ST38575	66	T	C	GAACATCCCA TGTTTCTGTTT AA	AGGGAAGGTA GTATAACACAT AAGAGA	AGTGGTCAAATGTAAAACTAATGGGGACACCAAGCCTCAGGAAGAACATCCCATGTTTCTGTTTAA[T/C]TCTCTTATGTGTTATACTACCTTCCCTTTCTTCTTTATACACATAGATTTTCCTTAATTGCAGC CCA
ST38616	101	C	G	CCTGCTCCGCC CTTC	GAGGAATGGAT GGTTGGC	CCATCTAGGCAGGCTACCTGAGCTCTCTGTGCTCCCAGAGTGGGTGCCTCACGCCCGGGGCCCCGTGG AGTCTCCGGCGGGGCCCCGCGCCCTGC[C/G]GCCACCATCCTCCCAGGGG
ST38652	59	T	C	TCTGAACTGGG CATTTCAA	TTGCAAAAATG AAAGGAAAAA	TATAGTAGGTACTTTCCTTGCTGCAGCAGGAATTATTCAGTCTGAACTGGGCATTTCAA[T/C]GCGTG GTATTTTTTCCTTTCATTTTGCAAGTAAAAAAATCAT
ST38654	42	T	C	AATGGTCATTT TAATATATCA GTTTTACA	CAGTGATGGTC CTTAATCTTCT ATC	CTCAAGCTGAGAATGGTCATTTAATATATCAGTTTTACATA[T/C]AGATAGAAGATTAAGGACCAT CACTGAGGTCACATAGCTCAGAGGCAGAGTTAAGATTTGGACCCAGGCAGGTTGGTTCCAGCATATA
ST38707	75	A	G	---	---	GGATCCTCACTCACCTGGGACAGCCTGAGAAGGGACATCCACCAAGACCTACTGATCTGGAGTCCCA CGTTCCCC[A/G]AGGCCCAGCCGGGGATGGTGTGCCCCTCCTCTCCCAACTCATCTTTCAGGAACACGAGG ATTCTTGCTTTCTGGAAA
ST38759	86	A	G	TGTCTCCCTGA GGGTGATATGG CA	TCACCATCGTG GACTTAAGG	TGACCTTGTATTCTTCACTAGAGGGGAGAAGAATCACCTTTGGATGCCTCCCACTCTACTTGT CTCCCTGAGGTGATATGG[A/G]CCTAAGTCCACGATGGTGACCTAAACTCAGTTTAAAATTCTTGCC TAGCACACC
ST38775	40	T	A	AATCAATAGG AGAGGATTGG C	GGCTTTGCTCT GAATTCAAA	GACTCTCAACCAAAGAGAAAATCAATAGGAGAGGATTGGC[T/A]TTTGAATTCAGAGCAAAGCCCT CTTACTGAGAGGTGAGCCCCAGCCCCTCCCAAATGCCCCTTTCATGAGTTAGGATCTCCTAAGTGGTAC AAACAAACCAACATGGTGG
ST38815	91	C	A	TGTTTATGAGA ACCCATTACA CA	GCTGACTGGCA CATGCTTT	CACCCCATATTTGACCAAGGGATGAAGCCTAGCCATGCTCTTTCACTTATGTGTGTTCATTCAACAAG TGTTTATGAGAACCCATTACACA[C/A]AAAGCATGTGCCAGTTGCCAGCAGATTCTGTAATAA
ST38858	98	C	T	CACGAGTAAA AAGAAACTCA TGAC	GGAGCGGAGTCC AAGGAGAA	TCTTTACTGTGCTTACAACTTTCCTCCAAGTTTGCGGTGGTTCCATATTGTTATTGTTATTA TTCAACACGAGTAAAAAGAAACTCATGAC[C/T]TTCTCCTTGGACTCGCTCCCCAATCTCGAT ACCGACTGCACTGTTG
ST38865	72	T	C	GCTGTAGAATT TGTGTCGATGC	GGAAGGACGCG AGGACACAG	CCTTAATGGATTTTACAGCTCATCTGAGTCTCTGCTGTCTGTGTTCTCTGAGGAGCTGTAGAATTTGTGTCG ATGC[T/C]CTGTGTCCTCCGTCCTCCCCAAATGAGCACATATGCAGGGCAGGCAAGAGCATGCTGGA TTTGTTTAGTTGTTAA

ID						Sequence
EST388789	47	T	C	AAACATCATT ACTAGCCTAG ATCCTAA	CCTTCAATAAA TCTCATGTCCT CA	CCAATGAGAACCAAGTAATTAAACATCATTACTAGCCTAGATCCTAA[T/C]TGAGGGACATGAGATTT ATTGAAGGGAAATCCTCAATTAATATGAACATTCTTGAGAAATGGGAAATTTGAAAACATTCCC
EST388826b	113	G	C	...	...	TTATTCAAGTGCATCTCACACATTCTTATTTTATTTGTTTCACTTTCTCAAATATCGGATTGTGC TCATGAGAATAAATGGCTGAGGGAGCTGGCACGGCAGTCTTCTCA[G/C]GCTCCCTGGATAGCTAAAT TTA
EST388826a	35	T	C	TGTCATCTCAC ACATTCTTTAT TTTT	CGATATTTGAG AAAGTGAAAA CAA	TTATTCAAGTGCATCTCACACATTCTTTATTTTT A[T/C]TTGTTTCACTTTCTCAAATATCGGATTGT TGCTCATGAGAATAATGGCTGAGGGAGCTGGCACGGCAGTCTTCTCAGCGCTCCCTGGATAGCTAAATT TA
EST389095	47	A	G	GCACAGCATG GCTAAAACG	GGTATTTGTTG ATTCCCATCTT T	GCACTAAACTAACTTTCATTGTGGATTGCACAGCATGGCTAAAACG[A/G]TAAAGATGGGAATCAA CAAATACCATTGAAGATATGGAGCAAAGAGAACTCTCACATACTGCTGGAGGGAATATAAATT
EST389119	85	A	G	GTTGAGGGAA ACTTATAACCT CAC	TGTTGTTTGT GAAACAAGCG	AACTGAATGGCAGTGAAAAACTACACATCAAAACTTAGGAAATGTGGTTAGTGTGGTACGTTGAG GGAAACTTATAACCTCAC[A/G]CGCTTGTTTCACAAACAACAGCAGACAACAGAGATTTCCAACTC CAGCAATGACAGGCTAGGG
EST389555	30	G	C	TGAATTCCCTT GGGTGCG	CACTGCAATCT CACCCCC	TAAACATTCCCATTGAATTCCCTTGGGTGGG[G/C]GGGGGGGGGGGTGAGATTGCAGTGCTCAAGATAAA TATCCAAATATATCAAAAACTTCAAATTGTCTATGCATTCACACACTGACACTGAGCCACAAACATT CCTTTCACAGGGACTGTAC
EST390020	42	G	A	GGACCCTTCGG TGACC	CTGGCAGGGAG CCTG	CCTGCTATGATGCCTGGGCAGATCCCGGACCCTTCGGTGACC[G/A]CAGGCCTCCCTGCCAGGGCTTGG CCCCTGACCGGGGCTCCCCAGCTGGCCCTGACGTGTGGAGGAGCTGAAATACGCTGACATCCGCAACCT C
EST390048	79	T	G	GGTGGTAAGG CCTAAGGAAT	ATCTCGGCTGG CGGC	CACGTGGCCCCCTAAGTTCCGGGGTCTTCCTCAGTCTGGATGGCTGTGTGGAAAAGCTTGGTGGTAAG GCCTAAGGAAT[T/G]AGGGGGCAGGGGGCGGATGCCGGCCAGCCAGGTCCGTGAAGCCTGTGGGTC AAAGACCTAACTTCTGGA
WI-16398	90	T	C	TCCCTATTATT CCATGATATTT TCA	GAATGGTTGT GAAAAAATATA TTGATAT	AAAGATAAATGTCATCACAACGCAACATATAGAAACATAAAGAAAATAAAGTATCCACCCTAAAAT CCCTATTATTCCATGATATTTCA[T/C]AGCAACTAGTATATATATCAATATATTTTTCACAAACCAT TCAGTTACAC
WI-16403	69	T	C	CCTTTGTCCTC AATTTTTAAC ACT	TAAGGGCTAAT TCCCTATATAA AAAG	GGTTGTCTTCATGTATTTTCTCATTCCTATCAGGTTCTGTGGTCCTTTGTCCTCAATTTTTAAACACT[T/C]CTTTTATATAGGGAATTAGCCCTTAAACTGTGGTACATGCTGCCAAAATTCCTCCCAGTT
WI-16406	24	C	T	GCTTTAATGGC TACAGAAAGA AGG	TAAGGGCTAAT ATGTGTTTAAA AA	GCTTTAATGGCTACAGAAAGAAGG[C/T]GGTTTATTTCTTTTTAAACACATCTGGTTCTGGCAGC AAGTTATATTATGCATTTAGAGCAATAGGTGCCCTGAA

ID	Pos	Allele		Seq A	Seq B	Seq C
EST39236 0b	57	C	G	TCATCTGAGA ATAAACTTCCT GTCT	CATTATAGGTA CTGAGTCATAC ATTAAACA	TCCTTTTATTCATGATTGTTCATCTGAGAATAAACTTCCTGTCTCTAATTTCCAA[C/G]ACTATGTT TAATGTATGACTCAGTACCTATAATGAGACTGGAAATATATTACCTGGCAAATGAATGAGGTGTCTC TTT
EST39294 4	63	G	T	CCTGAAACAG GGATGCC	GCACAATTAA ACATAGTACCG AGAA	CAAACAGACCTTTGGTTGAGCTCACCTGGTGACAGGAGACTCCTACCTGAAACAGGGATGCC[G/T] TTCTCGGTACTATGTTTAATTGTGCTGAGCCAGCAACCCTGCGAGTTACCCGGCCTTTTACCCCAGCC AGCTCTGCTCTGTCTGCAT
EST39366 2	72	T	C	...	...	AGAAAACATTCTGTCTGATCAGAGGAAGAGATGTATGTAGAAAATCAGAATCTGACTGAATTCCTAAA ATCTAT[T/C]ACACTGAGAGGAAAATGGAAAAGAAAATGTTTGCATAAAGCTTTTCCCTGACTCTCA GAGGGGTTCAGA
EST39371 9	86	A	G	CATTTGGATTA GCGTGAGAGG	TGATTTGAGAC ATTTCACATTT TT	AAAAAGCTGTAGCTGGCAAGTCAAAGTTTATTTTATGTGTGTAAATTCCCAGTTGAGCATTTTTCAT TTGGATTAGCGTGAGAGG[A/G]AAAAATGTGAAATGTCTCAAATCAAATGCTTCCTTCTAAAGATTA GACATTGCCCAACCCTGC
WI-17177	23	A	G	...	...	ACAAGTGACATATCCAACCAACC[A/G]TTCCATCCCCACCTGTGCCCTATTCTTTCCTTGTGTTCTTT AGAGCCTTTCAGCTATTTCCTGTGAAGCAAACTGCACGAAGGCCTCCCCGTACTCCTCCCCCTGGAA G
EST39428 8	31	C	T	GCTCCCCACA ATTTTGATT	GGTCCCTTATG AAGCCACC	AGGTTCCTGGTTGCTCCCCACAATTTTGATT[C/T]GGTGGCTTCATAAGGGACCCAGGATTCTGCATT TTCTGGGTGGGGGCCTAGGTAATTCTGTTGCCTTGGTCCACAGAGCACAATTAAAGAAGATCAGGTCT GGCTGTTGC
EST39430 2	45	A	C	GGCAGAGGAA TAACTGATGTT ACC	CAGGGGGTCGGG GTATTG	AATTTAGCAGAAACAATGAAGTTGGCAGAGGAATAACTGATGTTC[A/C]CAATACCCGACCCCTGA CCCAGTACCTTCCCCAGCCCAGCCTCCGGTGGGAGGATGTCCTGGG
EST39446 7b	117	C	T	CTACTGACAT AGGGACTTCA GAGTAA	TCCTGGAAAAC TGACATAAACC	AAAGCCCTGTAAACTGAAGCTAGACAACGTCAACTTTGGAAGAAATAACAGGAACCTATTTATAT ACGTAAATCACTTTCATACCTGCCTACTGACAGTAATA[C/T]GGTTTATGTCAGT TTTCCAGGATTGTTCTCCC
EST39465 2	80	A	G	AATGCAGGAG GGTGGC	CAATCTCGGCC CCTCT	ATGGTGTCATTAGAGGGCCACAGGGATGGGGGAGTAAAAAATAACATAAACGAACTGAACAGAAA TGCAGGAGGGTGGC[A/G]GAGAGGGGCCGAGATTGGGGTGTTCAGGGCAGAGGTGGAAGACCAG
EST39501 0	81	A	G	AAAGATTCCT GTAGACATCT AACATTAG	CACTTGCAATT CTGAAGGCT	TGCTTACAACCCATAACCATAGGCCATGTTCAGACATTCTTGACCAAGCCTAAAGATTCCTGTAG ACATCTAACATTAG[A/G]TAGCCTTCAGAATTGCAAGTTCAAGTCAAACCAATTC
WI-18387b	84	A	C	...	...	CACAAAATGGGACTGCTGAAGAGTGGACAGTTGGACCTTACTTGGTGACCCATACATTTGTGGTCA CATGCTTTAGCCATTAC[A/C]CATGGTAACATTGACTATGGAGTCTTGTGAAAGTGTAATGTGCGATG GCTATGTAGAGACATAAAGA

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ID	Pos					Sequence
WI-18387a	57	A	G	CCTTACTTTGG	GCTAAAGCATG	CACAAAATGGGACTGCTGAAGAGTGGACTTACTTTGGTGACCCCATAC[A/G]TTTGTG
EST406019	78	A	G	TGACCCCAT TGACTGGAACCT	GCTATGTAGACATAAAGA TTCTTGGAAGA	GTCACATGCTTAGCCATACACATGGTAACATTGACTAGTAGTCTTGTGAAAGTGTAATGTGCGATG TCCCAGGATGGTTTATTCCAAAGCTGTGGACGGTGAACATTAAGACGAAAGAGGTGACTCGCGTGGA
				GGAAACAC	AAGGCGTC	ACCTGAAACAC[A/G]GACGCCCTTTCTTCCAAGAAGGGCTGTGGCGATCAGGCCACTCAAGG
EST41935	32	A	G	AGTGTATCAC ATCTTCAGGAT AGGT	GCACACCCTTC ACACTGTTA	TCCATTCAGTGTATCACATCTTCAGGATAGGT[A/G]ATAACAGTGTGAAGGGTGTGCTCATTTTCTTC AGCTGTGAGTAGAGAGGAGTCTTCCCGAGAGTAGCAGTTGTTGA
EST43091	28	C	T	CATTCTGGTCT TTATTTTGGA CTAC	AAAACTGATTT GTTAAAAACATG	ATGTCATTCTGGTCTTTATTTTGGACA[C/T]GTAGCATGTTTAACAAATCAGTTTTCATAGGCAA CCTTTTGAAACATCAAAAGAAATACAATATATTTTCACAAATTCTCATCACTGTAAATTCA
WI-18420c	108	T	C	TTCCATTAAAC AGGAAGTTTC C	AAATTCTCAGC ATTGCTATAAG C	AGAGAGACAACAAGAAGAATAAGGGAAAATGGGAAGAACAGAGTGAAATTAAAGCAAATCTTGGA TTCAGATTCCATTAAACAGGAAGTTTCCTCAAAAAAATCAAA[T/C]GCTTATAGCAATGCTGAGAA TTTCATAGGTACTTCATGGGA
WI-18420a	38	C	T	GAATAAGGGA AAATGGGAAG AA	CCAAGATTTGC TTTAATTTCAC TC	AGAGAGACAACAAGAAGAATAAGGGAAAATGGGAAGAA[C/T]AGAGTGAAATTAAAGCAAATCTT GGATTCAGATTCCATTAAACAGGAAGTTTCCTCAAAAAAATCAAATCAAATGCTTATAGCAATGCTGAGAA TTTCATAGGTACTTCATGGGA
WI-18425b	101	T	C	---	---	AGCTGATCAGCTGTCGTTACTGTGTTTATGTGTGGCCCAGGGAAGCCAAAAGATCAGACACCCGTGTC CTAGACAGATTCAATGCACACAACAACAGGAGAGG[T/C]GGGGGTCACACGGCGGAGAGCCAAAGAC TAGGGC
WI-18425	81	A	C	CACCCTGTCCT AGACAGATTC A	CCTCCTGTTGT TGTGTGCA	AGCTGATCAGCTGTCGTTACTGTGTTTATGTGTGGCCCAGGGAAGCCAAAAGATCAGACACCCTGTC CTAGACAGATTCA[A/C]TGCACACAACAACAGGAGAGGTGGGGGTCACACGGCGGAGAGCCAAAGAC TAGGGC
WI-18449	129	C	T	CTTTTGGCTCT AAGTGGGACT	CTCCCCTGACT GTATCCAGA	AAATTGAGGTCCGGGTGGAACTATAAAAGGAAAGGAAGAAGTAATCAGGAGGAGGCCAAAGTG GGAAGCTGTATTGCTGATCTAACGTGCTGTTCCAGTTCCTTCTTTGGCTCTAAGTGGGACTA[C/T]TC TGGATACAGTCAGGGGAG
WI-18457	120	T	C	---	---	ATCGCTTCATTGAAGCCTGCTTAATTTCTCTCAGTCAACTGGTCCCCCAGACATTATTTTATTCTT AAATGTCCAATATCTGCCTGATGTCTGTGTTTGTGCACATTGGGCACCACAGT[T/C]AAATAGGCTAAA AGGCAGTCCCACCTGCT
WI-18462	39	A	G	CCACAATGGC AGAGGTGA	TTTAGGCTTTG AGATGGTTTCT	GGTGCTATAGCTGCTTGTGTACACCACAATGGCCAGAGGTGA[A/G]TAGAAACCATCTCAAAGCCTAAAA TATTTACCATACATCCCCTCACAGCAAAGTTTGCTAATCTCGGGTTTAGGGACTCCATTGAG
WI-18476	60	C	T	GGTGCGGGGTGC GAGG	GCACGATGGGA GTGACC	TGAGGACGTTGTGACAAGCTCCAGCAGGGGGTGGGGGCTGAGGGGTGCGAGG[C/T]GGT CACTCCCATGCTGCCCCATGCGTCGCCCCTGGCCGTCCCTCACCCACCACCTGCCCAGTCCACGTTGAGGT

ID	No.	Allele	Sequence
NI-18491	109	G A	AACAAATGGT AGGTGGTATT AATACTATT … CGTGTGCATT TCTTGTAATCC … CTAATGAGATGAATACATGGAAGGCGTTTAGCACAGTGCCTAAAACACAGTAAGTAACCAACAAAT GGTAGGTGGTATTAATACTATTATTAAATCCCAGAATGAC[G/A]GGATTACAAGAAAATGCACA CGT
EST50757	79	C T	GAGCTCGAGG CTGCTTCT … ACCCTTCACCC GCCC … AGCCCCCTCCACTCTGCTTCCACAAAGTCGGCTCCCGAGAGCTCGAGGCTGCTTCTTTTATAT GTGCAGGGCGC[C/T]GGGCGGGGGTGAAGGGTCAGAGA
WI-17675	103	T C	GGACATTTGG ATGGTGACTT … GGGGAACCACC CAGG … GATCTTGGAAAGCACTAGAAAACTAAACATCTTCACCAGTGCTGAAGAAAAGTGTCTTCGTTTTAAT TGCCAAGCAGGGATGTGGACATTTGGATGGTGACTT[T/C]CCTGGGTGGTTCCCATAGAATTCACCAT TGCCTCTAATGGTGTCTA
WI-16543	67	G T	AGATAAACTA CATTTGGGTT TGG	GATTCATCATT ACAGGGGACTT … GATCCATTACCTAGGGTAAATTCTCCTGAATGTCAAACAAAGAGATAAACTACATTTGGGTTTGG[G/T]AAGTCCCCTGTAATGATGAATCAGAATCCTCAGTGTCTTGCCACCCATTTAATACGTATT TTTGTTAAGGCTGAAGTT
WI-17687	107	C G	GCCAAAAAGG TTGGGGAA	CCGACCAGCA … ATCTGAGATGGAAGAGTTTCATCCCAAAACCATCTCCCCCTGACCCCAGTCCATGGAAAAATTGTC TTCCACAAAACCGGTCCCTGGTGCCAAAAAGGTTGGGGAA[C/G]TGCTGGTCGGTACAAAAGTAATT G
WI-17690b	79	A G	---	…	ACAACATGTGAAAGAAGAGATATGTTGTCTTTACTCACAGTGGAGGCATTTTCTAGCTGTGTGTTGATTT GGCTTCCCTAT[A/G]GATTCAGGAGCCATAAC TCTTGTTCTCACTCATCTGCTATGCTG
WI-17690a	63	G A	AGGCATTTTTC TAGCTGTGTTT … CAAGAGTTATG GGTCCTGAATC … ACAACATGTGAAAGAAGAGATATGTTGTCTTTACTCACAGTGGAGGCATTTTCTAGCTGTGTTT[G/A]A TTTGGCTTCCCTATAGATTCAGGAGCCATAACTCTTGTTCTCACTCATCTGCTATGCTG
EST51717b	128	C T	GCGGAAGACA GTGAGCTGTT	TTGAGGCAATA ATCCAGCTC … GATCCAATCTCAGTGTCTAACTCATCATCCCAGATTATTCTGGGAGAGGCAGGCGGGAGAGGAGACA GTGTGCTGGAAGCACCCTCGACCC CAATGGCAACATCACCCACTACCTGGTTTTCTGGGAGAGGCAGGCGGGAGACAGTGAGCTGTTCGAG CTGGATTATTGCCTCAAA
EST51717a	39	C T	---	---	GATCCAATCTCAGTGTCTAACTCATCATCCCAGATTATT[C/T]TGAAGTGGAAACCACCCTCGACCCCA ATGGCAACATCACCCACTACCTGGTTTTCTGGGAGAGGCAGGCGGGAAGACAGTGAGCTGTTCGAG CTGGATTATTGCCTCAAA
EST53012	97	C T	TGGTCACTTTG GGGCC	GGCTCTGCCCA CGCC … TTTCCAGGTTGACAGGTTTATTCCACCCCCTTCCATCCCATGGCCACCCCAGGCAGGAGGAGAGACAG GTGTGCTGGAGTCTGGTCACTTTGGGGCC[C/T]GGCGTGGGCAGAGCCCACTGGGTTTACATTCTCTGT GGGCAGGTGTGGACAC
EST53349	96	A G	TGTTGAAAGC AGTCACAATG TAC	CATCTGGATAT CTTGTCACATT TT	AAACTGCAAATAACAAAACAAAAACAGAAGTCCAAGAAGGCTAAAGTCTAAGCTATAATTACACATG AAGTATATGTTGAAAGCAGTCACAATGTAC[A/G]AAAATGTGACAAGATATCCAGAGTGTTTAA
EST53389	74	A G C A	GGAGACCTGC AGAACTTAAA GCA	GCCCTTTCTAA CAATAAATGCT C	TTTCGAAATGTCCTCCATGAATGTGACAGAGTGTCGGCGGAGACCTGCAGAACT TAAACAC[A/G]GAGCATTTATTGTTAGAAAGGGCAAGTCTTACACTCAAATAGGTTTTAACATGAAC ACATTAAAGGGAGATGGCC

EST	Pos					Sequence
EST53477	61	T	C	...		TTTGAGAGGTTGTGCAAAACTACTGTATTTACAAAAAATGGCACAAAAAGTGAATTCAACAGTT[T/C]AA TGCACATGCATACTTCATTCAACACATCTTCAACAACAAAGGTATTCTAACTCTACAGAAACTGAATATT AGCTTCAACGGCAGCTGTT
EST64622	91	T	C	CGAGATTTTCT TCTTTATTTTA TATTTTCA	CCAAAGAAAA TGGCTTCAGTA A	GGGGAGGAGGAGGTAGATTGCCAAATTGAGGCATTTTTTTAAACTCCCGAGATTTTCTTCTTTTATTT TATATTTTCATTTTCATCCTAA[T/C][T/C]TTACTGAAGCCATTTTCTTTGGTAACTTAGA
EST67268 a	77	C	C	TGTGTATAGCA CATACTTCAGG C	ATGGGGGTGGTG CCGC	CTCATCTTATTAAATGCATCGTGTGTGTGTGTGTGTGTGTGTATAGCACATA CTTCAGGC[C/T]TGCGGGCACCCCCATAGAGATGGTGAGGAAGTAACTTCTGCTTCTCATTGAAACT GTAGATCCATCGGGGA
EST78503 a	26	C	T	ACGACGCCGG CGAGT	GCATTTCCGCG GCAC	GAAATGCAGAACGACGCCGGCGGCGAGTT[C/T]GTGGACCTGTACGTGCCGCGGGAAATGCTCCGTTAGCA ATCGCATCGTGGTGCCAAGGACCACGCATCCATCCAGATGAA
EST80253	92	G	C	...		ATGCACTTTATTGGCTCCCAGGAGTGGGATCAGGAGGATCAGAGTGGACACGCGCAGGGGGGCTGGTGTG GGGGAGCAAAGCGCCGGCCCTGCCCC[G/C]GGACCCTGGTTCCCTGAGGACCAACGTGAATGGGGGCCC CACTGGAAAGATGCTTG
EST91254	73	T	G	---		TATTCTGTAGGGAGAATAACCATGCTGCTTATGGGACTATCCATGGATAACTTGGTTTTTTGTTG TTGTT[T/G]TTTAATTATAAGAATAATATGTCTCATCATCAATGTCCTTTCTCAGTAGAGCCCAG ACCTGG
EST91332	100	T	A	---		TCCAAACTGAAAGGAGGGTGGGGAAAACAAACGCATCATATGTAAAGCACTGAGTCCAGCCTGGCTC TTAGTAAGCCATTTAATCACCTTCAAAAATTAA[T/A]TGTGACTTACGGAAACAGGTCACTGAATAT TATT
EST91495 b	58	T	C	---		CTGACTCAAAAGACACTCCTGAAAGCAGGTCCATCCTGAGCAGCAGCTTGTATTACTT[T/C]ACAAG TCAGACCTGTTATTAAAGAGACGCAGACTGGCATTAAATCAGGCTGTGTCACCCATCCTGGGTCTT GTTCTCGGCTCCTATGGGTG
EST91921	114	A	G	---		CTGGCTGAGGGATCTCAAAGAGATTCCACCACATTGAATCTTAGGCTGGAGGACATTTCGTATTCTT CAGTCAGGAATAGCACACTTCCTTCATGAATAGCAGCTTTTAGGG[A/G]TTATATCATGAGGTACA AATAAAGAGGCCCTCACC
EST92026 a	56	T	C	---		ATAGCCAAGATTTGGAAGCAACCGTGACCATCAACAGATGACTGGATAAATAAAA[T/C]GTGGTA CATGTACACTATGGAGTACTACTATTCAGCCATGAAAAAGTCTAAGATCTTGTCATTAGCAACAACATGG ATGGAACTTGGGAACACTGT
EST92040 b	38	C	T	---		TTTCCATGAGGAATAAATTTGTGTTTATATAAAACCTG[C/T]AGATGAATATTTTTTAACAGCATG ATTCACAAATGCCAAAAACAATGCAAATGCCCTTCAACACACATGGATTAACAGACCGTGATAC ATGA
EST98276 c	69	T	C	---		GAGTCTTGCTATGTTTCCCAGGATGGTCTTGAGCTCCTGGTTTCAAACAATCCTCCTTCCTAAGCCTCC [T/C]AAAGTGCCAGGATTATAGGTGTGAGTCACA

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EST98276 b	61	A	C	---	---	GAGTCTTGCTATGTTTCCCAGGATGGTCTTGAGCTCCTGGTTTCAAACAATCCTCCTTCCTT[A/C]AGC CTCCTAAAGTGCCAGGATTATAGGTGTGAGTCACA
EST98276 a	22	A	C	GTCTTGCTATG TTTCCCAGG	AACCAGGAGCT CAAGACCA	GAGTCTTGCTATGTTTCCCAGG[A/C]TGGTCTTGAGCTCCTGGTTCAAACAATCCTCCTTCCTAAGC CTCCTAAAGTGCCAGGATTATAGGTGTGAGTCACA
EST98800	53	A	T	---	---	GCCTCCCAGCTGCATGACTCCTAAGCCATCATTCGAAGATTTGGCTAATTTG[A/T]TAGTCTTACAA AGGCAGTCTAGTTCACCAGGCAAGAAGGGGTTTGTGTTGGGAAAGCGCTGCTATCTTTGTTCAAAC TGTAAAGCAAGTTCCTC
J02931	138	G	A	CAGCATTAGTC ACTTTGAAAT GTAA	TTGGAATTGGT TGTAGTACCAT T	AGAGGATAGAATACATGGAAAACGCAAATGAGTATTTCGGAGCATGAAGACCCTGGAGTTCAAAAA CTCTTGATATGACCTGTTATTACCATTAGCATTCTGGTTTGACATCAGCATTAGTCACTTTGAAATG TAAC[G/A]AATGGTACTACAAACCAATTCCAAGTTTTAATTTTAACACCATGGCACCTTTGCACAT AACATGCTTTAG
L41680	88	G	A	GAGAAATCGA CTACCAGCTG A	TTTAGAGCACT TTGCAGGTATT T	GGATCCAAAACACGGCTGGGTTTCAGCATCCACCAATGAACTGAAAGGTGAATAAAGGACGTTCATG AGAAATCGACTACCAGCTGAT[G/A]AAATACCTGCAAAGTGCTCTAAAAATTAAATATTTGACTT AAGGGTCCTAGTAAGTGCCACTTCCACTAAGAATACAGTTTGAATGTATAATCAGTAGTGTTTACAA GATCCAACAGTGCACTCA
M15796a	84	C	G	CAAATTTGTA CCTCTAAGTAC ATATGTAGA	TTGGACTTTAT TCTTTAAACAA ATTG	CTTTTGTCACCAAATTTGTACCTCTAAGTACATATGTAGATATTGTTTCTGTAAATAACCTATTT TTTTTCTCTATTCTCT[C/G]CAATTTGTTAAAGAATAAAGTCCAAAGTCTGATCTGGTCTCAGTTAAC CTAGAAGTATTTTGTCTTTAGAAATACTTGTGATTTTATAATACAAAAGGGTCTTGACTCTAAAT GCAGTTT
M20472	103	C	T	GTTGAGTTCTT TGGACCAAA C	ACAATGAACA ACTCTAAAGAC AAAAA	AGAGCCACCCTGTGGAAACACTACATCTGCAATATCTTAATCCTACTCAGTGAAGCTCTTCACAGTC ATTGGATTAATTATGTTGAGTTCTTTGGACCAAAC[C/T]TTTTTGTCTTTAGAGTTGTTCATTGTTG TGATTGCATGTTCCTTCCCTGGCATTCAGAGAGGAGAGAGGAGAGGAAGA
M32315b	129	T	C	GCCTCTGCTGC CATGG	GCCTTCCGAGA GGGACAC G	CCCTCTGACCTGCAGGCAGGCCAAGAGCCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCAGTC GTCCCCTCTGCGGAAGGCTGCTGGGGCTGGGGGGCATGCGGACGTTCGGGGCCAGTCCCTGACTCTCTGT G
M33875a	131	C	T	GGTTACAGCTG GAGGTGTGT	ACCTTTGTTAA AATTAGGTGG TTAT	TTCCCAGGAGCAGCAAAGGGGCCTGCTGAGCTCTGGTTAGGTTACAGCTGGAGGTGTGTATATACA CACACACACGTGTATATACACATATATGTGTATATATACACATATATATATGTGCTTT[C/T]C AATAACCACCTAAATTTTAACAAAGGTTCCTTCCTAAGTGGTGGTATTTTTACCTTC CTTCT
TIGR-A003M18 a	29	A	G	TTTTTGTAGAG ATGAGGTTTTC CT	GGCAGACGGAT CACTTGA	TGTCTTTTTTGTAGAGATGAGGTTTCCT[A/G]TGTTGGCCAGGATGGTCTCGAACTCCTGACTTCAA GTGATCCGTCGTGCCTTGGCCTCCCAAAAGTGCTGGGATTATAG

ID	Pos	Allele 1	Allele 2	Flank	Sequence
TIGR-A003P30	117	C	G	---	ACAAGTTCAAAAGGAGAACTTCCTTGTTTAATGCAGCTGTGCTCAGAAGCCTGTGATTCCTAGGA AACCATCTGGGTTAGCCCATTAGAAAAATGCAGTTAAAGCAGTGTCA[C/G]ACTGGCTGCCTGAA GGTACCCTTGGAGATACT
TIGR-A004S34	156	C	T	CCAAACCTCCTT CATTCCTATAA A	TGTAAACAGCT AACTGTTTTTG GCTTGTCTTTTATGTTTAGGTTCGGGGGAAAGGAAGGGGCTGACAACCGCAGACATCTGGACACCAGC AAGGGTCCAGGGGAGGTTGCAGACTTCTTTGTCCTTGGCTAACAGTCTGTCATGTGACAATAGCCA AACCTCCTCATTCCTATAAA[C/T]TCTTAACAAAAACAGTTAGCTGTTTACAAAACAGTTAGCTGTT TACATG
TIGR-A004T44b	97	A	C	---	AACAACAGTGTAATCTTTAACAGGGGATGTTAAAGGTAAGAAGTCAGGAGGAGATAAACCAAAATGAT TGAGTATGATAAAGAATTTGCATGGCGATT[A/C]AAATAGAAAAACCTATAAATGTAGAAAAAGCA GGTCTCGGACTTAGCAAAGAAACAATATGACTTAGCAAAGAAACAATATAG
TIGR-A004T44a	69	G	A	GGAAGATAAA CCAAAATGAT TGA	AACAACAGTGTAATCTTTAACAGGGGATGTTAAAGGTAAGAAGTCAGGAGGAGATAAACCAAAATGAT TGA[G/A]TATGATAAAGAATTTTGCATGGCGATTAAAATAGAAAAATGTAGAAAAAGCA GGTCTCGGACTTAGCAAAGAAACAATATGACTTAGCAAAGAAACAATATAG
TIGR-A004V08	60	T	C	GCCATGCAAAA TTCTTTATCA CAGGAAAACA GGCATTCTCTT	CCTACAATCCTATAATATTGCAAGGGTTGGGAAGGATGCAGGAAAACAGGCATTCTCTTA[T/C]GCC TTTTGTGGGAAGGATCAATTGGGTGCATGGGGACAATTTGGGCAGTAGCTGTCAAATTTC AGTAGCTGTCAAATTTCAA
TIGR-A004V26	125	A	G	TCCTTCCCACA AAAGGC	TCTAGCTATAAGACCAGATTTAATATTCTAGATATAGAATTATCCAGAATAATTCTATTGAATTGA CTGATTACAAAATGTTAACAGCTGGATAAAACGGTAAAAATATGCATTATCTTCACATGA[A/G]AAGGT TTCAGTTTATAAATGCTTAAAATACTGTATCTATTGG
TIGR-A004V28 3	29	A	G	--- CGGAGGTTGCA GTGAGC	CCAGGCTATAAATGTTGTGGGGTGCGATCTC[A/G]GCTCACTGCAACCTCCGCCTCCCAGGTTCAAGCAA TTCTCCTGCCTCAGCCTCTTGAGTAGCCGGGACTACAGGCGCCGCCACCACGCCACCTAACTATTTTG TATTTTTAGTAGAGACATTGTATTTTTAGTAGAGACAGG
TIGR-A004X20	25	T	C	TGTTGTGGGTG CGATCTC GA	TAAGTTTTCCTTCTCTCTCTGTGTAGGA[T/C]GTCTCCCATGTCAACTATAAAACATGGCTCATGT TCACTCTGGGCTTCGCCTTCAGAGGAGTTGATATTTGGAAGTGGTACCTTGTCTGTGTGCTTTTCA GACCAACCGCCTTCTTCATTCTTCCAAGGAGTTAAATCATCATGTCCAATC ATCATCATGTCCTT
TIGR-A004X30	26	T	C	AAGTTTTCCTT CTCTCTGTAG GA TTTGAAATCTT AGAGTAGAAC CCAC	TTTTGAAATCTTTAGAGTAGAGTAGAACCCAC[T/C]ACTCTAGTAATACTTGTAATAAAATTAAAATAGTTTT AAACACTTCCATAAAGAATTAGGGGTGCCCCAGCTCCTTGATTCCCCCTAGGGATAAAGATATCCAT GTTAGGGGATAAAGATATCCATGTTAC
TIGR-A004Z04	102	T	G	TTTGAAATCTT AGTGTTTAAAA CTATTTT CTTATAATTAG TTCATTTGGGT ATGCAAAACT AAATTTCATGA AAGCAA	CACGGTATATGCCTATATATATAGGTATATATACAGATCGTACACAATATATTTAACAGTTTGACATG GGGTCCACAGTACCTTCATTGGGTATGCAAAACT[T/G]TTGCTTTCATGAAATTTCATTATAAGG ACTGTTGCTTTCATGAAATTTCATTATAAGGACATTATACAAAAATACAGTTCTTTAGTGATTTAAGACGTC TCTTTAGTGATTTAAGACTG

ID	No.					Sequence
TIGR-A004Z19	85	C	T	GAGAACAACT GCAGCATTTTT	AAGATGGTCAT CGGGAAGA	TAAGTGGAGACAAGTTATTGGAGGAGCTTGACACCCCTCTTCTGCCCTAGCTTGAGAGAACAACTGC AGCATTTTTCTTTTC[T]C[T]CTTCCCGATGACCATCTTTGGGCTGCGGCCAGGCCTGGCGGGCCCTGGGGTC TCCCATATCGCTGTCTTTAGTGACTGAGGATCTGGTATAAGGAAACAGATC
TIGR-A004Z42c	89	C	T	TTGGGGGGAGGT AGGAGACT	CAGGGCTGCGG GTCC	GTCTTAGCAGAGGAGATAACTTGAGGACAGCGCCCCCAAGGCGCCAGGTAGCCTTCAGGGGCGGGCA GGGTTGGGGGGAGGTAGGAGACT[C/T]GGACCGGCAGCCCTGGCTCCAGCTTCATCATCTGTGTCTT CATCATCTGTGTCTC
TIGR-A005D17c	81	T	C	---	---	TATGGACTGTGTGTAGAAATATGATTTGGACAAGAAGGGTATGATCTAATAGTAATAGACTGAGAGGGG AAACCCAGCAAGGC[T/C]G[T]CGTCTAGATTCTTCTTGGCCTCTGTGCAGGATTCCTTCCTTCTGGGCAC GGGGTGGGACCCTCTCTGGAATGGGTATCTTACGACAGTCAAACAC
TIGR-A005D17b	79	G	C	GGGGAAACCC AGCAAG	GAGAGGCCAA GAAGAATCTAG AC	TATGGACTGTGTGTAGAAATATGATTTGGACAAGAAGGGTATGATCTAATAGTAATAGACTGAGAGGGG AAACCCAGCAAG[G/C]CTGTCTAGATTCTTCTTGGCCTCTGTGCAGGATTCCTTCCTTCTGGGCAC GGGGTGGGACCCTCTCTGGAATGGGTATCTTACGACAGTCAAACAC
TIGR-A005D44	97	G	T	TTAACATTATT GAACTTAAAA CTGTTACAC	TTGTCTATTAT TTAAGCCAAC AAAA	CATCAGTAACATATACACAATGGTCATCAACTTGCCTCCAATATATTTCTATACAATACTT AACATTATTGAACTGTTACACT[G/T]TTTTGTTGGCTTAAATAATAGACAATGATTTTTG TCTATTACTTAGTGATAGACAAAGTGATTACTTGTTACTTTGTTAC
TIGR-A005E31b	27	G	A	---	---	GGAGTTCAAATTTATAACCAGCCTCT[G/A]CTCACAGCTGTACTGGCTAGGCAAAGCTTCCAGAC ACAAAGCCACCTGCCTGCCATGTGGGATAGTAGTACTCTTTGCCTGCTGCCCCTACAAAGCCACCTTCTAT TTCATACCAATACCTTCTATTTCATACCAATAAG
TIGR-A005E39	182	G	C	---	---	CTCAGTGTAAAAACTTTGTTTAGGGAAAAAAAAAATCCAATGGATATATGGGAAGAGAAGTG CCAGGCTGGATGGTGCTGAGACAGAATGACCCCTTGGGCTCCTTATTTGTTCTTTCAACAGGACC CCACAGATATTTGCGGTATGTCATGGGGATGTCTTCTATTG[G/C]G[C]CGGATGTCTTCTATTTT
TIGR-A005E42a	42	A	G	AGTAAGGTTA CTGCACCTTAC AGAG	CCTAAATCAGG GGAAATTGAG	GCTGAGTTTGTATCTTAGTAGTAAGGTTACTGCACCTTACAGAG[A/G]CTCAATTCCCCTGATTTAGGA AGGCGATGCTAATGGTATTGCATAGGTGTAAGTATAAAAATGTTGTATTTAAGAGAATCCCACAAG CTTGGTATAAGGCAGAAAAATAAATGGTATAAAGGCAGAAAAATAAATAG
TIGR-A005E46	76	A	G	CACCTGACTCG GTGCTTTAC	CCCTGGCTGTG AGGTAATGT	ATGACAATGATGATAGTAGTATTAGCCTACTACCGTTTGCTAAGCACTACTGCGTATCAGGCACCTGACTCGG TGCTTTAC[A/G]TGACTTTTAC[A/G]TACATTACCTCACAGCCAGGGTTGGCAAATGGTCATTTTGACAAATGGTCATTTTG ACAC
U20979	24	C	T	GCAGGGGTGA CGTATGTAGA A	GGGGAGGACAC CCTAAGC	AGAGCAGGGGTGACGTATGTAGAA[C/T]GCTTAGGGGTGTCCTCCCCACAGAGCAGATACTTGAACCG ACTCAATTCCTGTGTGAAAGAGCACTTTGTCCTGCTTCACGGACCTCCCAAAGTGTGCAGAGTTCTAT ATAGGATGCTGGATTAGTTCCTTGATATTTGTAAAAATTCCCCAAGAGCCGCATATGAATCTGCCCC

ID	Pos					Sequence
X57830	106	G	C	CT	AGTGGAACCA ACGATCATAT CT	CATTGACAGAA TAAAATGAGGC A	GTGGCAACTGTGGAAGGCACACTGAGCAAGTTTTCACCTATCTGGAAAAAAATATGAGATTGGA AAAAATTAGACAAGTCTAGTGGAACCAACGATCATATCT[G/C]TATGCCTCATTTATTCTGTCAAT GAAAAGCGGGGTTCAATGCTACAAAATGTGTGCTTGGAAAATGTTCTGACAGCATTTCAGCTGTGAG CTTTC
X74070b	72	T	G	CTTTTTAAGAA ATTTTTGTTTA TGGGATC	GGGCTTAAAAA TATTAGAGATC TAGATTT	AACCTGAAGAAGTTACTGGGAGCTGCTATTTATATTATGACTGCTTTTAAGAAATTTTTGTTTATG GATCT[T/G]GATAAAATCTAGATCTCTAATATTTTAAGCCAAACTGGACACTGCGAGCTCTTT CAGTTTTTGCTTATACACAATTCATTCTTTGCAGCTAATTAAGCCGAAGAAGCCTGGGAATCAAGTTT GAA
Z48804	44	C	T	---		ACTGCCGAAGTGTAGCGGCCCCCAAACCTTGCTCTCATCACCAG[C/T]TAGAGCTTCTTCCCGAAGGG CCTTTAGGATAGGAGAAAGGGTTCATGCACACACGTGTGAGAATGGAAGAGCCCCCTCCAGACCACT CTACAGCTGCTCTAGCCTTAGTTGCCCACTAGGAAGTTTCTGAGGCTGGCTGTAAAGTAAGTGTAAGG TCCA
D28513b	133	A	G	---		ATGACCAAAGCCACCACCATTTAGAACTTTGGCTGCCTTTGGAAGTCCAGAGCTGGATCTCTCAGCTCC CGCCCCCAGAGGGTCAGCACTTTGGACACTGGCTCACAAGCAGTTTTGATTGACTGCATGAATGC[A/ G]TGTGCGTGCAAGCATGAACCTTGTTTAAATCAAGAGGCTTACATAATTTAACCAGTTCTGTCTTC AGCTGTACATA
D29833b	85	A	G	---		CCACTCCATCCTGATGCCCCAAGTATCCACAGCCTCCTTCCCGACCAAGACCCTATCCACCTGGACC TCCATTTTTCCCTGTAA[A/G]TTCTCCAACTGATCCTCCACCCCAAATATGAA CAACTGCAGCAGGTGCCACCACCACCACCAGACACCACTACCCTTGTAACTACTGCTTCTGCTAC
D29833a	21	A	G	---		CCACTCCATCCTGATGCCCCA[A/G]GTTATCCACAGCCTCCTTCCCGACCAAGACCCTATCCACCTGG ACCTCCATTTTCCCTGTAAATTCTCCAACTGATCCTCCACCCCAAATATGAA CAACTGCAGCAGGTGCCACCACCACCACCAGACACCACTACCCTTGTAACTACTGCTTCTGCTAC
D31762	82	G	A	---		CTCCCTGCCTCCTCCTCCTGCCTGTGATGCTCCGTCTCGGTGGCTTCTTGGCTTCTTCTTATTCTTCCAACAGCCGAAACCTGCTTGCAATGGGGG GAGGGGGGCGTTTC[G/A]CTTCTTCTTTCTCCCCCTCAGCCACCTCCTATTCTTCCACAAACCATTCTCAATAAA GCCAAAAATCTTTCTTTCTCCCCTCCTGTCCTCCTCACTCCTGTCCTGTGGCTTTT CTGGA
D37931	64	T	C	---		ATTATCGCGAGTGGTTGACCTTACACTTACTCCTTAAATAGCAGTGAGTAATGCATTTGAGCTG[T/C] CCCAGGCTCTGTCTCCTCAGCTCATTTCCTACTCTTTTCTCTATAAACTCATTCTATTAAATACATT GCACCAAAGAGATATGGAGACATAAACCTGTAATGAATGAGGCTGGGCTTTTTCTGTAATAAGCTTCC TTT

ID	Pos	Allele			Sequence
D63807	101	C	T	--	CAGGCAGGACTTCAGTGTCAGTATCCCTGCCTTCAGTCTCTTCTTTAGAAATCACATCTGTGTTCAATCC ATTGTTTAGAGGGGAGTGTATTTTCCTGTTCCA[C/T]GAAGAGGACTTTTGTTCACAATTGGATCAC AATGCAGAGAGGAGTCTGTTCCTCCCCGGTGGCTTCTCGGTGTGCTGGGAGGGTGACCTGTCCCAGATGAC
D90145	21	T	C	--	TGGGAACATGCGTGTGACCTC[T/C]ACAGCTACCTCTTCTATGGACTGGTTATTGCCAAACAGCCACA CTGTGGGGACTCTCTTAACTTAAATTTATACTATTTAGTTTTATAAATTTATTTTGAT TTCACAGTGTGTGTTGTTGATTGTTGCTCTGAGAGTTCCCCCGTCCCCTCCCCTCACAGTGTG TCTGGTG
EST14035 1a	59	T	C	--	ATTATCACTCTCAAAAATTTGGTGTGTGTTAAGTACTTCTTATTTATGAGCCCC[T/C]GAGGA CCAGACATGTTATTATCAAGCCCCTTATATACCATCTAAT
EST16668 5	71	C	T	--	GCATTTAAAATTCACATTGAATCATTATTACTATTTATGATGTTACATAACAATTCAGTATCATT ATG[C/T]TTGTAGATTTCAGATGTAGGTCGTCAATACTGAGCACTTATCT
EST16904 7	57	C	T	--	ACAGACTATCGCCAACTTATAAATGCTTAAACTTATGATCAATAGTAATAAATTACA[C/T]GAGATA TTCACACTTTATTATAAAATAGGGTTTGTGTAAGATGATTTTCCCAACTGTAGGTTAACAT
EST21863 9	49	A	G	--	TTTTTAAGTACCAGAGGCACTGCTGGAACAGGATGAAAACTGATACACC[A/G]GTTACTACTTACTC TTCACTCTTCAAACTGATTCCCCTAAAGACTTCTACTTAGCAAA
EST21885 6	80	G	A	--	GGCTGTAAGTAGAATCAAAGGTTAAGAACATCATTTATGCACTTATTCCACAAACATTTACTGAGCATA CTAGGTGCTGGGA[G/A]TGTGACAGTGAGCAAAAACACAA
EST22623 3a	26	A	G	--	ATTTAGTGCAAATGACAAAGCCCAA[A/G]AGAACAGAGGATCAAATAAGATTGAAATGTATTACC TTCTCATAAGTATACGAAGTTTAACACAAGTATGGGAGT
EST22644 2	98	A	G	--	AAAAATGATTGAATTCAGCAAGTACAGTACATTTATGATCTATCTACATTGTTAAAACAGCACTAAAAATAA AAATTTTAAAATGATTATCCATTATTTACACAG[A/G]AAATGTGGAAAGATGGCTTTAAACCC
EST23587 1	31	T	A	--	CCTCATTTATTTAAAAAGACGGACACATAAAAAA[T/A]TATACAACAAAAAACCCAAGTCACATTTCAG GAGGTAAAAACTAAAAAGTCTGATATGAAAATATGGTGG
EST24246 7	106	T	C	--	AAAGATCTGGCATTATTCACATCACATCATCTCTAAATATTTGTAATTACTTTTCCATGAGTATTTTTCA TGTCCAAGCATTTAACTATCATTTTAGCGTAAATACC[T/C]GAATAACCCATAGTTACAGAATTGG GTCTGTGTAACCTCAATT
EST24308 3	45	A	G	--	TAGTTTAATTTCTGAACCTTTGGCTTATAAATTTTCTCAACTT[A/G]CATTTAAAAATGTATCAAT GCACCTTCTTCAGTAGTACCACACTGAAAAATAAACCTCGTTC
EST24435 6	73	G	A	--	CTTGAACTTCTGGTCTCTCAAGTGGTACGTCCGTCTCCAAACCTCCAAAATGATGCGGATTACAGGCATAAG CAGCC[G/A]TGCCTGACCCACATTTCTTTATCCGATCTGTTGATGGACATTCAGGTTGTTTC
EST25089 6	25	T	C	--	TATTGTTGCATTATCAAAATGGTTA[T/C]AGTTTTCAATTAAAAACTGTAATTGATTTCTATGTGTATAAA ACAGCTTTGAAGTTGTAAATGTAAAGTTTTCCAATCGTTAGTTAATGTCACATT

				Sequence
EST25476 9	33	G A	---	AATGATCTTATTTTCAGACCTGCTCCTAAAA[G/A]CTTTCTCCTCCTCCTAAAAACCAAACACA AGAGGTCCTCTTGCTGCCTTTCCATGACGCTGTGGCGGCTGTGGACCGTCTGCTGA
EST26183 2	70	T A	---	AGATAATGCATTAGAGCCTGCCCTCATTGTATCTTGATTAACTTGTAAAGATTGATCTCTAAATAAG AT[T/A]ACATTCTGGGGTACTGGGAGTTAGAACAAC
EST27231 1a	28	T C	---	AGAAAATAAGGTGCTACCAGAACTCATG[T/C]GATAGCGCTTCTTTCTTTAGGCACATATTATAGCATT CAGATGAAAGTTCTGTAATCACACACACT[T/C]TAAACAACAAACACGGTGACTCTGA
EST27816 5a	26	T C	---	CAACTCAAGGTACAAGACAATTGCAT[T/C]TAACATTGTTATAAATAAAAGGAACATCAGATCAAT CATT/AGGGGCTCCAGAGTGAACAGCATCTTCATAACTTCCATGTT
EST28588 0	78	A T	---	GTTTAATTGGCGTATGGTTCCACAGGCTGTACAGAAAGCATGATGGCTTCTGGGGAGGTCTCAGGAA ACTTACAATCA[A/T]GGTAGAAGGCAAAAGAGAGAGGCATCTCTTCCATGACCACAGCAGGAGG AACAGACAGAGGAGGGGGAT
EST30226 5	25	A C	---	TACTCACACCGACATACATATCTCA[A/C]GTAGAATTAGCTATACTGCATACTAACTTCATTGTAGT AGGGAATATAAACTACTGAACAAGACAGACTTGTCTAACTTAAACAAGACAGACTCATTCCTTTGA G
EST30935 9a	59	C G	---	AGCTATGGTAGAGCAAATTCCAGTGGTGGTAAATCAAGAACTCTAAAGTTCAGTAGAGA[C/G]AGGT GTTTGAATGTCAAGGAAATCACTGAGGTAGATTGGGGATTACAATAAGACAGCTGCCCTGTGAGGT CATAAGAGCTTTTGTGAGG
EST32515 7	25	G A	---	CCGAATATAAGGAAAAAATGGTGGC[G/A]TGCCTCTAAAACCTGTTGAATAGAATAATGGCCAAAT ATTACAGTTCTCACTTCCTATGAATACTGGCACTGTTTATTTCATGTTTATATGTGAGTTTCTATGC ATAAAAATCCCAGTAAGA
EST33274 4	27	T C	---	TGCTTTGTTGTTCCCTCCAAATCCTAAAA[T/C]GTGTGTGTCTTCAAAGAAATTCGTGGAAAGGACTTTGAA TACGAGTTGTGTACCCATATTCAAGTATTCCTGAATACAGGTTTCAGATAACTATGGAGATGATACCATT GGACTAGGTA
EST33352 7b	75	C G	---	TACACATTATTCAAGAGACCACCTGACATGCCATCTCCCGCAGAATACATTCGTCCTCTCTCTTAGAGA AGTTTAA[C/G]GCACATAGTATTTATTTACTAAGGAATCTGGTGTCATATCTAGGGG
EST33424 1	126	A C	---	ATTTTCCCACAGCAGAAGTATATTTATTGTGCTGAAATCAGGTAGCAGGGAATGAATAGCTCTTGG GAACCAGTACAGAAATGTTCACAAAGATTTACAAATCTCAGTGTTCATTACACACTGAGCAAC[A/C]AAA CAAAGGTGTTGAATCCTCTT
EST33488 7	90	A G	---	CCTTTGGGGGGAGTTTTAAGCCAGAATGTGACAAAGTCACTTACAGGAAGACTGGAATGTGTAGCCATAG TTGAACTCTAAACATCGTCTCTATAG[A/G]ACCATTTCCCGTCTCCAGTGGTTCTAGGCATACTAAGCT GCTC
EST33508 1b	45	C T	---	AAAAACATGCTATTTGAACAAACTTTTTATAAAGAATAAGTTGA[C/T]TGAAAGCAGTTTTAAAT AACATCAACTCACAAATGACTTTTAGAAGCCAAATAA

ID	Pos			Sequence
EST33508 1a	36	A	G	AAAAAACATGCTATTTGAACAAAACTTTTTATAAAGA[A/A/G]TAAGTTGACTGAAAAGCAGTTTAAAT AACATCAACTCACAAATGACTTTAGAAGCCAAATAA
EST33863 4	77	C	T	ACAACATAGGACTGGTTATTCTTGGTTTGAAAAATTATGTTGCCACTTCCTATTGTTTAAAAATGA TCATTTAAC[C/T]TCTTGAACTACAGCCTGAATCCCCC
EST34739 3	97	T	A	GAAGTATCCTTCCCAGTGGGCAGGAACTGAAGACTCCAGATCAACCAGGTGGACCTTTCGTTGATGA GCTGATAGCTTCTAGGCTGTGGGGGAACCTC[T/A]GGTGCCTTACAACTCCAACTACTGCAGAATTTCT TGTTGTGCCTCATAAACA
EST34792 6b	104	A	G	ACCTGACTGCTTTAAAAGCTCTTGTAAGCTGACCGTAGCACAGATCACGTGGCATCCACTATCAATA CTCATAAGTCTAATTTATCCTCAGGATGTTCCCTGA[A/A/G]GTATTCAGGAATTCTTAGTCCTATTACA AAGATTTGTTGCTGTG
EST34835 9b	93	T	G	GGAAAAATGTTCCCTTGCAAACAAGGTACGTTTATTCTGCAACTTAGGAGATAAAATGAGATTTCTG TGGGGGAGTCTATGTTGTGCTTTCTGG[T/G]GGCCTTAAAAGAAACAGACAAATTTGTGCTAAAGAT
EST34835 9a	82	G	A	GGAAAAATGTTCCCTTGCAAACAAGGTACGTTTATTCTGCAACTTAGGAGATAAAATGAGATTTCTG TGGGGGAGTCTATGTT[G/A]TGCTTTCTGGTGGCCTTAAAAGAAACAGACAAATTTGTGCTAAAGAT
EST35230 0	93	G	T	CACAAAGGTCCACTTACTTACATGAAGAAACATAAAGGCATGAGAAACAGTCATCTCAATAAAATG CAAGACATGAGCATAAAAGAGGTTCTC[G/T]GCCTTTCCAGCGTTGTTATTACAGAGAGAAACCT
EST35337 9	33	C	T	TCTTTTCAAATTTTTGATGTAGGCATTAATG[C/T]TATAAATTTCCTGCTTAGGAATGTATCTGCT ATATCTCAGAAGTTGGGCATGTTGTGTTCCATTTTACTTAGTTCAGAACTTTTCAATTTCATCT
EST35708 9	32	C	T	CTGCCCCAAATTAACTTTAGGCAAATGGAAA[C/T]AGACTTACTGTATGGGGACATTTTAAAAAG ACAGCTTAGTAATATGTTCATATGCAGCGTGTTGCTTCCCCTCTCTGAGGTTGGCACCTTTCCTGTGTG ATGTGCAAAGTGTGGCT
EST35747 9	51	C	G	ATCCAGTGCAGAGTTGTAGCTGGAGACATATTTCAACCCACAAAGGCTCCA[C/G]ATGTTAAAACGT TTCCCAACATCAACCTAATACAGTGACAGCAACACCTCCCTCCTGCCCCTTCCAGTAGGGTTGAGATT G
EST35751 9	89	C	A	TGGTCCATTATATTAAAACTGAGGGAACAAACGGTCGTGACATGGCAGAGACATTATTCAATGGAGA AGTTCCTCCCATGAAACCAAGA[C/A]CTTGTCCTCATGATAAAGTGGAGACAATAAGAAAGCCAGGT ATATAATTAAGGCCCTGA
EST36301 4	93	C	T	CACCTGTTCATTGGTTCACTGGGCTGCTATCTGTGGGGCTGATGCTCTACCAAGTGCTCTCCAGCCTACAGC AGTCAGGAGGCAGCCATGGCCCCCTG[C/T]GCTGATGGAGCTTGTAATTTAGCCCAAACTGATCTTCA GAAAGAGGTACAACAAA
EST36519 0a	33	G	T	GCCATCAGCCCCACAAAGACATGACTAAGAGCAC[G/T]GGCCCCTTGCACCCATACTGGCCTCAGCAC CTAAGACTGGACAACTTTGTACCTAATGACCGCCCCACCTGGCATATACTGGCTGGCCTCTTCTCGT CACAGGGGTCTTAGTCGT

EST366206	50	G A	GACTTTATTAGATAAGGGGTTTCGGCTACCCTCCAAAGCTCTCAGGACTGG[G/A]GCTAGGGTTTAAGGAAGGCTTATTTAAATATGGGAAATAAAATACAAAAGGGCCACACCCGATGCAAAAGACTTT
EST366900a	89	C G	CCTGTGATGTGCATGGGTGCCTGAGCAGTCGTACTTACTATGGCGTCAGACAGCTCACGTATGTCAGGAAAGGAAGTCTGGGGATTCCTA[C/G]AGGGGACATATCACACATATTCTAAGTCACTGTGTGACTCGGCTTGAGCAAGTCATTTCA
EST367299	62	C T	GAGACAGAAGCCATCAGTTAAAATGAGGTTAGGCCTCTCCTCCTAATATACTGATTGACAATG[C/T]ATATTAGCCAGGTAATGCACTTTAGCTACCCTGGACAATGCTATCCAGTGTGCTGGGAAGGGAG
EST368236	103	A T	ACTGTCTGGCCGGATGATTGGAGCTTGAAAAAAACTACCATGCCAGATCTCCACCCCAGACCAATTAGGTCAGTATCTCTGGGGGTGCTATTCAAGCAACAATT[A/T]TCTTTTATGTTCCTAAGCTCATCATGAGTTAA
EST369874	126	C G	ATGATCGCTTATGTAATTTGAGGGGCGACATGGGTAATGGGAGATACCCCACAGGACCTGTAAATATTTAAATAATATTTAACAGCTGATCAGAGGCTAAATTACAACTGACATTTTGATGCAGTTT[C/G]GTTAGGGAATTAAGACAATGCAG
EST370543	88	T C	GGTCTCACTCTCTTGCCCAGGACGGTTTGAAACTCCTGAGCTCAAGTGACCCTCCCACCTTGGCTTCCGAAAGTGCTAGGATTACAGG[T/C]GTGAGCCACCACCTGGTTCCTTGGTTTAAAGTAACCACTGAAC
EST372693b	105	T G	AATAGTCTATGGCTACGGGCCCGTGGGATTGTTAAAAAATTGGGATTTAAATTAAGATTGTGAACATG[T/G]CAGGAGAAAAAATGGGGTCCCAAACCCAGCAAATTTCTCAGCTTATATTTTGAAAGTC
EST372842	93	G T	AAAAGACCTTTCTCAAGCAGTAAACTTTGAGCAGCAGACTCAGATGAAGTAAGGGATGAACCAGGAAGCTCTCTGGATAATGTCACTCTAGGAA[G/T]AGTAAACAGGTGTTAAAACCCTGAGATAGCAACCCTCTTGGCTTGCTTGAGGAATA
EST373152a	90	A G	AGATGGGGTCTTGCTAGCTTGCTCGGGGCTGAACTAAAGATATCCTCCTGCCTCCAGGTAGTTGGAACTATAGTAGGAGTATCT[A/G]CCCTGCCCCTGCTAGAAACTTCAAGTTTGATGGGCAAATCCACCCCAGAGGACAGGACAA
EST373741	45	C T	CCTGCCATGATAATGTTAAAAACATATCAAGATCCTCCTCAAACTT[C/T]AAGGGTGAAAAGCATACCATTCCATTTAGTTGAAATATTCCTTCACATAGCCAACACATTTTTCAAGGCACTCTAGCTACTACAGGA
EST373768b	101	G C	GTGACATCATGTCTCTTCAATGCCCTTCAATTAATAGTAGTTGAGCGCTGGGGGGCTGGAAGTCAGACTCTCTGGGTTCAAATCACAGTGCTGTGTCCTCCAGGCAAGTTGCTGACTTCTCTGTGTCCAGG
EST373768a	41	T C	GTGACATCATGTCTCTTCAATGCCCTTCAATTAATAGTAGT[T/C]TGAGCGCTGGGGGGCTGGAAGTCAGACTCTCTGGGTTCAAATCACAGTGCTGTGTCCTCCAGGCAAGTTGCTGACTTCTCTGTGTCCAGG

EST				Sequence
EST37378 9	63	T	G	ACACACAAAAAAAATGGTGGCAGAAATCTGGAAAGATTCTAATAACCTCAATTCGTGAAAAC[T/G]AACATGCCTCAAAAAGAGGGGAAAAACTTAACAGAAAACACTGTGCTGACATGATTAGCTT
EST37452 4	46	G	A	AAGACATAAATCTGCAATGAAATCAGTTATGAAATATTAAACCTCT[G/A]CTTCTCAGGAGTGACACTAATCATGGTCTGGAAGCTAGCCTATCGCATTTAAAACACCTTAAAATCAATGACGTAGAA
EST37613 6	34	A	G	CTAGGCATGGGCGTTTACAGTCATTATTACC[A/G]GTCATGAATTCATTAAAAACCACAGCGATATAGCAATGAGCAAAACAGACCCTCCCCCAAAATCACCCTGCGTTCATGGGATCTTCCATTCTAA
EST38025 4	56	T	G	TTATTGAGTAGTCACTGTGGCCAGAACTAAGCTTTACATGTTTATATCACTTA[T/G]TTATCTCAACAATCTTGAAAGGGTGGGTATTATTTCCCGTCTTATAGGTGAAGACTCTGAGGTTCAGAA
EST38068 6	57	C	T	TCTACCAGGTCACCAAAGTATCTGTATATGCTTTAAGTGGCATTTCATGTCACTTA[C/T]CGCATGGAAGAACGCTCTCCTTTAATTCCCTAACTCTCTCTTCTGGGAAGACAGAACGTGCACAA
EST38420 6a	100	T	C	TAAATCAAGGCCTCTTCATTACCAAAAAACAAAAAAAAGGGAACAAAATACGATGGGGAGAGGGAAGAGAGATGATGCCGAAGTGTCATCCTGACTGAC[T/C]GTCCCTGCAGTGCCCATGGGTCCCGTGCCTTATTCATTCTCTCTCA
EST38950 5	25	T	C	TTTATTTGCAAAGTAAGCAGCCGG[T/C]TTGGTCCCTGGATTGAGGCTGAGGAAGACATTACTTCCTGCTGGAAATACTTGGGACTTACATTTGACACAGGCTAAAAGTATGGGATGAGAAGTATGAGAGGAACAAAAGCTTACAAACAAAGAGCAGCCA
EST39053 6	90	T	C	TTTTTGTTACTCTGTAGCCAGTCATTAATCTGAAGGTTTAATATATCATTTATTGGGATGAGATCATAGT[CT/TTACACAAATGCTATGT[T/C]AAACAAGTTACTGAATATTTTCACCTCGTGGAGTTG
EST39331 1	70	G	C	TCCTTCTTGCTCTCTAGCACTCAGAGCACCACCAAAGAAAAGCCTGGAAGACCAGCCATGGAAGGAAAGTATGC[G/C]GTGTTTTAGGGAGAGCTGGCACCTGGCACCTCTAATCTTCCCTCTGCCATTGACCAGATGGGTGCCTTTGGATACACTCACT
EST40544 7	31	C	A	GTCACCATTGACCTTACATAGTGCCTCTAGT[C/A]ACCTATGAGGCACTAGAACTCTATTGTACTTCTCACTTTATCACATTAGCTATCGAAGTTTGAAATTT
EST40548 4	37	T	C	TTCTAATAGCATGCCCTGTGACACAGGGAAACTAAGCTC[T/C]CTCAAAATAACTGAAACTAAATCTGTAAGATAAAAATGCTGGAATTTGAGAAGGCACATGCCTTTGTAGTTTTCTCCAGAGAGGCTCAAGGTGTTCAATAATCTGTGGGACTCA
EST40549 1	42	A	G	TGTTCTCTAGAGAAACCCTGTGTGTGATGAGATACACTACGCATGCACA[A/G]ATAAAGTCACATCAAGACTAATAATCTAAAGTGTTAGTTTGTTACCACCATTTCTCACTTGAACCTAGCTCCCTGCAAAGCACCTTCTACCCTGCACTTTGGGGAG
EST40579 1	81	A	C	TGTGAATTACACATCCAGTAAGGCAGTTTACAGAATTTCATTCTCTTACCTAAAGTCTGTGCTATCTGAGCTGGTGGAAAA[A/C]GGACTTGGAGACAGCGATTTAAATACGAACAAGGTCTTCCAGGAAG
EST40584 3	68	A	G	TTGTATGGTTGTGTAGGAATTTGGGAAGGAGAAATTATCTGTGAAGGAAGAAATTTGCCACTGTAATGCACACCCA[A/G]TCTGTACTCCCACAATATCCTATGTTTTAAGCT

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ST51340	51	G	A	GATCAAACTGTATTGCCCAGGCCAGCTCTGAGAAGAACTGTGAACTATGAAC[G/A]TCTCAGCCTAGAAGGATAATGTGACCTTCAATTGCACACCATCCATTGTCTCTTCAAACTAAGAGCCTCTCTAAGCTAGATAGGCCAAGGATTATT
04162	134	T	C	CATGGGAGTAATAAGAGCAGTGGCAGCAGGATCTCTGAACATTTCTCTGGATTTGCAACCCCATCATCCTCAGGCCTCTCTACAAGCAGCAGGAAACATAGAACTCAGAGCCAGATCCTTTATCCAACTCTCGA[T/C]TTTTCCTTGGTCTCCAGTGGAAGGGAAAAGCCCATGAGTCTTCAAGCAGGAAGCCCAGTGAGTAGCTG
K01506	63	T	C	CTGAACTCCAGCTGCCCTACAAACTCCATCTCAGCTTTTCTTCTCTCACTTCATGTGAAAACTAC[T/C]CCAGTGGCTGACTGAATTGCTGACCCTTCAAGCTCGTGTCTTATCCATTACCTCAAGCAGTCATTCCTTAGTAAAGTTTCCAACAAATAGAAATTAATGACACTTGGTAGCACTAATATGGAGATTATCCTTTCATTGAGCCTTTATCCT
18877	69	T	C	TGAGTCTGAGCACGAGTTGCAGCCAGGCCAGTGGGAGGAGTCTGGGCGAGGAGTCGGGGCCAGTGCCACCTTCCAAGGCC[T/C]ATCCATTAGTTCCACTGCCTCGTGTGACATGAGCCATTCTTCACTCTTTGAAGAGAGCAGTCAGTATTGTTAGTAGTGAGTTTCGTGTTCTATTGGATGACTTTGAGATTTATCTTTGTTTCCTGTTGGAATTGTTCAAATGTT
31848	36	T	C	GCTATTTTACATATCCCAAGCCCTTTAGGGCTACAG[T/C]CTCTCTGTCCTGGACCCTGTAGGGTGCCATTTGGAGTTCACAGCCTAGAGAAGAAAAGGCTTGGGCCTGGTGTGGCCATAGGCCTGTAATCGTAGCGGCTTGAGAGGCTGAGCTCAGGAAGATAGCTTGAGCTCAGGAAGTTCAGGAGAGTTCAGGAAGTTGAGACAAAACCTGGGCAATGT
38517	137	G	C	GGGTCCAGAAGCCTCTCAGCCAGGAGGAGGCTGGCTCCTGCCATCTCCTCTGCCATGAAGATACACCATTGAAGACTTGACTGGCAACCAGCGTCCCCACCC[G/C]CGTGGTGGTGTAGTCATAGAGCTGCAAGCTGAGCGGGGACTGGGGGGACACTGGCCTCCTAGAGACCTTGAG
39059	123	T	G	ACTTGAGAAGCAGAGCAGCTCGCCACCTTCTGGAGGCCACTGTGATGATGAGCCAAGCAATTTGGAGCCAAGTTGAAGGGACAGGGCAACAAAATACAGTAGTTTCTTTTGTATTT[T/G]CGCCTGAAGATCATCCCGCACCAGCCAGGTGCCGGTGCCTTGGCGTGCCGGTGGATGGTTGTTGACCCCTCTGAG
41268d	173	G	A	CAAAGTTGTCTCCTGCCCATGAGCACCACAGTCAGGCCTTGAGGGGATCTTCTCTAGGGAGGACAACAGCCCTGTCTCAAAACTGGGTTGCCAGTCCAATCGAACTGAAGGCGTGAGTCTGCATCTTAGGGGCATCGCTCTTCCTCACACCACAAATCTGAAC[G/A]TGCCCTCCCTTGCTTACAAATGTCTAAGGT

ID	Pos	Alleles	Sequence
L48728b	111	T C	AAGTGAACAGAAAGCAAAGATGGATTGTGTTCCTATAAAGCACATAGTTATGTTTACTGGTATCGT AAGAAGCTGGAAGAAGAGAGCTCAAGTTTTGTTGTTTACTTCAGAA[T/C]GAAGAACTTATTCAGAAAG CAGAAATAATCAATGAGCGATTTTTAGCCCAATGCTCCAAAAACTCATCCTGTACCTTGGAGATCCA GTC
M18079	52	G A	GCGCACAGTCCAAAATACAAAATTGGACAGAAGATCTATATTGTACCAGAACT[G/A]TTTATTTCACC CCATCAAGTATAAGGTTACTGATTGGTCCTTTTATAAACATTGGTATATTTCCATTCCATGCCAA AGCAAAAGAAGTAAAAGCTAA
M19169	113	T C	TAGGGATCTGTGCCAGGCCATTCGCACCAGCCACCACCCTCCCACCCCTGTAGTGCTCCCCACCCC TGGACTGGTGCCCCCACCCTGCGGGAGGCCTCCCCATGTGCCTGT[T/C]CGCCAAGAGACAGACAGAG AAGGCTGCAGGAGTCCTTTGTTGCTCAGCAGGGGCTCCGCGCCCTCCTTCCTTCTCGCTTCTAATA GC
M21539	114	T G	TCACCTCGTTCCACAGCTCCACCTGCATCTTCTCATCAAAGCCATCCAGGGATACACAGGGAGCTTCT TTCCCCTTAGCCTGTGATCTGCCCATGATGATCCCGACAGCAAAA[T/G]TTCCTTTCTGAGGCTG CCATGCTGCCACTGTCCAGGTGGAGACTGAGCAAAGGAAGTCCTCAGCTGTACCGGCCTTTCAGAGCT TCTCTTGGGTGC
M26041c	173	A G	CCTAGCATTATTTTCTGGCCCCATTATCATATCCCTTTCTCCTCTCCAAATGTTTCTCTCTCCACCTCT TCTGTGGGACTAAATTGCTATATCGTCAGAGCTCACAAATGCCTTTGAATTATTCCCTGACTTC CTGATTTTTTTCTTTACCTTACCTACTACTAAG[A/G]GATGCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M26041b	157	A G	CCTAGCATTATTTTCTGGCCCCATTATCATATCCCTTTCTCCTCTCCAAATGTTTCTCTCTCCACCTCT TCTGTGTGGGACTAAATTGCTATATCGTCAGAGCTCACAAATGCCTTTGAATTATTCCCTGACTTC CTGATTTTTTTCTTCTCA[A/G]GTGTTACCTACTACTAAGAGATGCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M26041a	45	C G	CCTAGCATTATTTTCTGGCCCCATTATCATATCCCTTTCTCCT[C/G]CAAATGTTTCTCTCTCACC TCTTCTGTGGGACTTAAATTGCTATATATCTGCAGAGCTCACAAATGCCTTGAATTATTCCCTGAC TTCCTGATTTTTTCTTTCTCAAGTGTTACCTACTACTAAGAGATGCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
A63967	57	G C	TAAGGCAGCTGTCAGGGAGGCCAGTCACAGTCCAGCAATTCCACAACCACCTTGAC[G/C]AATGCT TGCCAAGCTGTTTAAAGCCAAGAACACCCTTCTTGTTCCAAATTAACTCTTAGAAGAAACCCCA CAAATAAAGCAATTCAATC
A81695	34	G A	ACTTACTTACCCTCACCTGTCCAGGCTGCAGGGGA[G/A]GAACCACTGCACCACGAGAGAGGCTGGG ATGGGCCTGCTTCCTGTCTTTGGGAGAAAACGTCTTGCTTGGGAGGGGCCTTGTCTTGTCTTCAAGGTTC CAACTGGAAACCCTTAGGACACAGGGTCCCTGCTGTTCCCCAAAGGACTTGACTTCAATTTCTACC T

ID	Pos			Sequence
U06641d	166	C	T	CTCCTCCTTTATTTCAGCATGGAGGGGTTTAAATGGAGGATCTCCTTTCTCTGTGACAAACATCTTTC ACAACTTACCTTGTTAAGACAATTTAAAAAAGATCTTTCACAACTACCTTGTTAAGACAAATT TATTTTCCAGGCTATTTAATACGTACTTTAG[C/T]TGGAATTATTCTATGTCAATGATTTTTAAGCTA TGAAAATACAATGGGGGA
U09607	39	T	C	GAGGCCCTTATGAGGGGTCCTCTACTTCAGGAACACCCCCA[T/C]GACAATTGCATTTGGGGGGGCTCCCG TGGCCTGTAGAATAGCCTGTGGCCTTTGCAATTTGTTAAGGTTCAAGACAGATGGGCATATGTGTCAG TGGGGCTCTCTGAGTCCTGGCCCAAGAAGAGCAAGGAACCAAATTTAAGACTCTGCCATCTTCCCAAC CCCTTA
U09608	82	T	C	GAGCAGAAGGCAAGAGAGCGGCAAGATGAGTTTTGAGCGTTGTATTCCAAAGGCCTCATCTGGAGCCTC GGGAAAGTCTGGTCC[T/C]ACATCTGCCCGGCCCTTCCCCAGCCCCTGCCCTGCTCTCTTGTTCTTC ATTCATTCAACAAAATTTGGC
U10694	20	C	G	GTGACATGAGGCCCATTCTT[C/G]GCTCTGTGTTGAAGAGAGCAATCAGTGTTCTCAGTGGCAGTGG GTGGAAGTGAGCACACTGTATGTCATCTGGGTCCTTGTCTATTGGGTGATTTGGGAGATTTATCCTT GCTCCCTTTTGGAATTGTTCAAATGTCTTTTAATGGTCAGTTTAATGAACTTCACCATGCGAAGTTAA TGAATGACAGTA
U13877b	162	T	C	AAAAAGGACTCTGGTTCAAATCCAGGTTCCATTTGCTATCTTTGTGACCTTGCACAAGTTGTTTAAC CTCTTTGTTCAGAAATTTCTCCATGGAGTAACAATATCTAGGTGGGAGGATTAGTAGAAGTTACATGT AAAGCACAGAGAGGAACAGCCAAGAGAT[T/C]TACCGTGGTCTTACTAAGTACATATCCTAACTTGG GGTTTACCTTCAGCA
U15555	187	T	C	TTTCTGTCCACTTCACCTGGTTTTAATAGCCAGCCAGTCATAATAGTAGAGGAATCAGTCAAGCAA AAATGCTTTGGAAGAATTAAATAAGCAATGCTGAACATCAGGAATTGTAGATATCCGTACAGAGAGT TCCAGTAAAAATTTATGAGTCCACGACCCCTTTTCTAAGCAGTCGTGGTCCATG[T/C]TGGTCTCATAC CTCATATGCAGGATTCATTCA
U17077	122	T	C	TCCAATTATTGGTCCCCAAAGCAGCTTCCAACGTTTGCCATCTGGATGACAAACGGAAGATCCACT AAAACGTCCACGGATTAAACAGAACGTCCTTGCGACTGAGCGATGACACCACACT[T/C]TTGTTTGGG ACATTTAAATTCACTCTGCTGAATAGGAGGAAGCTTTTTTTCCTGGGAAAACAACTGTCTCTTGG AATTA
U18543	58	T	C	GCACATGCAGAATAGACTCAGCCTATGTCCTGATTCCAGCTGGGTAGTTCTAGAACTT[T/C]AGAAG CTCCATCTTTAATGTTTATTTGTTATGTCCCCGGCTTCCCACCTAAATTTAGAGCTTAAA AGATGCACTGCCCAAATAGGACACACGATGGTGTTAGCTGAAGTTTGATTAGCAATTAGGCACTTCC AAGGCTTTAGTAGTAGAGAGCC

ID	Pos	Allele 1	Allele 2	Sequence
J25975b	164	C	A	TCACTGCTGTGGCCTCATACTCTTTTTCCATTTCTACAAGAAGCCTTTAGTAGTATGAAAAATTATT ACTCTTTTGGGGTTAAAGAAATGGTCTGCATAAACCTGAATGAAAGAAGCAAATGACTATTCTCTG AAGACAACCAAGAGAAATTGCAAAAAGA[C/A]AAGTATGACTTTTATATGAACCCCTCTTTAGG GTCCAGAAGGAATTGTGGACTGA
J25975a	143	C	G	TCACTGCTGTGGCCTCATACTCTTTTTCCATTTCTACAAGAAGCCTTTAGTAGTATGAAAATTATT ACTCTTTTGGGGTTAAAGAAATGGTCTGCATAAACCTGAATGAAAGAAGCAAATGACTATTCTCTG AAGACAAC[C/G]AAGAGAAAATTGCAAAAAGACAAGTATGACTTTTATATGAACCCCTCTTTAGG GTCCAGAAGGAATTGTGGACTGA
J25997	61	A	G	CAGGGAGAGGTTATTCACAACCTCACCAAACTAGTATCATTTAGGGGTGTTGACACACCA[A/G]TT TTGAGTGTACTGTGCCTGGTTTGATTTTTTAAAGTAGTTCCTATTTTCTATCCCCTTAAAGAAAATT GCATGAAACTAGGCTTCTGTAATCAATATCCCAACATTCTGCAATGGCAGCATTCCCAACCAACAAA TCC
J28413	29	C	T	ATTCCTGACAGCTAAATTAGCCCTAAATG[C/T]GGGTAATATATTTTCCTCATGTTTTAAAATGAGGTT AATATTTGCATAAAAATCCTAAAACAGACTTCTGTATAGTTATTTAGTCAAAATGTGTTCCTTGATCC CAGATGTTGTGTGGGCCTGGGAAAGCCCCTCATTGCTACAGTACAACACAAGTCGTTGTACCTCAGTT G
J30884c	89	A	G	TAGGGGTAGCATTAAGATTCAGGAGTCATTAGCCA[A/G]GTGATGATTTGGGACCTGCCGTATAATCT GTTCTTCTTATTCCCACGTTAGCCAATTGTTCTTGATGAATCTATATGAGTCATAGAACACAAATCTAT TGACGGAAGTCATTAGAATGGCTTGTGATATCTGATGGCTTGAACTTGCCCACAGTTGAACACAAGT GCTGTGTCA
30884a	34	A	G	TAGGGGTAGCATTAAGATTCAGGAGTCATTAGC[A/G]GTGATGATTTGGGACCTGCCGTATAATCT GTTCTTCTTATTCCCACGTTAGCCAATTGTTCTTGATGAATCTATATGAGTCATAGAACACAAATCTAT TGACGGAAGTCATTAGAATGGCTTGTGATATCTGATGGCTTGAACTTGCCCACAGTTGAACACAAGT GCTGTGTCA
31216b	78	A	G	GGGACAGCAGCATATGTGGCACCGCCTCTCTGTGCACGTGAAGACCAATGAGACGGCCTGCAACCAAACA GCCGTCATCAA[A/G]CCCCTCACTAAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTCAGATA CCAGCACCAAGACCCTTTACAACGTAGAGAGGAGGAGGATGCCCAGCCGATTCGCTTTAGCCCGCC TGGTAGCCCTTCCAT
31216a	70	G	A	GGGACAGCAGCATATGTGGCACCGCCTCTCTGTGCACGTGAAGACCAATGAGACGGCCTGCAACCAAACA GCC[G/A]TCATCAAAACCCCTCACTAAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTCAGATA CCAGCACCAAGACCCTTTACAACGTAGAGAGGAGGAGGATGCCCAGCCGATTCGCTTTAGCCCGCC TGGTAGCCCTTCCAT

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U31416c	76	G	A	AGTTGCCAGCTCCCATGTACCAGCAGCTGGAATCTGAAGGCGTGAGTCTTCATCTTAGGGCATCGCTC CTCCTCAC[G/A]CCACAAATCTGGTGCCTCCTCTCTCTTGCTTAGCCCACAGTTGTCTAGGTCCCCACTGCTGCT GGAAAGAAAACACACTCCTTTGCTTAGCCCACAGTTCTCCATTCACTTGACCCCTGCCCACCTCTCC AACCTAACTGGCTTACTTCCT
U31416b	68	C	T	AGTTGCCAGCTCCCATGTACCAGCAGCTGGAATCTGAAGGCGTGAGTCTTCATCTTAGGGCATCGCTC [C/T]TCCTCACGCGCCACAAATCTGGTGCCTCCTCTCTCTTGCTTACAAATGTCTAGGTCCCCACTGCTGCTG GAAAGAAAACACACTCCTTTGCTTAGCCCACAGTTCTCCATTCACTTGACCCCTGCCCACCTCTCCA ACCTAACTGGCTTACTTCCT
U37519a	78	C	T	ACGGGTCACACAGAGAAACCTGAGTCTAGCCATGAGGGGCTTATGCTCCCAACTCACATTGTTCCTCC AGACCGCGCAGG[C/T]TCCCCCAGCCTCAGGTTGCTGGAGCTGTCACATGACTGCATCCTGCCTGCCAGG GCTGCAAAGCAAGGTCTTGCTTCTATCTGGGGGACGCTGCTCGAGAGAGGCCGAGAGGCCGCAGAAC ATGCCAGGTGTCC
U37690	54	A	G	GACCACGCTGAAACCCACCCACCCGCTGTGCTGACCATGGGCCCTGAGCGTCCT[A/G]CCCGAATTC ACGAGGCTGAGGCATCCGGGAGCTGGCCGTAATGCTGCGGCCGCAGTGTGTGTATCCCATACCCCACT CTGGAAGGAACCATCCAGTAAGGTCTTT
V00540	39	T	C	TGAAACCGTTTCAACATGGAAATGATCTGTATTGACTAA[T/C]ACACCAGTCCACACTTCTATGACT TCTGCCATTTCAAAGACTCATTTCTCCTATAACCACCGCATGAGTTGAATCAACAAATTTCAGATCTTT TCAGGAGTGTAAGGAAACATCATCATGTTTACCTGTGCAGGCACTAGTCCTTTACAGATGACCATGCTGAT A
X15943	106	A	T	TCAAGAAGGTGACTGCCCTTGTATGATGGGATGGGAAGATGAATGACTGGTTTTTACTGGGGTGTAA AACCACTCTGAGCCTCTCTGAGACCATGTGGTTTAAAA[A/T]ATCCATAAGGGAAGGTACCCACAC CAGTATCTGAGTTCCAGTAGCTAAGACCCTAGAAATTTGGATTCATCTCTGTTTTTCATGTCTCTCCTT GTAACCCTGAGATCATCAG
X52011b	148	C	T	AGGAAGATCCCACCGACCCTTCCTGGCCTAATCCTTTAGATTAGGTCACATTAACATTAGGA ACCCAGACCGAAAAGTTGCTGAAAGGGAAGGAGACACATTCACAAAGAAAGAAAGTTGCGAAAATTGCG AAATCTGTTTGTGCA[C/T]GCTCAAATGAAAAGCGCCTTTGGGCTTTATTTTTTGGAACTG CGAGTGGCTTAGGTCTAGCCT
X52011a	118	A	C	AGGAAGATCCCACCGACCCTTCCTGGCCTAATCCTTTAGATTAGGTCACATTACATTAACATTAGGA ACCCAGACCGAAAAGTTGCTGAAAGGGAAGGAGGAACATTCACAAAGAAA[A/C]GTTGCGAAATT GCGAAATCTGTTGTGCACGCTCAAATGAAAAACGCCTTTGGGCTTTATTTTTTGGAACTG CGAGTGGCTTAGGTCTAGCCT

ID	Pos				Sequence
X54741	24	A	G	---	CAGGCCACCTGTCTTCTCTCCCAC[A/G]TGCACAGCTTCCTGAGTCACCCCTCTGTGTCCAGCCAGCTCCT GCACAAATGGAACTCCCAGGCCTCCAGGACTGGGGCTTGCACAGGCTTGTCAAATAGCAAGGCCAG GGCACAGCTGGAGACGATCTTGCTGGCCAGGGCCCTGGTCCCCAGCCCACCTGGCCCCTTCTCC AGCAAGCAGTGC
X54869	99	A	G	---	AAGCATTTGCGTTTACAGTGCATCAGATACATTTATATTTCTTAAAATAGAAATATTATGATTGCAT AAATCTGAAAATGAATTATGTTATTTGCTCT[A/G]ATACAAAAAATTCTAAATCAATTATTGAAATAG GATGCACACAAATTACTAAAGTACAGACATCCTAGCATTTGTGTCGGGCTCATTTGCTCAACATGGTA
X66924	147	G	A	---	GCCGTGTCCTGACACCTCCAGAACGCAGGTGCTGGCGCCGTTCTGCCTGGGACCCCGGAACCTCTC CTGCCGGAAGCCGGACGGCAGGGATGGGCCCCAACTTCGCCCGTGCCCTGACTTCACCAAATCCCT TCCTTGGAGACT[G/A]AACCTGGTGCTCAGGAGCGAAGGACGTGAACTTGTGGCCTGAAGAGCCAGA
X78932	62	T	G	---	GAAATGTGAAGAATGTGACAAAGCCTTAAGCGGGTTGTCACACTTGATTGTATATAAGATAA[T/G]T CATACTGGAGAAAACTCCCAGAAGTGTGACAAATGTGACAAAACATTTAATTCTCTATACCTTA TTGCACAGGAAAGCATTTATACTTGAGAAAAATTGTATAAAAGAATGGAAAAGTCATTTATATCTGCT CATATCTTAACATCAGCGAGTT
X80026	25	T	C	---	CTCAACCCATAAACCTCAACCACATC[T/C]TATCCTCCACCCACATCCACCTCCATCC CCAACCCATCCTCATCCCCAACTCACAGCCCCAGACTAATCCAGCCATCCCAA CTCATCCTCATCCCCAACTGCAGCCCCAAACCCAAGGCCCATCCCCAAACCCAAGCC AAACTCAACACCATCC
X80197b	99	G	C	---	ACCCCAACTCAAGTCCCAGGCCCCAGGCATCTTTCCTGCCCTGCCTTGCTGGCCCATCCCAGTCCAGG CGCCTGGAGCAAGTGCTCAGCTGCTTCTCCTG[G/C]CACTTTGAAAGACCCCTCCCACTCCTGGCCTCA CATTTCTCTGTTGTGATCCCCACTTCTGCGCCTCTGCCCTTGCTTCCTTGCCCATCCAGTCC
X80197a	28	A	G	---	ACCCCAACTCAAGTCCCAGGCCCCAGGC[A/G]TCTTTCCTGCACTTTCTCCTGGCCTCA AGGCCGCCTGGAGCAAGTGCTCAGCTACTTCTCCTGCCCCCACTCCTGGCCTCA CATTTCTCTGTTGTGATCCCCACTTCTGCGCCTCTGCCCTTGCCCATCCAGTCCCCACCCTAGAAAG
X85106	150	G	A	---	GGCACCCAGAGTGACCACAAGTCCAGCAGGAGGCCGCCGCCCTGCCGGGGTCCGCGTGTCCGTCGT CAGCGCCCGGAGGAGGTCCTGACCTGGGGGCTTCCAAGCCTTCACCCATTTCACCCGCTCT CTTTTCTCCCAAGC[G/A]AJAAACCAAATGCGCCCCTTCACCCTGCGCGCCCGTGCGGAGGCCGGGGGCTT CTTTCAGAGC
X87160	128	T	G	---	ACCACCAGCCATGGTCTCTAAGGACATGGATCGCGGGGTGCCCCAGACGTGTGCACAGGGGACCCCTGCCC CACTCTCGGGCTTTTCAGATACTCTGACCAAAAAGCCTGCTTTAAACCGCAACAGAATGGGGCC[T/G]GGGGC ATGCGCAGGAGGAGCCATCGGGGTACTACGCGCAGCAACACTCACAACGTCCAGGCTGAGATAAAATCCC GGGA

ID	Pos	Alleles	Sequence
X87344	34	C|T	CATCCCAAGGCACTGGTGGTGACTCTGCTTCCTG[C/T]ACTGACCAGAGCCTCTGCCTGTGCACTGCAAGCTGTGTCTACTCAGCCCCAAGGGGACTCTCTGTTTCCATTCTCCCCCCAGACCTGTCAAGAGAAGCATGACAAACAAAATCATTTACCGACTTTAGTGCTTTTT
X87838	179	G|T	GGTGGGCTGGTATCTCAGAAAGTGCCTGACACACTAACCAAGCTGAGTTTCCTATGGAACAATTGAAGTAAACTTTTGTTCTGGTCCTTTTGGTCGAGGAGTAACAATACAAATGGATTTGGGAGTGACTCAAGAAGTGAAGAATGCACAAGAATGGATCACAAGATGAATTTA[G/T]CAAACCCTAGCCTTGCTTGTTAAAATT
Z14138	81	A|G	GTTCTGCTGCCTCTACACAGGGCCCTGTACAGTGAATGGTGCCATTTCGAAGGAGCAGCAGTGTGACCTCCTGTGACCC[A/G]TGAATGTGCCTCCAAGCGGCCCTGTGTGTTGACATGTGAAGCTATTTGATATGCACCAGGTCTCAAGGTTCTCATTCTCAGGTGACGTGATTCTCAAGGCAGGATTTGAGAGTTCACAGAAGGAT
Z18859	191	A|C	TAATCCTCACCATTCCTCAGGTATAAGTTCTATAAACAGGCTTGGAATCTGGTAATTAAAAACAGAAAATTATAGTCAATATACCATGAACATGAAGAATGAATCCATTCTTTGGAGATGGAGTATACACATGACTGCAACTGTATTTCATACGTTCTTTTCAAAGTGGGATAGCTATTGCAGCTTAAAGAGC[A/C]CAGGTTCCAGTACTGGTTTTCCAA
23091	159	G|A	AGAACCTGACCAGATGTGGCTCGGAGGGGAATCCAGACCCGCTGCTCTCCCTCCCCCCACTCCTCCTCTCTCTCTCTCTCTCTCCTTCCCTCTCCTCTCTCCCCCTCTCCGCTCTGTGTCTCATTCTCAC[G/A]GCCCGGCCCAACCCCTCTCTCGTCCCCGCCCGTCTCTGGAAACTGAGCTTGACGTTG
1595b	125	A|G	GTTGGCATTGTTAGTAAACTTCATAGGTGAAGAGGAGATCAGTCAGTGAGATTAAGTTATTTATCAAAGTGTGGTTTCTGCAAGGGCAGGTTGAAACCTGACCCAGTTGTGCTCCAGGACCTA[A/G]GCGTGCTCACTCTACCTTGTCTTTGTTGTTGAAAGGAGTGGTTTCCCATGACTGTTAAGTGACAAGTGCCATGGATATCTACACGTCACCAGACTAGATTGTCTCAATGTCCTTGGCTTGCGAC
11595	125	A|G	GTTGGCATTGTTAGTAAACTTCATAGGTGAAGAGGAGGATCAGTGAGATTAAGTTATTTATCAAAGTGTGGTTTCTGCAAGGGCAGGTTTGTTGAAAGGAGTGGTTTCCCATGACTGTTAAGTGACAAGTGCCATGGATATCTACACGTCACCAGACTAGATTGTCTCAATGTCCTTGGCTTGCGAC
1241	131	G|T	TATATCACATTAGTAGTATGTCACTGCCATGGTCACGGTAAGGACTTGATCACTAGGAAATAAGAACACTTTGAATGGTCTTGTCCTTTCAATAAAAGAGTGACAATGATTGAACATGTGTTTAGATAAAGGCACTTT[G/T]GCAGGAGTGTTAGGGATGAAGAGAGAGAGGATTAAGGAAGAGATCAGGAAGAAAAGTAGCAATGGGAATGAAAATAGGAGGGCCCTGAGATCCACTGGATAATCTAAAAAACCAAGAGAAAG

1282	130	C/T	GTGCGGATCACCACTACAGTCTAAATTCAGATGTTTCATTACCCCTAAAAGAAATCTTGTACCCATTA GCAATTATTCCTCATTCCTGCCCTCACCCCCAGCGCCCTACTCTTTATCGCTATAGATTTGCC[C/T]ACT TGACATATCATCACACATGGAGCCATACATATGTGTGCCCTTGGCTTCTTCACTGAGAATA ATGTTTTCAAGGT
6810	68	C/T	AGTATCACACACTACTTAATATATTAGATATATACACAATAATAAAAATCACTCCCTACCTTGAAAACTTT A[C/T]AGAAGGCATTTTAATTTACAACACAAAGCTCAAACAACCTACAAATGTCTAGTAGTCTG TTTCTTTTGGAGTTCTGCGAGAGCAATGAACAATGAACAATTAACCCTTAAAAATGTCTATGAACAAGTACAA GGC
6817	118	A/C	CCAAGTACAGTGGGTGAACGATGAGCTAGCTGTTCTAGTATTGCTTTTGTAATCCAGTTAAGACCA TCAGCATATACAACATCATCACTAACTCAACAATGTAGCTGCAGGGTAAC[A/C]TGTGGATACCCTG TGTGCTCTACTGGCCTCCAAAGGCATTCAGGGGGATCATCAAAGATGTTGGACACCTTGTGTTCAAATC TTGGTTCAGGTGCTGCGGCCGTGTGCAGATCGGCTTTTGGTTGGTTGTCTTAG
8819b	212	C	CCATTTTATTTTTCTCTAAATTTTAAAATAGAAGACTTTAATGGAAAACATTTAGTACCATCATGTCA CCCTGAATGCCAGCAATACCTCGACTTTACACACGCAGGAAGCCTAGTAAAAGCCCCGTCAGTAGT ACACATTTCTCTATGGTCCTTCAACAGTTTGCATATACAAAATTTCTGCTATTTTGCTATTTTTAGCAAA CAGCAATAACTTTGTGTTCCTATATGACACCTAATATCCA
8819a	166	G/T	CCATTTTATTTTTCTCTAAATTTTAAAATAGAAGACTTTAATGGAAAACATTTAGTACCATCATGTCA CCCTGAATGCCAGCAATACCTCGACTTTACACACGCAGGAAGCCTAGTAAAAGCCCCGTCAGTAGT AAACAGCAATAACTTTGTGTTCCTATATGACACCTAATATCCA CTGGTATGTCATAAGCAATCCATAATTGTTATAGCTATT[A/G]TTATACTATGGCACCATTTGGGACA TTAACAAAAGAAAATGAACGTCTAGG
81xx	39	A/G	AGGATTCCCTCTCTTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCCTCCTCTGTACCT CTGGTAGAAATTCGGCTGTGAATCCATCTGGTCCTGGACTCTTTTTGGTTGGTAAACTATTGATTATTGC GAGTGTATGTGTCGAGGAAT
972b	149	G/T	AGGATTCCCTCTCTTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCCTCCTGTACCT CACAATTTCAGA[G/T]CCTGTTATTGGTCTATTCAGAGATTCAACTTCCTCCTGGTTTAGTCTTGGGA
972a	122	A/G	AGGATTCCCTCTCTTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCCTCCTGTACCT TTGCCACAATTTCAGAGATTCAACTTCTATTGGTCTATTCAGAGATTCAACTTCTCTGGTTTAGTCTTGGGA GAGTGTATGTGTCGAGGAAT

	Pos	Allele	Sequence
598k	210	A|C	AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCAAGCCAAAGGAACTCAATGAAATAAGCCGCTAACCAGATTTTACCTTGGAGAAATGAAAATTATTCTTGAGGATGCCTTTAATATTTGATCCCCATTATGTGAGAGATTTCCTGATATTGTTATCTTATTTATATTTCCCGTATTTTCCTCAATGCAG[A/C]
598j	208	A|T	AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCAAGCCAAAGGAACTCAATGAAATAAGCCGCTAACCAGATTTTACCTTGGAGAAATGAAAATTATTCTTGAGGATGCCTTTAATATTTGATCCCCATTATGTGAGAGATTTCCTGATATTGTTATCTTATTTATATTTCCCGTATTTTCCTCAATGC[A/T]GA
598i	192	G|T	AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCAAGCCAAAGGAACTCAATGAAATAAGCCGCTAACCAGATTTTACCTTGGAGAAATGAAAATTATTCTTGAGGATGCCTTTAATATTTGATCCC[C/T]ATTATGTGAGAGATTTCCTGATATTGTTATCTTATTTATATTTCCC[G/T]ATTTTCCTCAATGCAGA
598h	144	C|T	AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCAAGCCAAAGGAACTCAATGAAATAAGCCGCTAACCAGATTTTACCTTGGAGAAATGAAAATTATTCTTGAGGATGCCTTTAATATTTGATCC[C/T]ATTATGTGAGAGATTTCCTGATATTGTTATCTTATTTATATTTCCCGTATTTTCCTCAATGCAGA
598g	142	C|T	AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCAAGCCAAAGGAACTCAATGAAATAAGCCGCTAACCAGATTTTACCTTGGAGAAATGAAAATTATTCTTGAGGATGCCTTTAATATTTGAT[C/T]CCATTATGTGAGAGATTTCCTGATATTGTTATCTTATTTATATTTCCCGTATTTTCCTCAATGCAGA
598f	120	A|G	AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCAAGCCAAAGGAACTCAATGAAATAAGCCGCTAACCAGATTTTACCTTGGAGAAATGAAAATTATTCTTG[A/G]GGATGCCTTTTAATATTTGATCCCCATTATGTGAGAGATTTCCTGATATTGTTATCTTATTTATATTTCCCGTATTTT
598e	83	C|T	AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCAAGCCAAAGGAACTCAATGAAATAAGCCGCTAA[C/T]CAGATTTTACCTTGGAGAAATGAAAATTATTCTTGAGGATGCCTTTTAATATTTGATCCCCATTATGTGAGAGATTTCCTGATATTGTTATCTTATTTATATTTCCCGTATTTT
598d	77	C|T	AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCAAGCCAAAGGAACTCAATGAAATAAGC[C/T]GCTAACCAGATTTTACCTTGGAGAAATGAAAATTATTCTTGAGGATGCCTTTTAATATTTGATCCCCATTATGTGAGAGATTTCCTGATATTGTTATCTTATTTATATTTCCCGTATTTT

7598c	56	A	G	AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGAGACACCCAAGCCA[A/G]AGGAAC TCAATGAAATAAGCCGCTAACCAGATTTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCTT TTAATATTTGATCCCATTATGTGAGAGATTTCCTGATATGTTATCTTATTTATATTTCCCGTATTTT CCTCAATGCAGA
7598b	47	C	G	AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGAGACA[C/G]CCAAGCCAAGGAAC TCAATGAAATAAGCCGCTAACCAGATTTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCTT TTAATATTTGATCCCATTATGTGAGAGATTTCCTGATATGTTATCTTATTTATATTTCCCGTATTTT CCTCAATGCAGA
7598a	30	A	G	AAAGGTAAATCAAAGTTCCCTCTATAAATT[A/G]TGATTTACAAAAGAGACACCCAAGCCAAGGAAC TCAATGAAATAAGCCGCTAACCAGATTTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCTT TTAATATTTGATCCCATTATGTGAGAGATTTCCTGATATGTTATCTTATTTATATTTCCCGTATTTT CCTCAATGCAGA
7998c	116	A	T	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCCTATTCAGACATCTTGCCAGCTCTCCTGTA ATACTTTAATGAATGGGTAGTCCTATCTTCTCAAGGTCCCCAAATA[A/T]CCTTGAGGTTCCT
7998b	94	A	C	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCCTATTCAGACATCTTGCCAGCTCTCCTGTA ATACTTTAATGAATGGGTGTAGTCCT[A/C]TCTTCTCAAGGTCCCCAAATAACCTTGAGGTTCCT
7998a	75	A	T	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCCTATCTTCTCAAGGTCCCCAAATAACCTTGAGGTTCCT ATACTT[A/T]ATGAATGGGTGTAGTGGT
8071	119	A	G	AAATACAGAATTTATTTAGAAACTGTTTAAAGTAGAAAAAAACCCTGTCAAGAAAGACCAGGTGG AAAATGGGTCCCAATAAAATGGAATTTAGGGCAACAAAAGTCTAAAAGGCC[A/G]CAAAAGAGA AATAGCACCACTGTCATTGAACAATGGCTAGTTACTTGCATTTTTGGCATTGTTAATCACTGAATC TGGGTTTCCTCTGAATTCCACACAGAGCACTGCACAACATTTTATCAT
8467b	93	C	T	AAGGCTTTCCTCTAAACATCAGTCCTACGGAGAAATCTGGGATATTGGCTTATCACTT TGACGCAAAATCCACTTGCTGTAA[C/T]GGTCATCCGAACTCCCTCAGAGAGCAAGCAAGCAAA TTAAGTGTGATACTGGAGCTTGCATGCAAAAGCTTGCAAAAAGTATTAAGGAAAAATTACTG
8467a	70	A	G	AAGGCTTTCCTCTAAACATCAGTCCTACGGAGAAATCTGGGATATTGGCTTATCACTT TG[A/G]CGCAAAATCCACTTGCTGTAACGGTCATCCGAACTCCCTCAGAGAGCAAGCAAGCAAA TTAAGTGTGATACTGGAGCTTGCATGCAAAAGCTTGCAAAAAGTATTAAGGAAAAATTACTG
8498	84	C	T	AGGGTTCAGGGTTTGGTTTTAAATCAGGCTGCACACCTTTCAAATCAATCTGACATCTCTCTATGTCA AACTGGCTTCCAGCTAGIC/T[AATACTTCATTCATTAAATGAAAAAATTGCTTAAGGAAAAAA AATCCAGTTTTAAGAACAATTAACATTAGTCTTTAAAATAAAAGGAGGCTAATGTTTCATGTTGCT TTATACATCCTTCTCCTCAATACAGAACCAGGAACTGTAATTTCCTAACTCAG

ID	Pos			Sequence
WI-18562	29	G	A	CTAAGGAAAAATTTAATGATGGAAATATC[G/A]ACAAATATTCAACATCATTAAAAACAAAGTAGCTTCTCTTATTCACATAGCTTAGTTTGGGATAGAAATAGAACTAATGTTTACAATGATTCTTACATTTAGCATTAATCAGAAACGA
WI-18618	51	A	C	ATAGCAGACTTTAATCAATGCCAGAGACAAAGTGAGGCCGAGCTAAGAACIA/C]CGCTCGAGCTTCGTTACAATGAAGAAATGGTTTCCTTCGATGCAAAGTATAATTGTAAACCACAGTGCTCGCACAGTTCAC
WI-18683	22	C	T	TAAGCTGTTCAGGACTGGACTC[C/T]GGTCCCTTATTGAGACTGACAGGCCAGTGGGTCCACCCAACAAAATAAATTTCTCTCCAAAGCCTGCCAGT
WI-18520	75	G	A	GACTTTGGTGATTTAATTGCTTTCCCTTAAATATGAGAAATAGGTGTAATTTCTCCTTTGTTCTTTACTACA[G/A]CCGGAGTGGTAAATACTACCTGCCAACAAACACGGGCATCCACTCTGTCTCAATGCCTCTTCCGTGAGAC
WI-18563	94	A	G	AAATAAAGTTTTATTGGCACACAGCCAAGCCCACTGGATGACACATTGTCCACGGCTCATCTTGCAATACAAATAGCAGGGGTTCACTAATGTGACIA/G]GACATGGTGTGGCTCACAAAGCCAAAGATATT
WI-18582b	69	T	A	GTCCTATTTCAATTTAGCTAGACCCCATTCATTCTGTTTAATGGCTACATTTGTTTTCATTGTGTGAGAC[T/A]GTGCCATAATTTATTTAATCAGTGCCATATTGAAAGACATTTGGATCGTTTCCCAG
WI-18723f	94	G	A	AACTTTATTTGATCTGACGATCAGCGATTAGTTCTCATCCACATTGACTGTCTGTAGATTTTTGAAAGTGGTAACAGGTACATAGGTAACCAAA[G/A]ATATATAGCTTATTTGGTGAATCTTCATCCT
WI-18723e	71	T	C	AACTTTATTTGATCTGACGATCAGCGATTAGTTCTCATCCACATTGACTGTCTGTAGATTTTTGAAAGTGG[T/C]AACAGGTACATAGGTAACCAAAGTATAGCTTATTTGGTGAATCTTCATCCT
WI-18723c	96	A	G	AACTTTATTTGATCTGACGATCAGCGATTAGTTCTCATCCACATTGACTGTCTGTAGATTTTTGAAAGTGGTAACAGGTACATAGGTAACCAAAGT[A/G]TATAGCTTATTTGGTGAATCTTCATCCT
WI-18619	44	G	A	TTTATTACAATATTTAGGTGGCACAATAACTAACAAGCTTCTGA[G/A]ACAGGAGGTAACATTCTCATAGACTTTGCAACTCAGCCAGAAGTAAAACTCGAAATA
WI-18715	76	G	A	TTATTCACAAAAAGTGATATTGCAGAGGGTCGTGGGGCTTGGTGAGCTTTGTACATGGG[G/A]CTGGGGAGACAAAGGGGAGCCTCCAGGTGGAAGGGTATTTTTAATAAAAAATAATGGAGCTACAACCACCCCC
WI-18535	107	G	A	GTAAAATAAAGTTTTATTGGCACAGCCACGCTCGTTCATTCATTGCCATTGACATCTGCTGTTGCCCTACACAGCAGGGTGGGGACCTGCTCTTCACGGGGAGAGCTA[G/A]TTGTTTAAAGCAGTGGTGCCCCAACCTTCTGTGGTCCCCGGTG
D17525	107	C	T	AGAGTGGTGCAGAACACAGGCCAGGCTCTATCACTTACTAGTTTTCAGTTCTGGGCAGGTGACTTCATCTCTTCGAACTTCAGTTTCTTCATAAGATGGAAA[C/T]GCTATACCTTACCTCGTAAAAGTCTGATGAGGAAAAGATTAACTAATAATAGATGCATAGCACTTAACAGAGTGCATAGCAATACACTGTTTTCAATAAATGCACCTTAGCAGAGGTCGATGTGTCACCTACCAGCAGAGAAG

DWU-133c	313	A	G	---	TAATTGGCCACTGCCTTATTATTACAAAACAGAAATGTCTCATGACTTTTTTATGTGTTACCATCCT TTAATAGATCTCATACACCAGAATTCAGATCATGAATGACTACAGAATATGTGGGCAGTCCT GATTTAAAACTAAGACTGGCTTGTGTGGTTAAATGAATATGTTCAGTTTTGAATTTAATAGTAACTCC AATTCAGTAAATGGTATCACTCGTTTAAAGATATGATTAGACT
DWU-133b	236	T	C	---	TAATTGGCCACTGCCTTATTATTACAAAACAGAAATGTCTCATGACTTTTTTATGTGTTACCATCCT TTAATAGATCTCATACACCAGAATTCAGATCATGAATGACTACAGAATATGTGGGCAGTCCT GATTTAAAACTAAGACTGGCTTGTGTGGTTAAATGAATATGTTCAGTTTTGAATTTAATAGTAACTCC AATTCAGTAAATGGTATCACTCGTTTAAAGATATGATTA
DWU-133a	199	C	T	---	TAATTGGCCACTGCCTTATTATTACAAAACAGAAATGTCTCATGACTTTTTTATGTGTTACCATCCT TTAATAGATCTCATACACCAGAATTCAGATCATGAATGACTACAGAATATGTGGGCAGTCCT GATTTAAAACTAAGACTGGCTTGTGTGGTTAAATGAATATGTTCAGTTTTGAATTTAATAGTAA[C/T] TCCAATTCAGTAAATGGTATCACTCGTTTACCCTTTAAAGATATGATTA
DWU-36	102	C	T	---	ATGAGATCCTTTAAATCCTTCCATGAAACGTTTGTGTGGTGGCACCTCCTACGTCAAACATGAAGTG TGTTCCCTTCAGTGCATCTGGGAAGAGATTTCTACC[C/T]GACCAACAGTTCCTTCAGCTTCCATTCGCC AAACAAATAAGACCCATAAGGGAAAGGATTCATGTGGAATATAAAGAT
DWU-387	169	G	T	---	GTGTATAAAAATGCAACTGTTGATTCCTCAACATGGCTCACAAATTTCTATCCCAAATCTTTCTGAA GATGAAGAGTTTAGTTTAAAACTGCACTGCCAACAAGTTCACTTCATTTATATAAAGCATTATTTTA CTCTTTGGAGGTGAATATAATTTATATTACAATG[G/T]AAAGCTTCTTCATATAATACTAAGTATTTTCA GGTCTTCACCAGTATCAAGTAATAACACAAATGAAGTGTCATTATTCAA
DWU-447b	172	---	---	---	ATTTTAGTGTCTTTGCGTTAAAAAATCATTGCAAAAGTATTCTGAACTGTCAAAAGTATTAGTTGATG GGGCTGTTGCCATTTAAQ[A/V]G}ATCACTGTAATTAATTAGTTTGATTAGAGCACAAAGCTTAGCTAAT CCATTATTTTCATTTGTTTGTTCTACAATGAGAGGATTGANAATCAGTTTAGTTTAAATGTCTTTCTTCTGTTAG GCCTTCTTTCTTCTTACAATGAGAGGATGATTCTTCTCTAGTTTATGTTA
DWU-447	85	A	G	---	ATTTTAGTGTCTTTGCGTTAAAAAATCATTGCAAAAGTATTCTGAACTGTCAAGCTGCCCAGTCAGAT CAACCATTATTTTCATTTGTTTGTTCTAAGAGGATTGANAATCAGTTAGTTTAAATGTCTTTATGGTTA TTAGGCCTTCTTTCTTCTTACAATGAGAGGATGATTCTTCTCTAGTTTATGTTA
DWU-476	63	C	G	---	GTAAAATTCAGTTTTTCCAGTTCTTTGCTTCTCCAATTACGCGTTTAAGGTGAG[C/G]AT AAATCAACTGTCCATCCAGTCAGGTGAGGTGTGCTCATTAGCGTTCATGAGTAGTGGGCTATGCA GGAGCTTCTGCTGGGGAGATTTTTT

DWU-505	67	A	T	TCATACTAGGGCAGTATCTCCCTAGCTAGTGCCCATACAGAGAAATTCTATCACCATACAAAATTTA[A/T]GCAGTATTATGTTTAAAGCACAGGTGTACCGAAAACTGTGAAAAGTTATGGGTTCTATGCATGCATTTTGCCTAACCTAGAGAAAGAGTTTGATAAATTTTACCAGCTTTATGGGATTAACTTTTGACTTTGAGCTTTAAACTTTAA
DWU-512	131	A	G	AAAATCCAGGCATTTCGAATCTGTTTTCATGATTTATAGAGGGTTTACACAAGTGCCACTTATTAAAGAGCTTCCCAGTTCCACAGTGAAGATGGAGAAGGTGAACTGCTTTGCTTGCACTGAAGTGTTGGTC[A/G]TGCCGTATGGCAGTGAGCAGGTATGTGTTTTATTCAAGATGTCTCCAGAGTGAAGATGCCGAG
DWU-525	97	A	C	AACTGCATATAGATAATTATCCAGGATGTGTGGCTCATTCTTTCGTTCTTGTTTCTATACTGTTTGTACCCAATTTTAAAAATAACATATTTTGCTTTCACAAATAGTTGAACAAGATTTCCCTAAAAATTAAACTGAAACGGTTTTTTATTCAAGATGTCTCCAGAGTGGAAGAAACATCTAGCTTAGGCCAGTCAGTACACCCACCAGGATTAATCTCTAAAATCTAGTCTCTGATTTGC
DWU-59	94	C	T	CATTTCTTTGTGAAGGTAATGGACTCACAGGGAAGAAACATGCTGAGAATGGAAAGTCTACCGGGTAGTTTGTTTGTGAACGTCACATTGGC[C/T]GAGCGGTGGTTTTACTTCCAAGTGGTGTTTACTTTCTGATAGCCCGGTAAGGCTCTGAGTCTTAGTGGTTAAGC
EST11	68	C		CTTGATCATGGGGGTGGAATTTGTGTATCTGGGCCTTCATGGGATGCATAAAATTTCCAGTTGGTAAGCAGCAGGTGCCGAGGGTCTGCGAGGGTCTGATCAGAAAAAGGCA
WI-19856b	63	C	T	CACACTGGCATCCTAGGCCTTCGCCCTGCCTGCGCAGAAGGAGGAGCCAGGTCCCCTCCTGGAGAA[C/T]GAGCTGTAGACCCACCAAAGCAACCACCAGCCGGCTTGCCACCACAGGCGCCTGTTGAGCGAGGAGGCCAGGTCCCCTCCTGGAGAAGGTGGTAAGACGTAAGTGTGTCATCCCATCCATTAGACACAAGACAACATCCTACACTAAAAAGT
WI-18014	40	A	G	TCCATTTACATTTGGTGGCATTTGGTGTGTCGTGTGTGACCCAGGAAGTGTCTGTTAAACAGAGATTTCTGTTAAACAGAGAAGTGTACAGAA[A/G]GAATGAAAGTGCACCATCAGAGTGTAATTAGGTCTGTGTGACCCAGGAAGTGTCTGTTAAACAGAGATTTCTGTTAAACAGAGAA
WI-18036b	97	T	A	TTCCAATGTAAGAGTCAAGTACCAAGTAAACTTCTAGAAATACAAAGAGAACATGATAAAATCTGATCACAGTGGAAAATTTAATTCTTCATAA[T/A]CTGACAGGTCAAGTAAGCTAAGGAAACATAT
WI-18036a	27	T	C	TTCCAATGTAAGAGTCAAGTACCAAGT[T/C]AAACTTCTAGAAATACAAAGAGAACAAGTCAAGTAAGCTAAGGAAACATATTTAATTCTTTCATAATCTGACAGGTCAAGTAAGCTAAGGAAACATAT
VI-18046	72	C	T	TGTAAGGTGACTTCTATAAGCTTCCTAAACTTCATTTACTGCAGATTATTTCAGGCCAATGTGTC[C/T]TTGTTGGGTCTGAGATTGATTATCAGCTGGGTAAGCTAAGGAAACATAT

ID	pos			seq	Sequence
NI-18063	105	G	A	--	AGGCTTAAACTGATAACAATTGCCTTTAATCACATACAAAAACTCTGCACTTTCATTCCTTCCTTCCCATGTTTCTGATTTGATGTAAACTTAAAATTGT[G/A]TCCTTTAACAATATACTGGTAGCTGCA
NI-18078	86	A	T	--	AGTTGAAAGATCAGAGAGGTTATGGTTGGTGAGTAGCCAAGT[A/A]TCCTTTAACAATATACTGGTAGCTGCATTGTTTTTCAGCATCAG[A/A]GTCCACTAGCAGTCGAACTGA
NI-18091	90	T	C	--	CCAAAGCTCACTCAGTATTTAATCATCTGCTAATTTCATCTTTGTTAATTCCATCAGACACTGTTAAGC
NI-18119	38	T	C	--	TTTCATCTCTAGAAGTTTGAC[T/C]GGGCCTTTTATACCTTCCATATCTCAACTTGTTAAGC
NI-18142	66	T	G	--	GCAATCTGTAACAGTTTGGTAGTGGTATTACAGAGGA[T/C]TTGTAAAATGGATTGGAGTACTTAC
NI-18178	68	T	C	--	CACTATTCATCTGCTCTGAAATAGTTCACTAACCAAACTACTGACAACAGTTTAATTTGGTTCTT
VI-18244	35	G	T	--	T/G]CCCAATAAAACTAAAGCCTTAAATAATCTATATAC[GCATAGGGTTGAGGGGTGTACAAGAGACAGAACCAGATTCAGTCCATGCCTGGAGGTTAGTCGGGCATACAG
I-18245	115	G	A	--	GT/C]CGGCGGGGATGGACAACAGAACCAGATTCAGTCCATGGGGT[G/T]GGGGGAGGTGATTATGGCTGGGGAAGATGGGCACTCACCCGACACAGCAGCATCTAGCACCACAGTGAAAACTTGCTGTAATTGGCCCCATTAAAGTACGAGAGAGTTGAGGTGGCAGAGGCTTT
-18261	26	G	A	--	AGGCTTGGCAAGAGTTGCTATACAACGGAGGAGGAGAAACATGA[G/A]CTGGGGAGTAGGCTCTGACAGAGGGTGGGCTGTC
18268	88	C	T	--	GATTTGAAGGATTGCTTTATTTAAC[G/A]TGAAAAGCGTGATAGAGGAACTGTTTAAGATAAACAACTTATAAATACTCCCAATTGTAGAAGTGAAAGATTG
8299f	107	C	A	--	TAGGAGGGAAAAGGAGGTGGGCCTGCCTGGGCCCTCAAGACATGTCTGCAGAAACGGGGTGGTTCCAAGCTTCCTTACTTCCCCCATAGATC[C/T]CCTGACAATGTCTGCAGAAACGGGGTGGTTCCAAGC
9e	101	A	G	--	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTGGTTTGCCAATTTTTTTATCTATTTGGGGTCTGAGAATTCCACAATTC[C/A]TTTTGCCAATTATTGACATATTCTGCAG
d	77	G	A	--	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTGGTTTGCCAATTTTTTTATCTATTTG[G/A]GTCTGAGAATTCCACAATTCTTTGCCAATTATTGACATATTCTGCAG
c	67	T	G	--	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTGGTTTGCCAATTTTTTTT/G]ATCTATTTGGGGTCTGAGAATTCCACAATTCTTTGAAGAATTCTTTGCCAATTATTGACATATTCTG

Marker	No.	Allele 1	Allele 2		Sequence
WI-18299b	52	G	A	---	TCACAAGTCAATCTCCCATCCAAATGACACAGTTTGTCTAAGATCATTAACTTG[G/A]TTTGCCAATTTTTTATCTATTTGGGTCTGAGAATTCCACAATTTTGAAGAATTCTTTTGCCAATTATTGACATATTCTGCAG
WI-18299a	48	C	T	---	TCACAAGTCAATCTCCCATCCAAATGACACAGTTTGTCTAAGATCATTAAC[C/T]TTGGTTTGCCAATTTTTTATCTATTTGGGTCTGAGAATTCCACAATTTTGAAGAATTCTTTTGCCAATTATTGACATATTCTGCAG
WI-18307	76	G	A	---	TCAACTTGTACCAAGTTTAGCAGCAAGAGGATACTTCCTTAGAGACTTCAGTGGACTTAAACTCAGTTTCCGGCTG[G/A][TGCTATGTAAAGCATCCACGATGGTTTATTGTACTCTGCAATCTGCTTGGTCAC
WI-18324	72	C	T	---	TTTGGTATGAAATCTTCTCTGACATTACCAATCATCACTTAAACCTCCGGGGGGTGGGGTACTGATTTATC[C/T]TTAGATCCAAATAAAGCATGCAGAAGTG
WI-18350	48	T	C	---	ATGAAAGTCACTTCAATCATCATAAGGGTCAAGAGAAAGAAATGTTTTCAGA[T/C]TAAATCTCTATGAAAAGGTGTGTATCTGCTTGCAATTTAAGAAACAACACAAGTCA
WI-18395	77	G	C	---	TCTTGACATGATGATCTGTGAAATAACGTGATTGTGGTTGAAATTCCTGGAAAATTTGAGAGAATAAATTGATTATTCAAG[G/C]TGTGCATTGGTTTATACATATCTCTCTTAATGCAAAGCTATG
WI-18398	62	G	T	---	TGCAGTGGCAAGACACTCTCTCGAGGAAAAAAAAAAAGAAAAACAACTCAAGGGTT[G/T]GATAACATTGCCAGTATAACCATAATTCAAAACAAGCAGCAGAATTTGGAGGATAATTGTT
WI-18396	21	C	A	---	CTCGTTGGTATTCTCTCATCC[C/A]TTCCTTTCGCTCTTTCTAAAATTAAGAAAAGCAATGGAATTTTAAAGATCATCTAAGAAATAGAACTTACATATGTAACATTAACTTATCAACTTGTACAAGTCAATGAAA
WI-18409a	20	C	A	---	AAGATGGGAAGAGAGGAGGAAATC[C/A]TTTTCTTACTAGAGATTTTTTCCCTTTAATCCTTTCAAATTCAAAGGATCATCAAAGGAGCAGGTGCAGAAGCTCTGGGGCCCCAGTGCTA
WI-18442	62	C	T	---	AAAAAGGAAAAGAAAAGGATGGAGTAAGAGAGGAGGAGAGAGAGGAACAAAATAAGTTTCTGG[C/T]TTGGCTGATCTGGGTGATCAGGTGGACACTATTATCCCAGAAGGGAAACACAAGAGAAAAAAAGGTTTATAGGTGGGAGAAGAGGA
WI-18452	38	G	A	---	TTGATGTTAATACTGTCATTCTGGAGATCGGCTAAAAT[G/A]AAAGCATAGTTATTATTAGCTTTGGTATATTCTGCGACAGATTAAACAAGTAAGACATATCAACCCTCATATTTCCAACCA
WI-18489	102	A	C	---	ATATAAAGCTGGAGACTGGAGGGTGAGAGCCAGTGGGGACTACTGTTGAAGAGAGAATGTAGCAGTAGTAAAGATGAAAGACTGCAAGGATTCAAACA[A/C]GGTTATGGCAATAGAGGGTGAAAGAAAGGCCATATAAA
?T5b	93	A		---	CTGGTGGGGAGGAAACAAATTGTGTATATTCATACAATGAAAAACTCTTCAGAAATAAGAAGGAACAAACCACTGAATCACACAACATGGACAAATCTCAAATCATTATGCTGATGGAAAGAAACCATTCATAAGAATACACAGTACAT

			Sequence
EST5	93	A	CTGGTGGGGAGGAAAGAACAAATTGTGGTATATTCATACAATGAAAAACTCTTCAGAAATAAGAAGGAACAAACCACTGAATCACACAACATGGACAAATCTCAAATCATTATGCTGATGTGATGGAAAGAAACCATTCATAAGAATACACAGTACAT
EST6	48	C	TTAGCTACTTTCAGAATTGAAGGAGAGAAAAATGCATTATGTGGACTGAACCGACTTTTCTCAAAGCTCTGAACAAAGCTTTCTTTCCTTTGCAACAAGACAAAGCCACATTTTGCATTAGAACAGAT
EST8	158	A	GGACAGGACCTCTATTCCCGCCTGGTGCAGCGGCGTGATGGACTGAGCGCCCAGGGATACTGGGCCCTCTTCTCAGGGGCGTCTCCAGGACCCCAGAGCTGTTCCTTGAGTTTCCTAGAGCTGTGTGCGGCCAGATAGCTGTTCCTGAGTTGCAAGCACGATGGAGATTTGGACACTGTGTGCTTTTGGTGGGGT
WI-18740c	104	GT	TCCTCATTGTTGGGGATGATGAGAAGAAAATGATTGGGAAAATTAAGTAACACGACCTAGAAAAGTGAGAACAATCTCATTTACCATCATGTATCCAGTAGTG[G/T]ATAATTCATTTGATGGCTTCTATTTTTGGCCA
WI-18740b	96	CG	TCCTCATTGTTGGGGATGATGAGAAGAAAATGATTGGGAAAATTAAGTAACACGACCTAGAAAAGTGAGAACAATCTCATTTACCATCATGTATC[C/G]AGTAGTGGATAATTCATTTGATGGCTTCTATTTTTGGCCA
WI-18985a	105	CT	CCAAAGTCTCCTGTTCGCTCATAAAGAAGTTTTGGGATGGGAGAGAATCCAGACCACCATCTTGGGGCAGCCAGGCCCTGCCTTCATTTACAGAGGTAGCACAA[C/T]TGATTCCAACACAAAACCCCTTCCCCTTTTAAAATGATTCTGTTCTAATGCATAGATCAAAGGCCTCAGAAACCATTGTGTGTTTCCTCTTTGAAGCAATGACAAGCACTTACTTTCACGGTGGTTTTTTCTTAT
WI-18746	114	GA	GCCAGCAGTCGAAGTCTCTCCTCTTTCTCTCGGCTGGAAGAACATCAAGATACCTTTGCGTGGATCAAGCTTGTGTACTTGACCGTTTTATCTTTGTAAATATTCTT[G/A]TCCACATTCTACTTCAGCTTTGGATGTGGTTACCG
WI-19112i	212	GA	CCGTGTTCACACACACAATGGCAAGCATAGTCGCCTGGTTACGGCCCCAGGGGGGAATATGCCAAGGGACCCCTTAATGGAAACACAGATCAGTAGTGCTATCTCATGACAACCACAAGAAAACCGACGACAAATCTTTGCGAGATTTCTTCAGTGGCTTAGAAACAGTTCCATACCAACTGCTTTGCTCTAGGGTGACAAGGC[G/A]TCTCTTCAAACAGTTCCATACCAACTGCTTTGCTCTAG
WI-19092	232	AC	TGGTGGCTGGCTAGCTAGTTTCTACAGAACACATAATTTGCCTCTCTATAGAAGGCTATTCTTAGATCATGTCTCAATGGAAACACTCTTCTTTCTTAGCCTTACTGAATCTTGCCTATAAAAGTAGAGCAACACACATTGAAAGCTTGTCTGATCAAACGGTCCTGAAATTTCATCTTGAATGTCTTGTATTAAACTGAATTTCTTTTAAGCTAACAAAGATCATAATTTTC[A/C]ATGATTAGCCGTGTAACT
WI-19057i	175	GA	CCCATTTATTATAGGCCAGTGATGTCTCAAAGAGTAGAGGAGCGTCTACTGGTCTTCAACTCCTTCAGTCTTCTGACGGGACTTACCGTGACAGCGAAGTGTATTGTACGTCCAGGCACCGCAGCCACTGTCTTCATGCAGGAACCACAGTGCCCACAGCTC[G/A]TCTCTTCATCTTGGTTTTGCCACA

Clone	Pos	Var		Sequence
WI-20103	168	C/T	---	TGGGACTTCCAACTCAGAGAGGATGTGGGAATCCAGCTCAAATGATACAGGATAAACTGGGATGGGCT AGGATGGACAGGCTGTGGATATGGGAGTCATGGGAGTCCAGATGGCTCCAGGTACAG TGGGCTTCCTGGCCTGGAAGCTGGGTCCTCCCCA[C/T]TTCATTCTGCTCAAAGCTTCTTGAAGGAGC TGGTTTGACTTCAACTTGCTAGAGAGCCTAGCCTCATCTTTCAGTCAACTGGGA
WI-20441	111	G/A	---	GCCTTACCCATTTGCACATATATACATATGCACCACCTTTGCAGTGGCAACATATATATCCACACTA TAAACATACCACCATTTATAAATCTTGTAAGGACAAGAAATGGA[G/A]TTGAATAAGTACCCCCAA CATATACAAGAAAGTTAGCATACTTACCCCGTTTTCACTACATCAGAGGCAAAATAAGAAATCTTT TAAGAAAATCTCAAGACTGGCTCATGGCAAAATGAATATGTCTAAATTTGGGG
WI-19911b	116	A/G	---	TGGTTACAAAACCTAAGCCCATATACAAATTAGGAACACATTTAGATGCCTCTTTGAAAGAAGCGT TTTAGTCTTTTAAACTGAGTTTAAAAAAATAACAATGCAATTTTA[A/G]ACACTGTTTTGAAA ACTTAAAAGTGCAGCAATA
WI-20613c	165	A/G	---	GTCCTCAAGGGGGAGAAAACTGGTTCTTTATGTACAAAGCACAGATGTAGGTACAGTATATAAACA GATACGTAGTACATCTGTAGTATTAAAATGGCATGGGAGGCAGTTAGAAAAAACATCTAAAAC AGCTCCTTAGAAGGCCAATAATA[A/C]AGTTGGAAAAAAAGGGAGTTTCCACGCCAGCCAGTGGTGAGC TGC
WI-20613b	156	A/C	---	CAGTAAAAGAGTGATTCAAGTTGCAGTAATAACACTGACAGGTAAATA[A/G]TATAACATTAGAAAA GCAAAATTCTTTAACTTAAGGACAGACTGAACCATCAGGTATGGGTCTGAGATCAAGTAATACAGG TAGGCAAGAGAGTTTTCCACACTGAAAAATGAAGGCAGTTTCCAAATACTGTGAATTTACAAACAT TGGGGGAAGG
WI-19984	47	A/G	---	GCCAGTTGGAATATGGCCTATACGAACCAAAGAGTGTATACAAAATGGAAGTGGTCATCAGGCAATA ATTGTTCCTTGGAACTCTGCACGCTGTCCATGCTGTGGGGACTTACACATTCAAGTTTGACAG[T/C]TGAAAAAACCAACTGGAGCTGCTTTCCAAGAATGTCGTTTCGTTGTCCTTCAAATAGGAATTCCATG TTATTCTTTCTTGCCTAAGCTCTTATATCTTTCAAATGACCTAAGCTGA
WI-20122	135	T/C	---	GAGTGCCATACCTTCTCCCCAGGCCTCTGCCCCAAGAGCAGGAGGTGCCT[G/A]AAAGCTGGGAGCGT GGGCTCAGCAGGGCTGGTCACCTGCCTAGAACCTTCCCTTCCTCGAGCAGGCCAAACATG GCCAGACTCCTT
WI-18846a	49	G/A	---	AGCAGTGGCCTTATTGCATCCCAAACCACCAGCCTCTTGACCAGGGCTGCCTCCCTTGTGGCAGCAACGGC ACAGCTAATTCTACTCACAGTGCTTTAAGTGAAAATGGTCGAGAAAGAGCACC[G/A]GAAGCCG TCCTGGCCGCCTGGCAGTCCGTGGGGACGGATGGTTCTGGCGTGTTGAGATTCTCAAAGGAGGAGCAT
WI-18959	123	G/A	---	GTCGTGGACACACAGACTATTTTGAGATTTCTTTGCCTTTGCAACC

ID	Pos.				Sequence
WI-20146	31	T	C	---	TGAGTCTCTGTAATTCATTGAGCAGTTAGC[T/C]CATTTGAGATAAAGTCAAATGCCAAACACTAG CTCTGTATTAATCCCCATCATTACTGGTAAAGCCTCATTGAATGTGTGAATTCAATACAGGC
WI-18922	74	G	A	---	TAGGAATTGGTTTCACGCCTGAGGCAATTAGACACTTTGGAAAGATGGCATAAACCTGTCTCACCTGGAC TTAAGC[G/A]TCGGCTCTAATTCACAGTGCTCTTTCTCCTCACTGTTCCCTCCCAGAG GAGCCACCAGTTCTC
WI-18763b	53	A	G	---	TTTCTGTGTTGTGGGGTCAACCGTACAATGGTGTGGGAATGACGATGATGTGA[A/G]TATTTAGAATG TACCATATTTTTTGTAAATTATTTATGTTTTTCTAAACAAATTTATCGTATAGGTTGATGAAACGTCA TGTGTTTTGCCAA
WI-18763a	38	A	G	---	TTTCTGTGTTGTGGGGTCAACCGTACAATGGTGTGGGA[A/G]TGACAGTGATGTGAATATTTAGAATG TACCATATTTTTTGTAAATTATTTATGTTTTTCTAAACAAATTTATCGTATAGGTTGATGAAACGTCA TGTGTTTTGCCAA
WI-18771b	75	G	A	---	CTCATTTCCATGCCATTGTGGAATTGAGCAGAGAACCTGCTCTCGGAGGATGCCTAGAAGATGTTGGG AACAGAA[G/A]AAATAAACTGAGTTTAAGGGGGACTTAAACTGCTGAATTCACCTGTGGA
WI-18771a	57	A	G	---	CTCATTTCCATGCCATTGTGGAATTGAGCAGAGAACCTGCTCTCGGAGGATGCCTAG[A/G]AGATGTT GGGAACAGAGAAGAAATAAACTGAGTTTAAGGGGGACTTAAACTGCTGAATTCACCTGTGGA
WI-18820	70	T	C	---	GGGAAAAATTTGAGACGCAATACCAATACTTAGGATTTTGGTCTTTGGTGTTTGTATGAAATTCTGAG GCC[T/C]TGATTTAAATCTTTCATTGTATTGTGATTCCTTTAGGTATATTGCGCTAAGTGAAACTT GTCA
WI-18742b	51	C	T	---	ACAAAGTCCTGTAGCCCCCTCACCTTTCCTGTTTTCACTTTTGCCAATGTA[C/T]ATCGGGTTTGGTTT TCTTGTATTATTAAACGGTTGTGGTTTCCTTTTCCACGGAGGTTCAAGTAAAGCCGCTGCAGGAGA GTTTTACC
WI-18882	94	C	T	---	GTGTGTCCAAAAATGGGGTCTGCTCCTGCTACCTTGACCCTTCCCTTCCTCTGTCTTCTCTCTCCTCATCA TCATTCCCAACAACATCCTCTGCCA[C/T]ACACAACAAAACGTAAGTTTCATTGGGCAAAAATTGA GC
WI-19970b	167	G	A	---	TATAAGCCCGAGTCACCAGGACGGCCTGTCTGGCCACAGACAGGGGCCTGCCTGTGGAGCCTGCCCACC GGCCCCGGCGCAGTGCAGTCCAGCGGCCCGTTCCTGCCAGTTCCTCACTGCGGGGGACC AGCAAAGGCCTTCTCACTGGGTTGGTCAAAG[G/A]TAGTCACCTGGCTGGTGCATCCACAGAGGA TGTTGTTCAAACCAGAAATCTTTAAACGACTGACCTTCCTTAAAAACAGA
WI-19970a	126	T	C	---	TATAAGCCCGAGTCACCAGGACGGCCTGTCTGGCCACAGACAGGGGCCTGCCTGTGGAGCCTGCCCACC GGCCCCCGGCGCAGTGCAGTCCAGCGGGGAGGAGCTGCCCGTTCCTCACT[T/C]GCGGGGG ACCAGCAAAGGCCTTCTCACTGGGTTGGTCAAAGGTAGTCACCTGGCTGGTGCATCCACAGAGGAT GTTGTTCAAACCAGAAATCTTTTAAACGACTGACCTTCCTTAAAAACAGA

ID	Pos			Sequence
NI-19067d	202	T	G	TATTGCTGCTGTCACTGCCTGCCCCCTGCTCCCCAGAGGCAGGCAAGGCTGCTGCAGCCTCCCCTGGCTGTGC ACATTCCCTGCTCCCCAGAGACTGCCTCCGCCATCCCAGAGATGATGTTTTTTTAATAGTGTTCATAAAGAA[T/ G]ACATAGTATTCTTCTTCTCAAGACGTGGGGGGGAAATTATCTCATTATC
NI-19067c	153	G	C	TATTGCTGCTGTCACTGCCTGCCCCCTGCTCCCCAGAGGCAGGCAAGGCTGCTGCAGCCTCCCCTGGCTGTGC ACATTCCCTGCTCCCCAGAGACTGCCTCCGCCATCCCAGAGATGATGTTTTTTTAATAGTGTTCATAAAGAA TTGGGCTCTGCAGGTCCTG[T/C]AGAATGTTGTGAGGGGTTTATTTTTTAATAGTGTTCATAAAGAA ATACATAGTATTCTTCTTCTCAAGACGTGGGGGGGAAATTATCTCATTATC
NI-19067b	151	T	C	TATTGCTGCTGTCACTGCCTGCCCCCTGCTCCCCAGAGGCAGGCAAGGCTGCTGCAGCCTCC[C/G]CTGGCTG TGCACATTCCCTGCTCCCCAGAGACTGCCTCCGCCATCCCAGAGATGATGTTTATTTTTTAATAGTGTTCATAAAGAA CTCTTGGGCTCTGCTAGGTCCTGGAGAATGTTGTGAGGGGTTTATTTTTTATCTCATTATC ATACATAGTATTCTTCTTCTCAAGACGTGGGGGGGAAATTATCTCATTATC
NI-19067a	57	C	G	TTAATCCCAGGCCCTACCCTTGTTAGTTATTTAGGAGGACAGTCTCAAGCACTAAAAAGTGGCTAATTC AATTTATGGGTATAGTGGCCAAATAGCACATCCTCCAACGTTAAAAGACAGTGGATCATGAAAAGT GCTGTTTGTCCTTTGAGAAAGAAATAATTGTTGAGGCGCAGAGTAAAATAAAGGCTCCTTCATGTGGC GTATTGGGCCCATAGCCTATAATTGGTTAGAACCTCCTATTTTAAT[T/C]CTGG
NI-19106	247	T	C	CAAGGCAAAAATATCAGGAGGCTTTTTACACACCTACTACACACATCTTTAACTAGTATTTTACCTAGCATTCAAAACCC AATGCCAGAAGGATAATATTGATTCCTCACATCTTAAATTTCACAATATAAAGTTCTACAGTTAATTATGTGCATA AAATGGCTAGAAAC[A/G]TGTTTAATTAAATTTCCTTCCTTCTTTCCTTAATAAATTAAGTTTT TTAAAACAATGGCCTGGTTCAATTTCTTTCTTTCCTTAATAAATTAAGTTTT
NI-18944	147	A	G	CCCATCCCTGTGAAGGAGTAGGCCCACTCTTTAAGTGAAGGATTGGATGATTGTTCATAATACATAAA GTTCTCTGTAATTACAACTAAATTATATGCCCTCTCCACAGTCAAAAGGAACTGGGTGGTTTTGGT TTTGTTGCTTTTTAGATTATTTAGTGTCCCATGTGGGATGAGTTTTTAAATGCCACAAGACATAATTTA AAATAAATAAACTTTGGGAAAAGGTGTAA[G/A]ACAGTAGCCCCATCACAT
WI-18952	232	G	A	CACACCTCATGCTAGCCTCACGAAACTGGAATAAGCCTTCGAAAAGAAATTGTCCTTGAAGCTTGTA TCTGATATCAGCACTGGATTGTAGAACTTGTTGCTGATTTGACCTTGTATTCAAGTTAACTGTTCCC CTTGTATTTGTTAATACCCTGTACTACATATCTTTGAGTTCAA[C/T]CTTAGTACGTGTTGGTTGGTCA
WI-18932d	177	C	T	CTTCGTGGCTGAGGTAAGACGTCTGTGGGAAGACAAGTCTGTGGCTTG

NI-19042	193	A	C	---	TTTGTCAGTGTTGCCTCTCGCAATGCCTCAGTAGCATCTCAGTGTGGTGTGTGAAGTTTGGAGATAGATG GATAAGGGAATAATAGCCACAGAAGGTGAACTTGTGCTTCAAGGACATTGGTGAGAGTCCAACAG ACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAATAACTCTAACCA[A/C]GGCTG TGTTTAGATTGTATTAACTATCTTCTTGGACTTCTGAAGAGACCACTCAAT
NI-18984	208	A	C	---	ATTGGCCCTGTACAGTTTGCTTATTTATAAATTCATTAAAAACACTACAGGTGTTGAATGGTTAAAA TGTAGGCCTCCAGTTCATTTCAGTTATTTCTGAGTGTGCAGACAGCTATTTCGCACTGTATTAAT GTAACTTATTTATGAAATCAGAAGCAGTAGAACAGATGTTGGTGCAATACAAATATTGTGATGCATT TATCTT[A/C]ATAAAATGCTAAATGTCAATTTATCACTGCGCATGTTTGACT
NI-18851	90	T	A	---	GCTTCAATTGGCGATTGATTCAGTGCCCACAATGTAAACAGGGTTGGTAGTTGTTACTCATTTTGAAT ATACCTTTTCCTTATTGTATT[C[T/A]GTAATATAGGATCCTGGAAATGAGACCTGGTGGAA
WI-18821b	76	T	C	---	TCAACTGCAGTGTTGCTTCCCTCCCCCTATAGGGCTGCGAATCTGTCTAGGGAGCCCTCTCTCGGAGGCC ACAGAGGC[T/C[C]GGGGGTAGCCATTGTGCAGTCATGGCCGGGGGAAACTTGCCAACCTTCGTGTCAG GTGCTGTGT
WI-18821a	69	C	T	---	TCAACTGCAGTGTTGCTTCCCTCCCCCTATAGGGCTGCGAATCTGTCTAGGGAGCCCTCTCTCGGAGGCC A[C/T]AGAGGCTGCGAGTCATGGCCGGGGGTAGCCATTGTGCAGTCATGGCCGGGGGAAACTTGCCAACCTTCGTGTCAG GTGCTGTGT
WI-18821a	69	C	T	---	ACTCCTCTGCTGCTCCAT[C/G]ACTGTCCTTTTGAACCAGGAAAGTCACAGAGTTAAAGAGAA GCAAATTAAACATCCTGAATCGGGAACAAAGGGTTTATCTAATAAAGTGTCTCTTCCATCACGGTTG CTACCTTACCCACACTTCCCTCTGATTTGCGTGAGGACGTTGCATGCTACTTACGTACGGTGGCATAAC ACATCGTGTGAGCCCATGTATGCTGGGGTAGAGCAAGTCAAGTAGAGCCCTGTC
WI-19021a	20	C	G	---	TGGAAATTCCCTTCATCTGGAACCATCAGAAACACCCTCACACTGGGACTTGCAAAAGGGTCAGTA TGG[G/C][T]TAGGGAAAACATTCCATCCCTTGAGTCAAAAATCTCAATTCTTCCCTATCTTTGCCACCC TCATGCTGTGTGACT
WI-18908	70	G	C	---	CACGGTTCTCTGCATCGTTACCAGAGCGCCTTCTGGTCCTCAGCCACGCCCTGTATGACCGGCGCAAATA TCCCCAAAGCTTTGGGTCCTCCAAGTCATGCCGAATTTAGATGCTGGTCATTTTCTGGAGAGGGGGTC CCCTCCCCTTACGAACACA[A/G]AAACCCAGCCACCAGCCCACATGTGGTGACACAGTGAATGGGAGGTGG GTGCCAGGCACTGGGGGGGTGGAAGTGTGGGGTGGAAGTGTGG
WI-19037b	155	A	G	---	CACGGTTCTCTGCATCGTTACCAGAGCGCCTTCTGGTCCTCTAGCCACG[C/A]CCTGTATGACCGCGCAA ATATCCCCAAAGCTTTGGGTCCTCAAGTCCTGGTCGTCATTTTCTGGAGAGGG GTCCCCTCCCCTTACGAACACAAAAAACCCAGCCCACATGTGGTGACACAGTGAATGGGAGGTGG
WI-19037a	47	C	A	---	TTTGAGGAGGTGGGGTGAACTGTCCTTGGCAGGGATTTGTGACACTGCATTGCTGGGCTGTGTTCC[T/ C][C]GGGCTGGTCTTCTGGACCGTTGCACGGTGGATACCGGGCCATGTGCCATGGTATTTGGGTCCTGGAGAGGG
WI-19064	66	T	C	---	TGGGGTGAAATAAAGGC

ID	SNP		Sequence
WI-18972a	112 A G	---	AGGGCCTGTGGCTTATGTCACCCAACAGAGGGGTCCTGAGAAGTCTGGCTGCTGGGATGCCCCTGCC CCCTCCTGGAAGGCTGCTGCAGAGATGACTGGGCTGGGGAAGCCAG[A/G]TGCTTGCTGGCCATGGAGCC TCATTGCAAGTGTTGTTCCTGAACACCTGAGCGCTTCCTGTGCCCACCAGCACTACGGCTTCCTCTCC AGATGTGCTTTGCCTGAGCACAGCAGTCAGCATGGAATGCTCTTGGCCA
WI-19016b	184 C A	---	GTTTGCAAACCAACATGTGCTCTTTCAGTCATTCACTGTTTAATATGACATGGTAGAGAAGATAAG GTTTATGGCCAGGTAATTTTTGTAATGTGTATTAAACGAAGTTCAAAGATTAGAAATACATCTGTGTC CTGAAAAACCTTAGATACATAGCCGACTGTATACAGAGAGGTTCATCTCAA[C/A]CTCAACACTATTGAC TTTTGGGGCTGGATAGTTCTCTGTTGTGGGGGGTTTGTCTTGTGTGCACTGTAG
WI-19016a	161 C T	---	GTTTGCAAACCAACATGTGCTCTTTCAGTCATTCACTGTTTAATATGACATGGTAGAGAAGATAAG GTTTATGGCCAGGTAATTTTTGTAATGTGTATTAAACGAAGTTCAAAGATTAGAAATACATCTGTGTC CTGAAAAACCTTAGATACATAGCCGA[C/T]TGTATACAGAGGTTCATCTCAACCTCAACACTATTGAC TTTTGGGGCTGGATAGTTCTCTGTTGTGGGGGGTTTGTCTTGTGTGCACTGTAG
WI-20096	21 T C	---	GGTTTTGGGGGCATTTATTTTC[T/C]GATAGAGACTGGCACAAGCTTTGGGCTAAGGACACCCGCCCCCC ACCCTCATCTAGAAACAATCTCTCGCCAGACTTG
WI-19591b	156 C A	---	TGGGGGCAATTTTAACAAACCAGGCAAAATATCACATATACCTGAATATAAGGTAACTCCAAGCCATG AGTATAAGATTAAGGCAGTTACTTTATTTTGAACAAGGAAGTGGCATAAGCAACTCAGTGTGTGCCC CTTAGGGTGGGGGAGCTCTTCCC[C/A]CTACCACTCCCCACCCCCAAGGCATCATTTGGGAGAAAAA GTGTCTTCTATCTGGCTAGCTGTGTTATCTAGGGATTGCACCTTCTTACACGG
WI-19591a	45 T A	---	TGGGGCAATTTAACAAACCAGGCAAAATATCACATATACCTGAA[T/A]ATAAGGTAACTCCAAGC CATGAGTATAAGATTAAGGCAGTTACTTTATTTTGAACAAGGAAGTGGCATAAGCAACTCAGTGTGT GCCCCTTAGGGTGGGGGAGCTCTTCCCCTACCACTCCCCACCCCCAAGGCATCATTTGGGAGAAAAA GTGTCTTCTATCTGGCTAGCTGTGTTATCTAGGGATTGCACCTTCTTACACGG
		---	TCCTCCAGCTCTGTCATCCTTGTCTTGTGTTCTTGAGGGTTCTGTGTTCACGGCCCCCTCCAGGCATGGTTTCTTCAT TTAGGTAGGAACAAAAGCCAAAAGAACATACAAGCCCAGCTCTCTAGAGGCTCCA[G/A]TCAGAA CTGGACCCCTTAACTACAAAGGAATCTTGGATGAATTATTTTAGCGGGGCTTCAGGAGCAGGTAGC AGAGCCAAAGTGCACACTCAGGCCATCTCAGGGGGGG
WI-20310	125 G A	---	CTCTCCCCTAAGGAGCCTTGGCCTTGCAGCCCCATTCAGCAGGGATGGAAGTCACAAGACAATGAGT GGAGCCTCATGCCCCTCCCATGAGGAAGCCCTTAGTATTGCTGACATCTGCCCTTATCCTGTCTCTCCT CCCCAGTGTGTCACACTTGGGCAAGCAGAGTGGTGGCAGACCAGCCTTGAGAGCTCTTGTAGACC GGAAGGAAGGGGGCGGGTCATT[G/A]GGTGATGCGTCTCTGGCTT
WI-20860	224 G A	---	GACGTGGACAAAGGAGGAGGTTTAAATGAATACTTTGTTTGT[T/C]CATGTTCAAAAAAAGAGTATTAAT ATTTTGTGACTGCATCTGTGAATGAAGACACTCAAAAAGCCATGTTCCAACTTAGGTTAATAATAA GGCTATTTGTCCACCCACTCTTCGGGCACATTGCTGCAATATTCCTGGCCTCAAGTGGGGAGGCCACGTG
WI-19359a	39 T C	---	GGAACAAGGCCTCAGAAAACAAAGGACACAGCAGCATGCAGATTGCAGCCTCCCTGAGCCAGTTCCT

WI-19766b	93	A	G	---	TGGCCTCAATGACTGGTACATTGGAGAAGCTGTGCAGCAGCATCCTTTCTGTGGTGGGCAGGCAGG AGATGAACCATAGGAGCCAAAAGTC[A/G]ACAAACAGAAGCACACCAAGCCTGAAACCCTC CGGACAACAGCAGAGTTACCAGCTGCCCTGGAGGATGTCCCTGGAGGTTCTGACCCATGAGAGGCCCCCTC ACCCTCCTTCACCCTCCTCCTACCACCAAGCTCTCCGGCAGTCATGGACTTAT
WI-19766a	31	G	A	---	TGGCCTCAATGACTGGTACATTGGAGAAGCT[G/A]TGCAGCAGCATCCTTTCTGTGGTGGGCAGGGC AGGAGGAGATGAACCATAGGAGCCAAAAGTCAGAACACAGAAGAGCAACCAAGCCTGAAACCCTC CGGACAACAGCAGAGTTACCAGCTGAGGGATGTCCCTGGAGGTTCTGACCCATGAGAGGCCCCCTC ACCCTCCTTCACCCTCCTCCTACCACCAAGCTCTCCGGCAGTCATGGACTTAT
WI-20512d	126	C	G	---	CTTCTCTGTTTGGCTTTGCATTGTGTGCGATTGGAAAAACCACTTGGAAGAAGGGACTTCCTGCAA AACCTTAAAGACTGGTTAAATTACAGGGCCTAGGAAGTCAGTGGAGCCCCTTGACTGA[C/G]AAAGC TTAGAAAGGAACTGAAATTGCTCTTTGAATATGGATTTTAGGGCGGGGGCGTGGGTGGGCTCACGCCT TATTAATCCCAGGCACGTTGGGGAGGGCCAACGCGGGGGTGGGATCACCTGA
WI-20512c	59	T	G	---	CTTCCTCTGTTTGGCTTTGCATTGTGTGCGATTTGGAAAAACCACTTGGAAGAAGGGACT[T/G]TTCCTG CAAAACCTTAAAGACTGGTTAAATTACAGGGCCTAGGAAGTCAGTGGAGCCCCTTGACTGACAAAGC TTAGAAAGGAACTGAAATTGCTCTTTGAATATGGATTTTAGGGCGGGGGCGTGGGTGGGCTCACGCCT TATTAATCCCAGGCACGTTGGGGAGGGCCAACGCGGGGGTGGGATCACCTGA
WI-19599	230	C	G	---	GGGCTTAAAATTCCCCTCTGTTTGGGGACTGGTCTCTCCAGTTACAGCAAAGGATCGCACCCTTTCC ATAACCCCTTCTACATTGGAAAGAGCACACCTGTATACAGAAGATGGCTCCGTGAAGTCTTTAAACG GACAAAGGTAAAATCACAGCTAACAAAACGTGATGTTGGCTCACACGTAACAAAACACCTCTTTTCA GAACAGAGAGAGCGTTAAAAGTAAAGGGCA[C/G]TTCCAAGAGTAACACTGCTA
WI-20679	82	T	C	---	TGTTTGAAATAAAAAATTTCCATGGTCTTAATTGAACTGTATGTTCTTTCTTTCTTTAGAATATCCTTTT TTCATTAAAATAATT[T/C]TCTAAACCACTCTATGTTCAACCTCTCTGTTAACACTAAGATATGGGT TTTTGGAAAGGCCACAGTCACCCAGCTCCATGAAGTGGGCGAATTGGTCCTTGTTTGGAAAGCTCTC CAGGGTGTTTCTCCAGAAA
WI-19909a	29	T	C	---	CCAGAAATAAAGCCTGAATATTCTCTTTCT[T/C]TTAAAAAATATAATTTTCCTTCTTTCTTCTTCCAA GTAAATCTTAAAATGAACCTGTTCTAGTCTATTTTAATCTAGGCAATTATAACACTACCTAGGCGGGG TTTTTCCTTTATACCTTGTTTCGTTACTGTGTGGAATCAACTAA
WI-20341	221	G	C	---	TTGAGAGGCTGAGAGAAGGCTGTTGAGACATTGTAATAAGTGCTTAGGGGCATGAGACATTAGGAAG GCCACAATTATGAGTAATGAAATGTGGAGGCTGATGAGAAGCTACTGCTCCCATTTGTTTAGCAGGA GGCAGGAAAGTGATCTGGGGTCTCTGGCAGCAAAAGCGTGTGGTAAATATTTGGGTGGACGTCATGC ATCCCCCATGCCATTGTGTTTTT[G/C]TATGTCTCCAGTGAGCTGTTCCAGTGAGCTGTTGGGCCAAGTCT

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WI-20113	60	T	C	TTCTGGTACATGGTAAGTGCTCAGTATTACTGAGTGAATGAGCAAAGACCTGAAATACTGT[T/C]GGA AACAGTAAAAGCAAATTGGAGCATGATTATTTTCAGACATAGGATATTTAAAACAT CACTCAAATACTGGAGCATGATTCAGCAATAAAATTCTATTCCATAAACCAGGTAGATAAATGTCACA GCTTTAAAATATTAGTTAAGTACAGTTGATCCTCGTTATTCATGGATTCCGTATT
WI-20895	107	G	C	TGATGGCAAAGTACAAAGGCTCTGAAAGAACAAGAGACGGCAGTGCAGCGGTGTGGC CACTTCCCACCAGGCAGAACAACTTGACTTCATTAAGGCAAA[G/C]CTTTACTCTGTTTTCCTC CCACATAGTTTAACCCAAATAGAAAGGCATTCTATTCTCACACTACTGCTCTCTAAGGTCCTAGGAA TATAACTGGTACTATAGGCAAACAGATGCA
WI-20721	72	T	C	CCTGCAATCACAAAAGTGGAACTAGTTGATATTTTGAAATCATACTTGATTTAACCACCTTCAGAAA TTCTA[T/C]AAAAACACTAGCAACTTCCTTTATCAGA
WI-19415c	161	A	G	CTGGATTTAATATTTCTGGCCTAATAACCAAATGTAATCAATAAAATTGGTCAATATCTCCACCTC ATTTCTGCTAACATGTTTGCAAGATTCCCTAAGTAAGGTATTGACGACTAGAGTCCGGCAAA GTCATGAGACCCTTAGCTGATCTCAT[A/G]AAGTCCACCTCATGAAGGAGATGATTCAACATCTCAA GCTAAGGTATAAAGTGTGGACAATACAAAGGCTTACAAGTTTACACTTCCTG
WI-19348c	103	C	T	GCTGCTCACTGGTAGCCAGCTGCCAGGATGGTGGGGTAGCAAGTACGGATGGGCCATGCACTTCTG GCGGGTCGATGAAGAGACTGTTGGTCATGGCGGTGA[C/T]GTCCTTCTCCAGGCTCATATGGATGTCCT CGAGGTTGCACAGGGAACTGCTCTGCTTGTAGAAGCTTCTCC
WI-19348b	98	G	A	GCTGCTCACTGGTAGCCAGCTGCCAGGATGGTGGGGTAGCAAGTACGGATGGGCCATGCACTTCTG GCGGGTCGATGAAGAGACTGTTGGTCATGGC[G/A]GTGACGTCCTTCTCCAGGCTCATATGGATGTCCT CGAGGTTGCACAGGGAACTGCTCTGCTTGTAGAAGCTTCTCC
WI-19635	98	A	T	ATTAGTTCGTGTTGGGCCACATTCAAAGCCATCCACACAAGCTCTTGTAGGCCATTGTAACACAATG TTAAAAGGTACAGTAAAAATACAGTATTAT[A/T]ATCTTATTGTGTAGCACGGCTGTGTGAGGCTCATT GTTGAATGAAGCATCCTTAGGCACGTGACTGCATGCAGATATGTGCTGAAAGAACTTTGCCTT T
WI-19641a	46	A	G	TCCAATTTCAGAAACATGTTCCATGTTTATTGTGATAAGCACTAG[A/G]TATTATTAGTCTCATGTTT TTAATTTATGAATAACGTCTGATTCATTGTATTTGATTTTACAGAAGATGTCAGGGCTATCTCATTC AGTTATTAATAAATGGATCAGAGTAGTAAGTCAAGAATAAGTGCATAATGTGGTTTAAAATTTTAAAA AATACTCAGAATGAGGTAGTATTTAATTTTAATTTCATCCACCTTG
WI-19642b	52	C	A	ATATAGAGTAGTACCATCCATGGTTTCAAGCATGGCCTGGACACATTATCCCCTC[C/A]GGGTAAACCAG GACTATTGCATGAGCATTCTTTAATACGTATTTTGATGGACACAAGTTTCATGTCTATTA
WI-19673b	180	C	T	TCTGCCATGATCACATTGTGATGAAGAAACATGATGGTCACTAGTAGGTAACTTTCTGTGTCATTGCCT TACTCTCAGTGAGGTGCTAGTGATTACCTACCCCTGCTTTGCATCACCACTGTAAATCTAATAGT GAAAAGGCAAATGTGTCTCAGTATCACTGTGAAAACATTTTC[C/T]CT]CTTGGACCAGCTGAAAGAA TCTTGAGGAGCCTGAAGGCTTCAAGGTCCACACGTCAAAAAAACACAGCCC

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WI-19673a	35	G	A	---	TCTGCCATGATCACATTGTGATGAAGAACATGATG[G/A]TCACTAGTAGGTAACTTTCTGTGTCATTG CCTTACTCTCAGTGAGTGCTAGTGGATTACCTACCCCTGCTTTGCATCACCACTGTAAATCTAAT AGTGAAAAGGCAAATGATGTCTCAGTATCACTGTGAAACATTTTCCCTGGACCAGCTGAAAGAA TCTTGAGGAGCCTGAAGGCTTCAAGGTCCACACGTCAAAAAACACAGCCC
WI-19724	35	A	G	---	TTTATTTGGGAAACAAAGGATTGTAATTTGGGTAA[A/G]CTGAGTCACGGTGGCCCTGAGTGAGTGTC CTAGAAAGCAAACACAGAGAGTTTTGGTTTTCTCTT
WI-19307	196	T	C	---	TCCTCCTCCCCCAACTAGATGGTATTGATCACTCTGCCCACAAATGGTACCCCCTTCAGCAAGAACTG CAAGCCCTTCTTGGATTTGCCTTCATGAGAAAATGGTGGCTTGGGATGGAGGTGACATTCCTGCTGT GGTGAACTGCAAAGAAGGAAACCAGCAATGTATTCCATAGAGGCCTTAAAGAGACCCG[T/C]TGG AAATGGCCATGGTCTAATTTGGTGTTGAAATAAACTAACCTCTTTGGCTG
WI-19269	85	A	T	---	CTTTCCCTCATCCCTCTTCCACCACCATCCGGAACAAGTGCTCCAGGATTCCCTGCCCACTGGC CATTTTGGAGTGTGTCC[A/T]TTGGGTAGCAATGTGGAAACCACCAGGGCCTTTGTGGAGAAAATGG AGGGGGGTTGAGGGAGTCCCAGGAGGGCCTTATTTGAGGGGCCTTGCCACTTGCTCATAGGCGAGCTCG ATCTCCTCATCATCTGACACAGGGTGGAAGCGAATTCTTCCCGGGCGTAGGCA
WI-19946	122	C	T	---	CAATGGACTGAATGAGTGCGTGCTGGGTGGGCACACACACCTTCAATACACGTCAAGGTCG CTTCCAGTTTTAGAAAACAGAAATCTGCATCTCAGCCTGAGACGCACAGAGAGGT[C/T]TCTTCCTG ACCCAGACGCACTCACGAGTCCAGGTCCTGGTTTCAAACTGCATTTAACCTGCGCCAGAGAGTTCAC CGTAGGCATCTCTTTAATAAAACTAACTCCAGCAAAATGTGGGTACGGTTACTAA
WI-19956	141	G	A	---	CACAGCATGGTGTAAATAGCATCAGATTGAATGAAAAGTTTGTTAAATGCAACCATAAATAATTATA ATAAATATACACCAAGTAACTTACAGCACACACATTTTAGGGCCAAGGTTTGATCTGTCTGGACCT CAATGTT[G/A]CTCTCGGAGAACAGCTTCGAACTCTACCTTACAGCTTACAGCTTGTCATCTACTCAA GTGATGGCCAACAGAAGCTTCTGAACTCCTCCTGGGGAGGTAGCTGACAAG
WI-19076	40	G	A	---	TTGGTTGGATACTTGCTGGAAAAAAAAAGCAGTTTAAT[G/A]GTATTCAAAATACCTTTTAAAAA GTATTCTAGCACAAGATTTTCTGTAAACTAGATTATGTTGTAAACTTTTCTAAATCTTGTGTAGGAG TGTCGGTTGTTAAGAACTAGAGCTTATTCCTATTCCAAATCTATCTTGCGCTCCTGAAAAACTGCAGA AAGGCACTTGAAAGCTGTTTCTTAAGATATGGGATTTCTTTTATTCTT
WI-20218	26	T	C	---	CCACACACTCTGGTTTTATAAAGCTA[T/C]AGGACGAGAGCAGAGATGGAACTGAAAAACAGGGTAG AAAAATAACATAAATTGGAGGGAACAGTGGGATGCAGAAAGAATGACAACAGCCACATGTGCCCCA GTCAAATACTTTAGTCCCTGCGACAAGAGAATGCCAACCAAGTCTCTATACTGGCTGGGGGATCCTGCC ATGGGATGCAGAGGAGAAAA
WI-20295g	154	T	G	---	CAACCTTTTGACAAGGGGACGTGAATTTCTGATGAAAGTTATCTTACCAAGTTTAAATTCATAATTG GGAATTCCTCTTTAATATCTCCAGGCTGAATTGGGAGGGGCTGGGCTCTACCCTTCTCTTCTTCCA TCCAGTCTATTGCCAGA[T/G]CTCAGAGAAAAGCGCGCGGGAAGCCCAGCTCTCCAGCATAGCCACTGTGG GTCGGCCTTCACCTTCTGTCGTCGACTCCTCATGCTGGGGACTTGTCTTTCGGGG

WI-20361a	192	G/A	---	CTGGGAGTGCTGACCTAAGTGACATTTTTTTAATGCCAAATACAGTAATCTCCAAGCTTTAATGG CTTATGCAAGATGACAGAATATGTGAAATCTGATTGTCCCAGAGTTACACTCTGCACTCCAAAGCTA CAACAGTGCCACAGCTGAGAGGTTCCCTATACTTCCTGTGCAATTTAGC[G/A]ATCCTTC AAATGGGAAAATTCCTAACTACACGAGACAATGGGTCCTACAGTAGGCCCG
WI-20572	75	A/G	---	GAGCCAAACCCAAAACAAAAATAAAACAGAACTCTTTTGTAAACTAAGTCATACCTACTTTCTTCT TCAGAATT[A/G]TCATAAAAACATCATCTTTACAACATGGAGAAGCGAGGTAGGCCATAATTGTTCA AATTTCATCTTTCTCAAATTTAAAATTGTTTAATCCCAAAGGTGCCTATTGAATTCTTCAAAAATA AACTGCCTATCAGGTATCATCACCTGCAAATGCTTCTAATATCTCTTGATTAT
WI-20588	133	G/A	---	CATGACAAAAGACAAAGATCAAGGAGTAACATAAATTATAAGTTGAATAAATAGTATACAGCAATC TTCACTTTTTAAGAAAAATGTGAGATCCTTTGTTGGTTTTATTTCCTTAAGTACAAAAATGCTAAAC[G/A]GAGCCGAGCTCTTCCGCATTCAGG
WI-20593	79	A/G	---	TGACCTCATACTGGGTTCTGGTTAGAACACAGCCACTAGAACAAACTCCAGTCTTTTCAGTCTGTTG CTGTACTTCAG[A/G]TTTAAAATCTGGGAATGAGCATGCAGCAATGCTCCACCAGATGAGGAAGAAA AGCTGTTAAAAGGAACTCAGGATGTTGTTAGGAAGGGGAGTGGATGCCAGCCTTCACCAGACTAT CCAGAAGCCATTCCATGGGGTATTGGTCTGCATACTGTGAGACACTGAGCT
WI-19765	57	T/C	---	TTCTTTGCCAAGCCTGTTCTTCAAGTTATTCAGAACTGGGTGTATACCTTGTCCTCA[T/C]ATGTATCT TGTCCCTGCTGTCTTTAGGTTAGCAAGGTGTATGAATACTTTAAGTTTGTTCTTTCCTCGT GGTATCAGTGAAATACTGATCTATTCTCTGGCTAGGGTCAATTACAAAATTGCCATGGAACTGAGC AAAAGGCCCACGTGGGATAAAATCACTCACCATGACGCGCCACCAGTATT
WI-19066i	239	A/G	---	TGACAAGGGAGAGAGAAGGGAAATTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAAACCCATGAACCTTCAGCTGATCGTCCTTAGCCAGTCCAATCTCTACGAGGAACTGG CATATGTTCTTGCGTTGGTCACCCTGAATTAGTTCTCCCATATTC[C/T]GGATGCTCAATTACAGT ACCATTGCAGGCAAACTTTTCTTAAAGCCCTTCACT[A/G]TTCTTTTTA
WI-19066g	184	C/T	---	TGACAAGGGAGAGAGAAGGGAAATTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAAACCCATGAACCTTCAGCTGATCGTCCTTAGCCAGTCCAATCTCTACGAGGAACTGG CATATGTTCTTGCGTTGGTCACCCTGAATTAGTTCTCCCATATTC[C/T]GGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTTCTTTTTA
WI-19066f	148	T/C	---	TGACAAGGGAGAGAGAAGGGAAATTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAAACCCATGAACCTTCAGCTGATCGTCCTTAGCCAGTCCAATCTCTACGAGGAACTGG CATATGTTCTTGCG[T/C]TGGTCACCCTGTAGCTGAATTACTTCTCCCATATTCCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTTCTTAAACGCCCTTCACTAGTTTCTTTTTA

NI-19066e	147	G C	TGACAAGGGAGAGAAGGGAAATTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAAACCCATGAC[G/C]TTGGTCACCCTGATCGTCCTGAGCTGAATTACTTCTCCATATTCCGGATGCTCAATTAC CATATGTTCTTGC[G/C]CAGGCAAACTTTTCTTAAACGCCTTCACTAGTTCTTTTA AGTACCATTGCAGGCAAACTTTTCTTAAACGCCTTCACTAGTTCTTTTA ···
NI-19066c	100	G A	TGACAAGGGAGAGAAGGGAAATTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAAACCCATGACGAACCTTAGCCAGTCCAATCTCTACGAGGAAC TGGCATATGTTCTTGCGTTGGTCACCCTGTAGCTGAATTACTTCTCCATATTCCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCTTCACTAGTTCTTTTA ···
WI-19066b	87	C T	TGACAAGGGAGAGAAGGGAAATTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAAACCCATGAA[C/T]CTTCAGCTGATCGTCCTTAGCCAGTCCAATCTCTACGAGGAAC TGGCATATGTTCTTGCGTTGGTCACCCTGTAGCTGAATTACTTCTCCATATTCCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCTTCACTAGTTCTTTTA ···
WI-19066a	72	C T	TGACAAGGGAGAGAAGGGAAATTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCA[C/T]TTAAAACCCATGAACCTTCAGCTGATCGTCCTTAGCCAGTCCAATCTCTACGAGGAAC TGGCATATGTTCTTGCGTTGGTCACCCTGTAGCTGAATTACTTCTCCATATTCCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCTTCACTAGTTCTTTTA ···
WI-20660	105	G C	TTTACAGCGAGTTTTCCCGTCTCAATAAGTATGAATCTAAATAGATTAGGGTGAAAAGAAAATGTG TGTCTAAATAAAATCTCCCTTTTGAATGTATATTTGT[G/C]TTAATAAAGGAAGCATTAATATTA CAGACATATTTACAAGGTTCTGAACATGAGTAGTTCCATTACTGTTTCTGTACAAGATAGAACAAA AAGCTATCCACCCGCCCCAAAAATACTGTTTAACACACTATGTTTTAAGA ···
WI-18768	120	C T	CTGCTGCCAGCTTCTCTTGCCCTGCTCCCAGATGGCGGGTCTCCTGGCAGCCTCCCCTCAGTCTTCC TCCACCCGGCCTCTCCTTCCCTTCCCCAGCCTGCCATGTGCACCCTTGGT[C/T]TTCGCTCCATCGCC TTGAAAGCTCTGAA ···
WI-19087	37	A G	TTCCCCAGGGTTCTGTATTGCAGCTAAGCTCAAATGT[A/G]TATTTAACTTCTAGTTGCTTCTTGCTTTG GTCTTCTTCCAATGATGCTTACTACAGAAAGCAAATCAGACACAATTAGAGAGCCTTTTCCATAAA GTGTAATTTAATGGCTGCAAAACCGGCAACCTGTAACTGCCCTTTAAATGGCATGACAAGGTGTGC AGTGGCCCCATCCAGCATGGTGTCTCTATCTTGCATCTACCTGCTCC ···
WI-18790	49	A T	GAAAGCCAGAGATTAGCCCCGCATTCGCTGTCAACCAGGACAGACAGAA[A/T]GCATGGACAAGGGA TGAGCTTTACAAAGATGATGCACTTTGGAGATCAGAAAATTCATATTTAAGCAAAGTGATACAAACA CAGTGATTTGGGAATGCCT ···
WI-18987	35	G A	AGGAGGGCTGTTCCAGGAGTCCTGCCCAGCAGCCTC[G/A]GTGGCCAAGCCCAGACACTCACCCACCTT CCCAGTGGCCCCGTGGATCCTGGTCCTAGGCTGGACACAGGATTCAGAAAGACACCAGGCTGCACA GAAAGAGCCAGATGGCACCTGAGTGTGTCGGTCACAGCCCCCTCACACTCAAGGCTGAGAGGCCTCAGGAA AGTCA ···

WI-18919	26	C T	---	TGGATGAAAACCACAGGGATTCCGGA[C/T]GCCAGACCCCATTTATACTTCACTTTCTCTACAGTG TTGTTTGTTGTTGTTGGTTTTTATTTTTTATTTTTTATACTTTGGCCATACCACAGAGCTAGATTGCCCAGGTCT GGGCTGAATAAA
WI-18741c	64	G A	---	CTTTCTGGTCAAGGCTTTGGACATCTCTTCAGTCATCAGACAGAGTATCTCTGCTCTAGACCTC[G/A] CTGGAGTTCAAGCTTGAATTATTATATGCAAGTTAATTTACAAGCCTGGATGAGGCTACTGA
WI-18741b	38	G C	---	CTTTCTGGTCAAGGCTTTGGACATCTCTTCAGTCATCA[G/C]ACAGAGTATCTCTGCTCTAGACCTCG CTGGAGTTCAAGCTTGAATTATTATATGCAAGTTAATTTACAAGCCTGGATGAGGCTACTGA
WI-18741a	23	T G	---	CTTTCTGGTCAAGGCTTTGGACA[T/G]CTCTTCAGTCATCAGACAGAGTATCTCTGCTCTAGACCTCG CTGGAGTTCAAGCTTGAATTATTATATGCAAGTTAATTTACAAGCCTGGATGAGGCTACTGA
WI-19179a	170	G A	---	TCAGAAGCAGACATGGCATCTGTTCCTTGCTTGGTTGTTGTTGTACCTTTCACGAGACCTGAATT TTAGAATTGCCCAGTGCTGCCAGAGTGAGTGGTGTAATTCTCCTTTCAGGTAAAGATAGGCTATCTC AACACTGCTGAGTGATTCATAAACATATCAACCA[G/A]TAGCATTAACCCATTTATTTCCTGTCCTT AGTGTCTGAAGATGCTCACCAGTTTCTGTGTACAGTAAGGCAGCATGCT
WI-19212	46	T A	---	CCAAGTTGCATCCATGTTGATTTCTGATGAGACTAGAGTGACAGT[T/A]GTTTCAGAACCCAAATGT CCTCAGGTAGTTGGAGCATCTCTATGAGATGGGATTATGCAGATGGCCTATGGAAATGCAGCTGC ATAATTAACACATTATCAAGTCCTCTACAATTTATTTCCGCAGCATGTCAGCTAAGTAGACCCA ATGGGGAGAGAAAATGCCTGCTTCTTCTTCCCTCTTTTTCTGCACTGCCATAT
WI-19183	210	G C	---	CTGTTGAAGGCTTCCTCAGGCAAACTCCAGCTTAAAGCCCTAGACAGGTAAAGCACACATTGGATG GCAGCATGGGGTTCTTCCCCATTTATGGGCATGAAATATGTGGTTTAGAATAAGGAACAAGCAATATT CCTTTGCCAACAGCCTCACTCTGACCTGTCTCTAAGAGAGGCTTTTTGCTGAGTCAAGCAAACACTTGCCTGCTCTGCCC CTTGGGAG[G/C]TGCATTGACCTGCTCTCACTGGTAAGGTGACTTGGTGGC
WI-20014b	214	T C	---	TTGAAATCCCAGTCTCCTGGCCCCCAGGCCCAGGGTCGTGTCACCATAGAATGTCTTCCTCTACTGGGGTC GTTCTCGGCTTTTGTTAGAAACTTGGTCTGAGATGTTCTTCCCCTGTCCCTGTCCATTACCATTCGATGTTCTTT TGTTCAGAGCAATGTTCTTGTATTCTGAAACTGGAAACTGAACCAGTTTGCCTTTCTCCTCTAGTCACC AAGCATACT[T/C][T/C]GCCTGGCCTCCCCAAGTTACTTAAATGTTCTCATCTGT
WI-19041	198	T C	---	GTCTCCCCAGAGTGCTTCTGCACCCAGCCCCTGTCCTGCGTGTAAGGGATCAGAGAAGCTCCCCG TCTCTGCATCCCTTCCCAGGGGGTGCCCTTAGTTGGACATGCTGGGTAGCAGGACTCCAGGGCGTG CACGGTGAGCAGAGATGAGCCCCAAGCTCATCACCACCAGGGGGCCATCCTTCTCAATACAGCC[T/C]G CCCTTGCAGTCCCTATTTCAAATAAAATTAGTGTGTCCTTGCCTGTCTGT
WI-19135	20	G A	---	CAGTTACCCTGCGCTTGCCCTC[G/A]AAAGTGTCATCAATTTGTAATTTTAGTATTAACTCTGTAAAGT GTCGTAGTAGGTACGTTTTATATTATATAAGGACAGACCAAAAATCAACCTATCAAAGCTTCAAAACT TTGGGAAAGGGGTGGGATTAAGTACAACAGCACATTTGGCTTACAGTAAATGAACTGATTTTATTAACT GCTTTTTGCCCATATAAAATGCTGATATTTACTGGAAACCTAGCCAGCTTCAC

ID	Pos	Allele		Sequence
WI-19236	54	G	A	TACACAGAGGGTCGCACTTGGACTCTGAGGGTTGGGTGTGGAAGGGGAAAAGG[G/A]GATGGAGACCTGCTCCCCAGCTCTTCCTGTCAGCCGGTTTACATGGGAAGAGTGTCACACTCCTGGCTATCTCAGGGGGAATGGGGAAAAGCACCTTACCCTTTTCAAGGGCAAAGAACTCGTGGGAGGATGTCTCTTGTTGTATGTAATACT
WI-19144	222	G	C	GTGCCAGTCTTCCAGAAAGCAAGGACTGCCCTTGCTGACCTCCCAGCCTTTCTAAGGCTCAGCCCCACGGACTCTGGTGGCTGCCAGCTTGTGAGCTATCTATATTCATTCATAGCCAAACAGGAGACCCCTTTGCAGGACTTGCACACAGGGAGCCGTGTAGCCAGGAAACCCTCTTCTTCCCTGGTCTGGCTCTGCTGGAGCGG[G/C]TGGGAAACCAAACACCTTCAGTGCTGGTG
WI-19139b	110	C	A	CCCGTCTAAGGGAGAAAGCTAATGTTTTCCACAAGACTGAACAACGTGTATTTACACGAGGGTAGACGGCAGATGCCTGACAGAGAGTGGGTTGGCAGACAACACACTAG[C/A]ATTTTCACGGGTGTGGGCACATGGGTGTGCACCTGGCACGTGTGCAGCAGTGGCGGTCTCTGTGTGAAGCCACCGTGCTCTCTTTGGGGGGCCGCGAGATCTAGCATCTCTGAAATCCTGGCTGTGTCGAGGCTTTGAAG
WI-19139a	66	C	T	CCCGTCTAAGGGAGAAAGCTAATGTTTTCCACAAGACTGAACAACGTGTATTTACACGAGGGTAGA[C/T]GGCAGATGCCTGACAGAGAGTGGGTTGGCAGACAACACACTAGCATTTTCACGGGTGTGGGCACATGGGTGTGCACCTGGCACGTGTGCAGCAGTGGCGGTCTCTGTGTGAAGCCACCGTGCTCTCTTTGGGGGGCCGCGAGATCTAGCATCTCTGAAATCCTGGCTGTGTCGAGGCTTTGAAG
WI-18910	112	T	C	GGCTGGGACCTTTAGGAAAGTGAAATGCAGGTGAGAAGAAACCTAAACATGAAAGGAAAGGGTGCCTCATCCCAGCAACCTGTCCTGTGGGTGATGATCACTGTGCTGCTGCTGG[T/C]GGCTCATGGCAGAGCATTCAGTGCCACGTTTAGG
WI-19235	173	A	G	TTCAGGAGGTGGAGTTCGTCGTCAGCTCTCCTGCTGGTGGATGTGGAAGCTTCTGATATTTGAAGAAACACGAATGTCTCTGTAGCTTCCTCTTCACTGCCCCAGTATTGCTCTGTATTTATCAGCGATGCCCCTCTGTCACTCATGCCCTAATTGTTCACAATGGTGGAA[A/G]GCTTCATGTAATATGATCAGGACCACCTCCAGTTCTCTGAAAGTGTGACAGTGTCCAGCCGGTTCTGTCAGCACTA
WI-19222	179	C	T	CGTTTCCCTAACTCACCCAGTTAGTTGGGATGATTTAGTTTCTGTTCTTGTTGTTGATCCCATTTCTAACTTGGAATTGTGAGCCTGTTTCTGTTTCTAGGTGAGTGTTGGGTTTTTCCCCCCACCAGGAAGTGGCAGCAGCATCCCTCCTCTCCCCTAAAGGGACTCTGCGGAAC[C/T]TTTCACACCTCTTTCTCAGGGACGGGGCAGGTGTGTGTGTGGTACACTGACGTGTCCAGAGCAGCACTTT
WI-19117	134	A	G	AAATAATGCAACGCAGGAGGAGAAAAGAAATGCACTAAGACAAGAACATTCTCTCATAGAACATTGATCTGTTTTACAGGAAAACAAACCTTGCCTTGAAATTACACAGTGAGACTGAGACTGTACATAATTGCATGAAA[A/G]TAGCTATTTTTTCCTAAGACATTTTCATTCATGAATATTTCAAGTTTTTCATACTACTGTACACATTTCTTAAAACACATTGATACCAGCAACTGAACTGAAATGAATGCGAATTTG

Marker	Pos	Allele 1	Allele 2		Sequence
WI-19134c	263	C	T	---	CTCCTCGTTCGTCGACCTGACACAGGGTGACACAGCCCCTTTCACACTCTGTCCTCCTATCTTCCTGGGTAGA TGCCCTGGTGGTAGGGCTGAGTACTGAAGTGTCTTCCATCCCAGCAAGGGGGTGCAGCCCAGGGTCAG GCCCTTCAGAGCACAGGCTGCTCCTCCCTACACCCTGGGCTAGAGCCCTGGGTGGGAAAGGG TTCATCCACTTGCTCTCCCTACACCCTGGGCTAGAGCCCTGGGTGGGAAAGGG
WI-19134a	162	T	C	---	CTCCTGTTCGTCGACCTGACACAGGGTGACACAGCCCCTTTCACACTCTGTCCTCCTATCTTCCTGGGTAGA TGCCCTGGTGGTGAGGGCTGAGTACTGAAGTGTCTGAATGGTCTTCCATCCCAGCAAGGGGGTGCAGGGGTCAG GCCCTTCAGAGCCAGGCTGGCTAGAGCCAGGA[T/C]GCACGGTGGCCCTAGAGCCACTACTCTTTTCAGAG CACTTCATCCACTTGCTCTCCCTACCCCTCGGCACCCTGGGTGGGAA
WI-19224	112	C	T	---	GGTTTCACCAGTCTTTCCCAGGGAACTCCGATGAAGTGTTCCAACAAAATGAGCGAGTGAACCAAGA AGAGGATGACATTAGATCCAGGAGATACAACAGAGGAGATAATCT[C/T]CAGGATGCCTGTGAAGA AAGATCCCTGGATCCCAGGATGATTATAGGACAAGTTGTTCATAATCCAGCAGGCCAGAAGACTTCC AGGGAAACTCATTCAAGGAGGTGAAAATGATGGATGACTCCTCCAAGATGAAAA
WI-19201	179	T	C	---	GCAGCCTAAGGACCACTGGCCATTAGCTCTTGTCTTTTGATGGCATTCTCTTTCCACCTTGTCTTGTCTCTC CTTTGCTCCTCTGTGTTAGTGTGGCAGGTATGACAACTCATCCAGTGGAAACACAGCCTCACACTGCC CTTCCGCCCCCCACACTTGCCTGCAGGTGCACCGAAAGGAC[T/C]TGGGGGGATAAAATTCAAAAAA GTGTGATGTGTGCTGCTCAGAAGGTCAGACTCCATGTGTGCCTTGGCCTCAA
WI-19034	45	T	C	---	GAAATGGCTCCACTCAGAGCTACCCCGGTGATGAGGATAGGGAA[T/C]ACTTCTATTACATTAAAG GCAACAGCAGTTAGTAAAAGGTTTTACAGTGTTTCTGCTGTTGAAAGTGCAATATAAATTTTTTG CTAGCCCATGCATCAATGACACTTCTATTGTTGATATACACTTGATCTTCTTTAAGTTCTGTCGAATTGAC ATTTGCTACTTATAAACTTAGTCCCTAAGTCTTCTTATGCTGTATATA
WI-19102	25	C	G	---	TGTTCCTGAGTCACGCTGAGGAGAG[C/G]CTTCACTCAGGAGTTCATGCTGAGATGATCATGAGTTCA TGCGACGTATATTTCCTTGGAAACAGAATGAAGCAGAGGAAACTCTTAATACTTAAAATCGTTCT TGATTAGTATCGTGAGTTTGAAAGTTCTAGAAGTTCCTGTAAGTTTTGAACTCAAGGGAGAAGGTAT AGTGGAATGAGTGTGAGCATCGGGCTTGCAGTCCCATAGAACAGAAATGGG
WI-18548b	65	A	G	---	AAAGGAGGGAGGAGAATCTTTTACATAAATGCCTTGCATCATCCTCCAGTCCCCTCACTGGGGGAA[A/ G]AAAAAGCATCNTCAAGTCTTTGTCCAACTTTGGCTGC
WI-18548a	62	G	A	---	AAAGGAGGGAGGAGAATCTNTCAAGTCTTTTACATAAATGCCTTGCATCATCCTCCAGTCCCCTCACTGGGG[G/A]A AAAAAAGCATCNTCAAGTCTTTGTCCAACTTTGGCTGC
WI-18700	97	T	C	---	GGCAGCAGCTTTTTTAATTGAACACTTCTTCTTGAGGACACACCTTCAGTACAGTTAACAAATGGT TACACCTGAAATCTGCTGAGAGCAGAGCT[T/C]AAGATCCACAATTGCAAAGGCCACTGCTGGCTCA CTTCCTCACA
WI-18501	121	C	T	---	CAGAGGGAAAAGTTATTGAGTCAGCCACAGAGGAACAGAGAAAACAGACACAAGGAGGTTCTGTGT GCATGGAGGAAATCAGGGCGCCGNACAGCTGAACCCTGCGCAGGACAGAGGGGCG[C/T]GGACAGCA GCGCATGCCACAAACATTCA

WI-18017	87	C	A	ACAAAAGAAAATGGAAATAGGTTTGCGAAAACTTATCTGCATGTACAAAGTAATCCCGTAGATAAGGAGAGGCAACCCNGGAACA[C/A]ACTGCTGGATAAATCGTTCATTAAAATTATATCTCTTTGCATCAGAGCTGGTGGTGAAAATCAT
WI-18148b	101	A	G	TTATTGCGTTCCTTGGGACTATGAGATCATCACCAGATGTGAAAACGAAAGCAGTGATTTCAGAAACCNTCGATTCTGAATATCCC[A/G]TGGCGGGCATATGCAAAGGAAGATGA
WI-18254	64	T	C	TATACGGATCATGTATTTGTGACCACCACTACCACAGTCAATTTGTAGAGCAGTAAATCAC[T/C]GCCAAAATTCCCTCTTGCTTCCTTGTCAGTCCTTCTCCAACCCCAGGNACTTGGCAACCTGTTTCCGTTCCTAGACATTT
WI-18265b	117	C	A	CAAATGGGTGGACTGAGTGATAAACGCATATTGAGAACAAGACGGCCTTCTGGCCNCTCTGCGTCCAAGGCTGTAAAGGTCTCAGGATTGCTGCTAAGTGAGCCATGAACTGGCTG[C/A]GTTTTCAACCTTTCCTTGGGTGGTTCTTCAG
WI-18295	40	C	T	ACCACACATTGTTGAGAGCCTATTGTGGAGAACAAACAG[C/T]TTGGGAAGTAAAGGTTGATTACTTCCTCTCCAGGATGATATGTTTAATGAATTCCCTTNCCTTAGCTTCATTCTTCATAATGCCAAA
WI-18459b	64	T	C	GGGCAAGAGACAGAGATTAATTGAATAAAAACTCCAGGTCGTGTGACACGGGTGGGAGACAAA[T/C]GAGTAATTAACAACATAATATTTANATGACAGTGCAATTAATTAACGTCCTGGGTAAGCCAGAGGGGGAGGAGGCGTCTTTCA
WI-22585	56	A	G	TTTATTTAAATTTGCATCCTGAGATAATAAAATTTATCTGACAAGTAACAATG[A/G]CAGAAGCAGCAGTGAAAGTTTCGGAGGAGGCAGGTATCCTTCATTTGGCACAGCTGTATAGATTGA
WI-21155	36	A	G	GGGCTGTGGAGTAACAGAACTTGATGGAAAATTGGC[A/G]TCTGTGTGTAGAATGATTCTAAAGCTTTCAGACAAATGGCAGA
STS-F02766b	88	G	A	GCCTTTGCTCTGTCTGTGCTGTCCTCCAGAGGCCTCCAGATGGTATACGCAGCAACTTCCTTTTGAACCTTTTTATTTTCCTGGCAGGAAGAAGA[G/A]GGATCCAGCAGTGAGATCAGGCAGGTTCTGTGTTGTGCACAGACAGGGAAACAGGC
WI-19888a	98	C	T	GGCACGATTCAACCCATAACAGAGAAATAACTCCTTATTGGAAACAAGGTTTATTTGATATGATGAAAATATTTTGGAACTAGAAAGTAGCAGTGA[C/T]TTGGACAACGTTGTAAAGATATTAAATGCCACTGAACTGTTCATTTAAAATGGTAATTTCATGTTGTATTTCATCTGTATTCACCTGAAGTGTATACTTATTAATTGTAAATTACATGAGANCATATTTATGTTGAAGTGAACACAAG
WI-21485	82	C	T	TGAGACCATCCTCCTCACAAAGAATCAGTCAGTTCAGCACCTAATTTCCCACACTGAAGTCTACGCAATTTCATGCAGA[C/T]TGTGCACACAGTACAAGTGCACAAATCCAGAGGGCAACACATTGTAATTCATATCATCCGTTCCAAA
WI-20601a	125	T	C	TCAGAATTGCTTTCCACTGCCCCAAACCAAAAGAATTTAATGAATGCNCTTACAATTGAGATGACTTGAAGTTAAAGAAAGGTACCTTCCTTGGAGGTTGCATGACAGGATTAGTCTTCTCTGTT[T/C]CTTGGTGCAAGTTTGAACCAGTCAGTGATTATGTACCATTGCATCAGAGCATCTGTTCCCTGTCAGATCCCCACTAG

Clone	Pos				Sequence
WI-20561b	94	T	C	---	CGTTGCTTATTTAAGATGGCTGTGTTATAAGTAGTAAAAGCAGTTGAGCAACACTGATTGTGCATTATTG TACTTCAGATGAAAAATCCTTACACATG[T/C]GGAATCAATGTCTTTTAAAATTTCAGATAAAGAATTT NCATTTGAGGAGACATACAATTGTAA
WI-20561a	25	A	G	---	CGTTGCTTATTTAAGATGGCTGTGTTT[A/G]TAAGTATAAAAGCAGTTGAGCAACACTGATTGTGCATTA TTGTACTTCAGATGAAAAATCCTTACATGTGGAATCAATGTCTTTTAAAATTTCAGATAAAGAATTT NCATTTGAGGAGACATACAATTGTAA
WI-20116e	69	T	A	---	GCTTTCATTTTCTGTCACCCACCCTGTCCACCAGTTATGTTGGCCTTCAATATATGGCGTTAGAACAT A[T/A]ATAAATCTATATCATATATTTATACACACAAACACATTCTACCAGCACTGTGAAGACACAGA CTAGGCTTACTAGGCTTGGGGCCCTCTCCCATGCCACTTAAAAATGNGCACAGGTTTGCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI-20116c	59	T	A	---	GCTTTCATTTTCTGTCACCCACCCTGTCCACCAGTTATGTTGGCCTTCACCAGTTATGTTGGCCTTCAATATATGGCG[T/A]TAGAA CATATATAAATCTATATCATATATTTATACACAAAACACATTCTACCAGCACTGTGAAGACACAGA CTAGGCTTACTAGGCTTGGGGCCCTCTCCCATGCCACTTAAAAATGNGCACAGGTTTGCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI-20116a	22	C	G	---	GCTTTCATTTTCTGTCACCCAC[C/G]CTGTCCACCAGTTATGTTGGCCTTCAATATATGGCGTTAGAA CATATATAAATCTATATCATATATTTATACACACAAACACATTCTACCAGCACTGTGAAGACACAGA CTAGGCTTACTAGGCTTGGGGCCCTCTCCCATGCCACTTAAAAATGNGCACAGGTTTGCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI-20466b	133	G	A	---	AAAGATTTGCAGTCCTGGGACACAGTTGGAAAACACTATTTATAAGGTTGCACATATTACAAACAG NTCCCAAATGGTGAAACTGGTATTCTAAGATGAAAGCTTAATGAACATAATGAAGTGAATAAACGC[G/A]TGTGAACTAATGTTTAAAAGTTAGAGCTTGTCTCCAAGTCAGTACAGCTCTTAAGATAATAAAT ACAGTAACACTACTTTATTTCTTGCTCTTTATTCCCTTTCAGGTTCGATT
WI-21444	39	A	G	---	CTGGGCAGCAAGTAACCATTTAAAGAAATACTCTCAAC[A/G]AGTTCTTTTTTTATGGGGTATTTCA GTTGTTAACAAAGTTAAAAATACTTATTGGAACTAATTCTTGTATTTATTCGAGGAAGAAGAATCT ATAAGATTGACTTACTCATTGTTGACTGGTTTTTGAAGCCTTACTGGGG
WI-21034b	148	T	C	---	AGAATGGACAATGATGACGAGATGATTTGTGAGCATTTGATGAGAAAGTGGTGATTAGAAGGATACAG CATAAATTTAATTGTAAACATGCTTATCTAGCTAACCTAATCTGTTTCTGTAGAATTACTGGTCATGG GAGATTGGATAGA[T/C]GCCTAACCTATCTCAATTTAAGTAATGTGAGCAA
WI-22091c	205	G	A	---	GGCGTGTATTTGATGCAATGTCCAACCAGTCAAGCTATCATTGAAATCCAAATATTTCCCAGTAGAG ACATGCAGAGCAATGTCAATGTAACATACAAGCATATTACCTCCCCCCTTAAGTGACTCATAATTC ATTACTTGTGTCTGTAGCTTTAAAGGTTTAAAAATGTGTAGCAACACACTAAGTGGTATTTACTTGAGGGCA ACA[G/A]AATTACGGCTTAACAACAACTAAATCATGAGGCTCAGGGATTG

805a	45	A T	---	CAACTGCTCTGAGGTCTTTCACTAGCTGATTTATAATCCTATATT[A/T]AAAAAAATCTATAGTCTG CAGTCTTTGACATACTTCTCAAGGGTGGATATGTGGTGGAATGCAGACTCCATCAATATGTGTGGTT TTGTTTGCTTTTTGTAGCTTAACTGCTGTTTAGNAAATCCCAGAGGAATATGATTGAGGCCAGAGTTA CATTGGTTCATAAAAATTCGAACAGTTGAAGGCTGTTTTGTTAATTGCTG
778b	155	T C	---	AAAAATCCATAATTATTGAAACCCAAGTTACAGAGAAAGTTCGTAACTTTTTTATTGAATTATTGAC TCTGCCCGCGTGTCGTTCGTCGCTTCAACTCCAGTCTGTCAATGCCCCTGTGTGTGGGGTCCCCAG GTCTGGGCTTCTGAGGTCCT[T/C]GGTAGAAGGAGGGGCAGGTGGT
I-20907	241	A C	---	TGAGTCAGTGGTCAGATGGGGCAGTTGCGCTCAGCTGCAGTCCCTGACTCCGGAAACACTGTGCCTCT CAAATGATCTAGAGCTCATCCTTGGGCGGTACATGAGGGGCAGTTGTGTTCTAGTACCCATTTAGCCC ATGGCTCTTCAAGCCAATTCACACTGGGAAAAAACACACCCTCACAAGATGCCTATCCATTTGAGTTC ATACAGTTTTAGTAGCTAGAAACTAAAAAAACATTTTTA[A/C]AATTATCTA
449b	222	C T	---	AACAGCAGCAGTCACTTCCAAAAATGCAAAAAAATTACAATTTTTAGAATAAAATTATAATGTTTA TAATGCGGGTCAGAAGANTTGAAGGTACAACAGAATCAAATCACGCAGCACTGAGGCGGCTGGAG AAGCCAAAGCCACTGGTCAGGGGTCAGGGGTCCAACTGACAAGAGTCCAACCTGAGAGGTCTCCACACCC AAATCATACCCCTCAGCTTCCCA[C/T]TGACAGAGCCAGTGTCCTCTGGGTTAG
558a	157	G A	---	GCTTACAAGGAAGCCTGTGGACAGGCGGAGNTGGGTGGAACCGACTCCAGCCTGGAAAACCTGCCCTC CCATCCCCCTTAGCGCCTTCTTCGGCTGATTTTCTTGGACAGCCAGTTCTGGCCAGGGCAAGG AGCTGTGGTGGGGGGCCAGTAT[G/A]AGCCCAGGGACTCCCCTTCCCACAGATGAGGGCCTAGGGCTGCAA AAGGGGCCCGTGAAAGAGAGATGTGGTCAAGGCTTTAATGGGTCTCTCCACC
2187b	178	G A	---	TTTGCTGTGGAATCCATGAGAGCCGGAAGCATCGTTGGGGCCGTGCTAGCAGAGCTCATGGNGACCA GTCCTGGGCCTGACCAATGGGCTGATTACATTTAAAAACCAAACAAAATACCAAGA ACAGATCACTTGCCATGGACATCAGTAATCTATTGGTAATGGTG[G/A]AAATTTCATGAAAATTTCC CCTAAACCATAACAAAAACTGTCCTCCTTACCCCAAAAGTGCTGGAGGAAAG
2187a	110	C A	---	TTTGCTGTGGAATCCATGAGAGCCGGAAGCATCGTTGGGGCCGTGCTGCCTAGCAGAGCTCATGGNGACCA GTCCTGGGCCTGACCAATGGGTGATTACATTTAAAAACCAAA[C/A]CAAAACAAAATACCA AGAACAGATCACTTGCCATGGACATCAGTAATCTATTGGTGAAATTTCATGAAAATTTCC CCTAAACCATAACAAAAACTGTCCTCCTTACCCCAAAAGTGCTGGAGGAAAG
1609b	146	G A	---	TCATGAATATGCAGCCTCCATAATCTTCTCCCTTGTAACAAACGTGCAGTTCCGTTCACAAGCTGTAAA AACAAGCCCAAACCCAAGCACCCAAGAACATCCAAGAGGCAAGAGCAGTGCAGTAGGGAGAGCCTGTAAAG GATGTTTCAAAG[G/A]AGGGTCCCGGCTATGTGGCCACTGGACGTGAGAGAGCAGTAGGCAGTGAGCTGAGTCCAGGC TTTCGGTCTGGGAAGTGGCAGAGAGCTGGAGGAGGGCGAGAGACANTGGCCAAAGAGAGGAGTTGGAG

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WI-21609a	42	C	T	---	TCATGAATATGCAGCCTCCATAATCTTCTCCCTTGTAACAAC[C/T]GTGCAGTCCGTTCACAAGCTGT AAAAACAAGCCCAAACCCAAGACATCACAAGAGAGGCAGAAGCAGTGGCAGTGAGAAGGGAGCCTGTA AAGGATGTTTCAAAGGAGGGGTCCCGGCTATGTGCCCACTGGATGTGGCAGTCAGTGAGCTGAGTGAGCCAGGC TTTCGGTCTGGGGAAGTGGCAGAGGCTGAGACANTGGCCAAAGAGGAGTTGGAG
WI-22512a	104	T	G	---	ACATTCCGAGCCAGTTTTTTCCATATTGCTCCACTGCCTAAAATCCCTTGGTGCCTCCTAGGGCTTCA GGGTAAGCCCTGACACATCATGGTCCTTGTGATCTG[T/G]ACCTCACCCATGTCTCCCACCTNAGTTCC CACATTTCCCCCACGTCTCAAGGGCAGGCAGCTACACTTGACTGCA
WI-21028b	139	A	G	---	ATCGGCAAGCTACAGCCTTAAAATCTGAGCTCCTCAAGTGCACAATTTCTGTCCCTTTAAGGGCTCA CAACACTAAAGATTTCACATGAAAGGGTCGTGTGATTGAGCAATCTAGGGATATGTGACAGGGG TTTC[A/G]TTGCACTGGTACAGAACACACAGGGAGTTTCACAATTTTTTATACAATGCTTGGGAAT CTACGG
WI-21028a	121	A	C	---	ATCGGCAAGCTACAGCCTTAAAATCTGAGCTCCTCAAGTGCACAATTTCTGTCCCTTTAAGGGCTCA CAACACTAAAGATTTCACATGAAAGGGTCGTGTGATTGAGCAATCTAGGGG[A/C]TATGTGACAG GGGTTTCATGCACTGGTACAGAACACACAGGGAGTTTCACAATTTTTATACAATGCTTGGGAATC TACGG
WI-18829d	58	A	G	---	ACAACATGCCTGTTCACAGGGGGAAAAATCCTAGGNAATAACTTATGTGTACTTCTTG[A/G]TTCA TCATACAAGACAAGCACACAAAAGCACCACCCATGCCTCTGAGGAACATTGGACCATGCCACCCTTGAAA AA
WI-18829b	35	T	A	---	ACAACATGCCTGTTCACAGGGGGAAAAATCCTAGG[T/A]AATAACTTATGTGTACTTCTTGATTTCA TCATACAAGACAAGCACACAAAAGCACCACCCATGCCTCTGAGGAACATTGGACCATGCCACCCTTGAAA AA
WI-20964	87	G	A	---	AGCCAACTCAAGGCCAAAAAAAAAATTTCTTAATATAGTTATTATGCGAGGGAGGGGAAGCAAAGGA GCACAGGTAGTCCACAGAATA[G/A]GACACAAGAAACCTCAAGCTGTGAGGTCAATTGTAATTAA AAGAATAACTAAGATTAGATGAACACAACACTCAGAAATACTCTAGGAGAGCTGAAAAAGAGGAAC AGATGTTAACAAACAAATTAAGGCTGTCTGGGGAACCTGAGTCCATGTTAAGCTTG
WI-20059a	59	T	A	---	CTCTGAACTAAAGGGCCGTGAAAGGCATGATTGGTTTGGCACACAGAGTGGATAACCA[T/A]ACAT TGGCTGGAAATGAGGTGGTCAGGAAAATAAANTGCACAAATCTAACACCATGTGAAATCATGTCTGA GTTCTGTGGAGAAAGTTAAAGTGTAATAATTACAAGACTGCAACTCTTTACCTTACATTATT CATCTACAGACTATTTTCTCCCTTAGGGAGATGAGGAGTATGGGCCTTAGGT
WI-22130b	165	C	T	---	TGTTTTTGAGGGCTGTGTAGCAGACTACATAATGAGGCGGTGAAAGCGCTGCCTTCCCCTCCTCTGACAC CAGCAAGGGGGAGGGAGGCACCATCACCGGCCCCTGGCCACCATCCATCCAATGAATTACTAGCACTAGGAA GCCAACGGAAANAGGACCCCGCGCGCTTGCT[C/T]GTGTTTAATCCAGGTTAAGCTATACACGTTTAA ATACATGTCGGAGGTTACATGGTCTCATGCAGTCCCTGTGATGGGAATGAC

ID				Sequence
WI-21661	117	G C	---	GCTTAGTGTCTCCACCCTTTAAATGTACTCTAGGTACAAAATAAACATTATACACATATAAGATCAGT CTTTCCAACTTAGAATGTATAAATAAGAATGACATTTTAAAATAAAATA[G/C]TTAGTCACAGTC ACACAAAACTACCTTCTAAGGAAAACTGTCCAGTGAAGCCGTTAAATTGTGCTTCAGCTATGAAG GA
WI-21980a	25	T C	---	TCAGTTTAAACACATTCATCAAGGA[T/C]AGATTAATTAATGTCAGGTGAGCATAAAGGGAGATTA TAAACCAGAAATGTGTTTCTGGAACCAAGTTTCAGTGACTCAGGATAAGTTTATTAATTTCAT GGGTGAAGCCCCTGGGATAAAG
WI-21636	71	A G	---	TGCTTGTATTAATGTGGTGTTTACATTATCCTATTTCACAGATGGAAACAGAAAATACCAGCTTTTT AAA[A/G]TAGCAATATCTATTATTATAATAAATAACACCATAATAATATCACTAAGGA AGTAATCTAATTGTGTTGATTTTGCAGAGGGAGAAAAACATTACCTCTAGAGCTGAGGCTATTGTGC TCATGCAAACTCCAATCTGAAGGTGGTAGAAACTAGGAAGGGACAGGGATTTC
WI-22457a	112	G A	---	TTGCTATAATTTCCTTAAAAAATGCAAAAGAGTACATCACAGCAGAGTATAGCCAATCACTCATTAGA CAAACAGTAAACATACTGGACACGGTTTCAGGCATGAAGGATACA[G/A]CAGTTAATTAACTAAAG GAACAGAGTCCCTGCATTCCTGAAGCATAGGATGGGGAAACAGTAATGCAGATTAATACCTGGGGCC AAAACCCACTGAACTCACCCCAGCTGAAAACACTGAAAGGATACTGGGTAAGGA
WI-21524b	97	C T	---	GCCGTGAGGGTTAGCGTATAATGAAAAGGTGTAATAGCCTAGTTACGACCTTCGCGTCATACTTAT AATGGTTAATAACAGCATTCCTGTCTACC[C/T]GAATGATGCTTCTCTCTGCAAATGGACTATTTGCC CAGTTGCAACAGGCTAAGATTGTCGCACTATGTGACAATGAGTTGTTGATTGATTGTTTGGAGTTGCGGTGTC CTGTCAGAAAGATTTCTTGACTTTCTTCCAAGTTACTTCCTTCCAGGGGATG
WI-21524a	35	A C	---	GCCGTGAGGGTTAGCGTATAATGAAAAGGTGTAAT[A/C]GCCTGATGTGTACGACCTTCGCGTCATACT TATAATGGTTAATAACAGCATTCCTGTCTACCCGGATGATGCTTCTCTCTGCAAATGGACTATTGCC CAGTTGCAACAGGGCTAAGATTGTGTCGCACTATGTGACAATGAGTTGTTGATTGTTTGGAGTTGCGGTGTC CTGTCAGAAAGATTTCTTGACTTTCTTCCAAGTTACTTCCTTCCAGGGGATG
WI-22652a	32	G T	---	TTACCTTCCAAACCAGGCCCACTTGGAGAAAG[G/T]AAGGAGAATGCTATTAATCAATAAGGCCAAGAC AATAGGGACTTACCTGGGGTAGACCAAGATGGGCAGTCACCATCACCACCATCCTGCCACAGAACC TTTGCACATGCTGCCCTCCCTACTCCGCACTCACGTCTCAATTGGGACCTGAAGCTTCAGCATCCCTT CTTTAGGG
WI-21703d	197	A G	---	CAACAGGCTCATGGAACAGAGCCTAGGGATCCAGGAGGCATAGGAGGTGGTGCTGGGCAGGGCTC TGCATCCCCTTTCCTCAGCACAGCACCATCTTCACCCTCCTGGGAAAGCAGCATTGGAGCCTACACCA CTTGTGCTTTTCTCACCCAGGGGTAAGAAAATGCCAGGTATTTGCAGAGAGGGGAGTGAGTTGGGAA[A/G]G TGGGGCAGAGAGCACAGCTAGGGGCAAGGAACTTAAGGGAACTTGTGTGGGGAAGAG

WI-21703c	134	A	G	---	CAACAGGCTCATGGAACAGAGCCTAGGGATCCAGGAGCATAGGAGGTGGTGCTGGGCAGGGCTC TGCATCCCCTTTCCTCAGCACAGCACCATCTTCACCCTCCTGGGAAAGCAGCATTGGAGCCTACACC[A/G]CTTGTGCTTTTCTCACCAGGGTAAGAAATGCAGGTTAAGGAACTTAAGGGAAGAG TGGGCAGAGCACAGCTAGGGCAAGCAAGGACTTAAGGGAGC
WI-22663c	139	G	A	---	CCCTTGTCAGTCTGTGCCTCGGCTTCTCACTGCACTGGCGGAGGTGAGCGCGGCGCTCGCTAATCTTATTC CCAGTCTCGGTGAACATGGGCTCAGTCTCTCCCGGGCTTTCCTGAGGGTTTGCACTGGTGCACTTACAG GC[G/A]GAAGAGCTTCCTCATTTGCTGAGGGCTTTCCTGAATCCGTGTTGAATGTGGGT
WI-22663c					CCCTTGTCAGTCTGTGCCTCGGCTTCTCACTGCACTGGCGGAGGTGAGCGCGGCGCT[C/T]GCTAATCTTA TTCCCAGTCTCGGTGAACATGGGCTCAGTCTCTCCCGGGCTTTCCTGAGGGTTTGCACTGGTGCACTTAC AGGGCGGAAGAGCTTCCTCATTTGCTGAGGGCTTTCCTGAATCCGTGTTGAATGTGGGT
WI-22663b	55	C	T	---	CCCTTGTCAGTCTGTGCCTCGGCTTCTCACTGCACTGGCGGAGGTGAGCGCGGCGCTCGCTAATCTTA TTCCCAGTCTCGGTGAACATGGGCTCAGTCTCTCCCGGGCTTTCCTGAGGGTTTGCACTGGTGCACTTAC AGGGCGGAAGAGCTTCCTCATTTGCTGAGGGCTTTCCTGAATCCGTGTTGAATGTGGGT
WI-22663a	38	C	T	---	CCCTTGTCAGTCTGTGCCTCGGCTTCTCACTGCACTGGCGGAGGTGAGCGCGGCGCT[C/T]GAGGTGAGCCGGGCCTCGCTAATCTTA TTCCCAGTCTCGGTGAACATGGGCTCAGTCTCTCCCGGGCTTTCCTGAGGGTTTGCACTGGTGCACTTAC AGGGCGGAAGAGCTTCCTCATTTGCTGAGGGCTTTCCTGAATCCGTGTTGAATGTGGGT
WI-22668	99	A	G	---	TCTTTTATCCTGCCTGCCTGAGTATTCTGGAATCCTACAAGGATTTGAGGGAGCCCCTTGGGATT CCAACCTAACAAATTAGTTTTCTGTAATATTA[A/G]TTCTAGTCCATTTAGATTGTGTAAATGATCTAA ATGGNGTAACCATTTAATATCAAAAGTATAACAGCATTTAAGTCAGCTTTCGAAGAAACTTTTATT
WI-22631a	52	T	C	---	AAGATATAGTGGCAGGACAAGATTGGTCACGAAATCCTGGCTTCAGTTCTGA[T/C]AGCACCATTTT CAAGTTTAGGCAAGGTATTTAACCTCTCAGGCTCATTTCTCTTTGTAAAATTGTGATAAATGGACC TATGTACCATCATCATAGGGTACTTGGACAAATCAACTGAAATTTT
WI-20258	157	G	T	---	AATCCACACTTTCACGGAGGGGGACCCAGCCTGCCATGTCGTCCCCAGGCTCACAGCAGCGGCGGCTAC TCTGCTGGTGGTTTGGTGGCAGGTGGCAGGTGGAGATGGTGACGGCGGCATTGGAAACCGTAAGGCATGACAACG GGAGGCCCGCCGGGGGTGTTCAG[G/T]CGCGTTGACGGCAGGTGCATGGCCAGGCGGCCTCTACAGA AGGAGGGGACGGCCAATTCACAGCCTCTTGACGTAGTTTCCGGGGAAAGTACC
WI-22714	212	C	A	---	ACTACACATATGCTGATTTTCAACAGTAAAAATAAACATTTTACATTTGTAGAGAAATCTAGGGTCT ACTAAATAATCTAGTACTTGTTTCCACTCTCCTGCTAACTCTGACAGGAGTGTTGTGGGAAACGAAGT CTGAAAAGGATTCAAAGGGGGCTAGGATTTGCCACAGATCCTGTAAAGGAAGGATGAGGTGAGCTT ACCAACCCCA[C/A]T[GA]TGAGTAGGGGCCAAACATCCTTAACAAGCTAGTTGCT
WI-22734a	44	G	A	---	TGGGGCTACTTTAGATGGGATGGCCGTCAGGGTCTGGGAAGGCCT[G/A]TCTTAGAAGACATTACCCA AATGATGAGAGCAGCAGCCAGTCGTCGAAGCCATAGTTTGGATGGCGAGACTTTTCCGGCAGAGGAAAT AGCAAGTGCAAAGGGCCTGAGGGAGAAATGAACTTGGCGTTGTCCTACAGGGTGAAAGGGCGGCCGGT NTGGCTGAGGTTTAGTGGGATG

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WI-22724	117	A	G	---	TGATATGATGTCTGAGATTTGCTTCCAAATATGCCTAGGAAGGAAGAAGTGTTTAGAGAGATATAGGACAAATCAAGATTGTCAAAATGTATAACTGTTAAAGCTTGCTAAGGGT[A/G]GTTATTCTATTTTGGGATATGTTTGGGAATT
WI-22750	48	G	A	---	TGTAACCTGTGTTTTCCTGAAAGTTGAGGGAAAGCTGAGCCAGCTAAT[G/A]GGCTCATACAAAGGTTTGGAAGACCCATTCTGACTACCTAAAGGAGAGAGTGCAGCCATTCTGACCATTCTGACTGTGCT
WI-22775a	60	A	G	---	TGCTGTTTCTTTAGTTCATGACGTTTATCACAATGTGCTACTGTTCCATTGTTACATC[A/G]TAGTAGGAAAGGGAAAATAAACTCCCTAAGGGCAGCAATAATTCTGTCTTGAATCCTTCATTCAGGCAAATATTTGTTGAGCACCAAGGGCCAGATGGGAACTGAGGTATGTAGGTGTTGGGAGCCAGGAAGGAAGGGT
WI-22808	143	C	T	---	CTTTAGCTAATGAAACTGGCTATGTGGACTATGATAGACCAAGAAAGCTACCCAAGTCCTGAGGGAGCCTAGTCCTCCTAAATGCAAATGCAGACAATGTACCCATGACAAGGGCTACAGCTTGGCTTTAGCAACCAGGAGGATGAAGA[C/T]AGCAAACTGATTAAGAGAGTAGGTATAAGAACCAGGGAGAGTGGGGTCCAAATATC
WI-21016	207	G	A	---	TCTCTCGGTGTCTTGAGCGCCTCATCCCCACCCCTCCAAGCGCCCTCATGCCCACCACCGTGTCCCACATTCCCCATCCTCCCCGTGTCTGCTCCCCATCTCAGTCCAATTCCCAAGGCCAGAGCCCTGGCCAGCTTTTCTGGGAGACAGCATGAAAAGGAGGGGAGTGGAGATGGCAGAGATGGGGTGGAGCCCAGTGCGCGTGTGGGTC[G/A]TTGGGCGGTGGTGATGTGGGGGCCAATCCTGAGGGCCAGAGGTTCA
WI-21031	31	C	T	---	TTGAACACCTGACCTCTGACCTGTGACATGTGG[C/T]TCTCTGGTCCCCATTGTCTCCAACGGTGGCACATCTTCATCTTTGTTATATCTGCAGGAACCACTCAGTCTCTTCAGCAGCCGAGAAAACACACACA
WI-21314	122	A	T	---	CCATATCCAGTCTTCTTGAAGCTTTCTATTGACTTTAGGGGTTCAGTTATTATATCCTTTATCACTATGACTTTCATTTGATTTTTTATTTGTTTCTTCCATTTCTGTCAAACTTTC[A/T]TTTTTTGTTTATAAACTGTTTCTAAACTTCACTTAATTCTCTATCTGTATTTNCCTGAACTTCTTTTAGAGG
WI-21186	95	G	A	---	AGCGGAGCATCAGAATCACCTAGAGGGTTGACTAAAACGACTTCTGGACCCAACCCCCAGAGCTTCTGATTCAGTAGGCCTGAGGTGGGCTTAC[G/A]AATTAGTATTTCGAAGAACCTTCCTAAGTGTTGCAGATGCTGCTTGTCCCGGGGGAACACACTTTGAGAACTATTGTTCTAAAATGTTCTCTCTTTCTTTTAAAGGAGAGACAGGAATTCCAGAGAAACTGCTAATTTAAGCATAAGTGTATTGAAT
WI-21187a	94	A	G	---	CCACGATAACTATAAAAGCAGAAAATTAGCTTTGAAAATCAAATAACATATTTAGTAACACACATTCATTTTTATAAAACACACATAAAAGACACC[A/G]GGNTCTCAGTAATGCTCTAGTCCAGGGGTTCTCAAAGTATGGCTTCAGAGACAAGCCCCATTTGCATCACCTAGGGAATTGCTAAAATGCAGATTCCTCAGGCCCTACCTACTGATCTCACTGAATCAGAAACTCTGAGGGTGAGACCAAGCAACCTGT

ID	Pos				Sequence
WI-21190	39	T	C	---	TTTCCCCACATACCAATGCACCTGTTGTATAAACTATT[T/C]GTGGGTAAGCCCTTCTTGGAGAC CAGTGACATAGAGACATGATTCCCATTATTATTATAACAAATAATTAATAAATCTGTACTATTACTGC TTTAGTTATCTAGTGTTATTGAGAAAGGAGAAGTCAGCAGTAGTTTATTTTCCATGTAATAAAAGCTT AACACA
WI-19937d	186	G	A	---	ACCATGTGCATTTATTGGCATAGGAAATAGTGACCAAGAAAATGCAGCAANCTAAACTTGGAAGGAAA GAACTATTGCACAACCAAAACATTGTACATATCTGATTTAGACAAGCAAAAGCACTTCATGTTGTCT GTAAAGGTGTTCTATGGCAACAGTGATGACATTGGTGTGTTCCTCAGCAAGTC[G/A]TCCAAACCTTC CAAAAGAAGCAGTCATTGAAAAATGCTGACTTATGCCTCAGGAAGAA
WI-19937c	185	C	T	---	ACCATGTGCATTTATTGGCATAGGAAATAGTGACCAAGAAATGCAGCAANCTAAACTTGGAAGGAAA GAACTATTGCACAACCAAAACATTGTACATATCTGATTTAGACAAGCAAAAGCACTTCATGTTGTCT GTAAAGGTGTTCTATGGCAACAGTGATGACATTGGTGTGTTCCTCAGCAAGT[C/T]GTCCAAACCTTC CAAAAGAAGCAGTCATTGAAAAATGCTGACTTATGCCTCAGGAAGAA
WI-21117b	227	C	T	---	GAAAACGGGGTGCTAAACAAAGAAAGTCTCAGATCCCACTGAAAATCTGTTCAGTTTCACAGGGCTC TCTCCAGAAAAATGCATATGTACCAATTTGCATGTACAATTTCAGAGCCTTCAAATACATTCTGGGG TCCAATCACATACTTCAGGTTCAGACTCCTCCAATATTCCTACAGTTCTGAAGANTTAGCAGT CCTCTCATTCATTCTACAGTCTGTATT[C/T]TTCTACTGAATCTTGGGTGGGAG
WI-21122a	42	C	T	---	TCACTTTTGATCATAATCCCCTGTAAAAGCTAAAGTTATTCA[C/T]TTAACAGGAACTCTGTTTTTCC TTATTCAAATGTCACAAGCCTGACGCGTTACTGTACATATTGCTAGCAGGAGCAACTGGAAATACT AAACAAATACTACTGGAATTCACATTACACAGACAGAAACCAACATGGATGCCACACATAACTTCCT TTGTAGGTTTCACAGAGAGCCTATTTGTGGGTTGCT
WI-21254	53	A	G	---	CAGTTTTGGTACAGGAAGGGCCCATGAATGTGGGCGGGAACTATTCCACAGGAG[A/G]CAAGGAGAAG CTGTTCTCTGG
WI-21054	23	G	T	---	AAGGAAACTGCATGGGTACAAAT[G/T]TCCAATTCATACTTAACAAGGTGGGGAAACGGGTCATTCT TGGCCTGCTCCAGAACAAGGGCGAGTCTATGCACTCCTG
WI-21059b	181	T	C	---	GGGACCAGGGTAACACCATTAGCAATATCCGTTATCAGCCTTATTCTTTCCCACTGAGCCTGGCTGAA CTACAGCTGCCAGCATTTCCTGGGCTTGCATTTCGTCGTCATTTCTCTATTC[T/C]ATTGTAGCCAGGGCAAAA AATCCTGGGGAAGAAGACATACTTCACTGAAGTCATTTCTCTATTC[T/C]ATTGTAGCCAGGGCAAAA TGAGATTAGGGATTAGCTCAGCGCCAGAGTTAGGGTGACTATCCTTGCCTAAT
WI-21059a	63	C	T	---	GGGACCAGGGTAACACCATTAGCAATATCCGTTATCAGCCTTATTCTTTCCCACTGAGCCTGG[C/T]T GAACTACAGCTGCCAGCATTTCCTGGGCTTGCATTTCCCAGCTTGTCACATCTTAATTTCAAGCTG AAAAATCCTGGGGAAGAGACATACTTCACTGAAGTCATTTCTCTATTCTATTGTAGCCAGGGCAAAA TGAGATTAGGGATTAGCTCAGCGCCAGAGTTAGGGTGACTATCCTTGCCTAAT

ID	Position	Allele 1	Allele 2		Sequence
WI-20442	37	T	C	---	TCCACGTGAAGGAAGAAGAAAAAANGGGGGGGGCT[T/C]TAAGGTGGCACAATTTTAAGAAAAT ACCATCCATTTTCTCAGTCTAATCTGAATCCATCACATTAAAACAAAAGTGCAAGTGATGAGACGAA CA
WI-21235	43	T	C	---	GTGACAAGAGGTGAAGCAAGGGACAAGGGGCAGCAGGGGCAGTC[T/C]CTCGGCCGGCCGATGTTCCAGGG CAAGCTACGTA
WI-22012a	57	T	C	---	ATCAGAACTGCAATCTGCACATGAAAAGACCTGGGGGAATGCCTACACTCTGAATT[T/C]CATTAC ATCAAACGTTAAATTTGTCCGACCAGTTCTTCATTGCTGATCATCTTTGATAATGACAGATCCAACAT GAAACTCCTGAAGCAAATGAATATTTACCTTGCTTTCATGCAAATTAGGGACCAAACTCAAAGG TTTCATCCATGCTGGGACACCAGATCTAAGGAATTGTGACAGGGATCTCT
WI-21149a	167	G	A	---	AGGACCTGCTCTCACACGTTCCCTCACCCCCACCAGCTTTGGCAAAGATAGTTGACTAAATACCACT AAATAGTTGGCTTTTTTTTTTTTAACAATGACCTTATTTATCTTTAACTTAACTGAGTCTTTATATA CAGACCTGCCCAACTGGAAAGCTTTACAC[G/A]TGCTTCAGAATGCGGCAGTATTGCACAATGGTT TGGGGCAGGTTCTGTGGTTAAACATGGGATGGAACCCCAGCGCTCACCTG
WI-21376b	188	A	G	---	GGTGTCAACTTGGAAATAATGGTTAAAAACAGGATAAGCATTAAGGAAAAACACTTTCAATGTGTC TTCCATTTGATGAATTTGTTTTCTCTTTATCCCCGCAAATCTGGGGAAATCTGGGCATGGGGAGAGCCT GACAGTGTGAATCTGTTCCAGCCCAAATCTGCAGCATTAGGGATGAGTTCTC[A/G]GAAGTGATTCT GAACTGAGCACGCACTCATGTCTGCTGCATGGGGAACTCTGGGGAGAAGAGCCT
WI-21382d	125	C	G	---	CCATTGCAGTCCAGAGATGAGAAACTGGACCAGAGAGGCAAATCATGAACAGAACGGGAGTCAAGAGA AGGGGTTCTAAGATGGAGAAGTGGGGGCGGGGTTGGATCCAGTGGGATNTGGCTTCCC[C/G]AGGTT GCAACCCCAAGGAAGTTCTCTGGAAGCAGCACCAGGTCTGATGGGGGAGCAGAAGAGAGCTGCCATCCTC AGTCAGGGTCCGAGTCAGGGTCCGAGGAGAGCTGCTCTCCATAGTCTCGCAC
WI-21437a	201	G	A	---	TCCCTGAGGTTGGAGTCCTAGCATAGCTCCCCTCCCTCAAAGAGGAGACAAGGGGTCAGGGGCAGAGC AAAAATCCAGTCGCTTCAACCACGGAGACTGCCTTTGGGATGGAAAGTTTCTGGAGCTCCCTCCATT CTATTCCTGTGGGGCAGGAACATGCCAGGGGTCTGCTGGTAAATGCAGGGGGTCACCTTTACCAGGGGC[G /A]CAGGCATAGTGTGGCCCCTGNCTGCCCCTGGGGGGCCACCCTGGGAACAGT
WI-21202b	156	A	C	---	CAAAATAGAAATTCTTGTGAGTGGATTGACTTAATTTATTTCTGTATAAGCTAAATATGTTGATCT GTTTATGAACATGTATTTATAAAAATGGTCACAATATATTTTAAGTTAACTGATTTATTATTGAGGG AGGAGAGAGAGTTGACCAAGCTCACATGCATGAGAGTCTACCATGCGATATCTCAAACATG A
WI-21202a	61	T	C	---	CAAAATAGAAATTCTTGTGAGTGGATTGACTTAATTTATTTATTTCTGTATAAGCTAAATATGT[T/C]TGA TCTGTTTTATGAACATGTATTTTATAAAAATGGTCACAATATATTTTTAAGTTAACTGATTTATTATTGA GGGAGGAGAGAGAGTTGACCAAAGCGTATCCTACACATGCATGAGACAGTCTACCATGCGTATCTCAAACATG A

ID	Pos	Allele		Sequence	
WI-21627b	153	A	G	GCATGAAAAGAACTCCAATCAGAGACTTTATTCAATAAAGCAGCTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTTCCAGTATCAACTTGAGTACCTCATTATGGATATTTATGCTAGGAATGACAA CAGTAAGGGCCATTGCAAA[A/G]TCCAAAGTCATCTAATATTAAACCATATTTACATAATTGTAGG GACAGTATACTAATACTCTACAATAAATAAGGGTTTAAAAATGTGTTGCTTA	---
WI-21627a	106	A	G	GCATGAAAAGAACTCCAATCAGAGACTTTATTCAATAAAGCAGCTTTCATGAATGCTTCAGGTCAGTG TATGTGATCAGCTCAGCTTCCAGTATCAACTTGAGTACCTC[A/G]TTATGGATATTTATGCTAGGAATGA CAACAGTAAGGGCATTGCAAAATCCAAAGTCATCTAATATTAAACCATATTTACATAATTTGTAGG GACAGTATACTAATACTCTACAATAAATAAGGGTTTAAAAATGTGTTGCTTA	---
21399a	75	C	T	GGATTTGAGTGCCCAACTTGATCTCAAATTCACTTCTTGCATGTAAACAAGCTCATTCCCTCTAAAGTT TCAGTTT[C/T]TTCACCAGTAAAGGAAAGGTTGGACCAGACATGTTGGACCGTAATGCTTGGTAA CTGCCTTCTGCATTGTCTCTGAGGTGTGTGTCCTAGGACTAGGTAGGATCTCTCTTGCTTCTGCC TTACCTAGGCATAGTGCCTGATAGCAGGCTGAAGCCAATTCATACTTGT	---
WI-20329a	68	G	A	CGATGTCTGCTAAGATAGGAGGTTAATTCTTTACATGGTGAGTGGGTCACAGAGACAAGAGCATCAAT C[G/A]TCTGTTAGCAGCGGAGAGACACTTTAAGTTGCCCCAAGAGTACAAATCCCATCTATGAGAC AGCAGTGCTGGCTTCTTAAAAACAGTAAAACCAATCAAAAGAAAAGATTTAGAGGTTCAGACATT AGGAACAANTGTGGCCAGAGATACCACACAGAGCCCTTGAAGGGAAAGGCCTCACT	---
WI-21249	155	T	C	TTCTGGCATTCAAATGTACATGTAAAATCCAATTAACAGATCAAATTGTTACACTAAGTTTCACT TAGTATCTAAGTATCCAATCACAATTGTATCTAAGTTTCACTTTAAGAAACATTATAAAGGTAATT AAAACTCTAGGTGTATACTTA[T/C]ATGGAACTAGTTTATTTCCNATTAACTACTGTTCATTGCGTA AAGTATGTTGTCCCAATTTGTTTTAAGGAATTATAAAACATTGAGA	---
WI-21504	147	C	T	TGACACAGCATCAATTTCATGAATACTTTGAAAGGGCCATTAGAAAAAATAAGAGCCAATTTGGGGTC ATTTGAGAAAACATTTTCAGCACAATTACAGTGGGGGCACGGGCGTTCGGCTCCAGCTGGGTTTCCC AGATGCAACAAT[C/T]GCGGTTCTGGCCTTTCTCCCACTGGTGGGGATCGCGCCCTTCGGAGCTCT CAGGG	---
WI-21242	115	G	A	CTGCACCAGGGAGGAGGACAGCTGCTGGCCAGGGACTAATAAACCCTTCCACCTGGCCATGGTGGTGTGTT CTCTATGGACCGAGGCCCTGAAACGCGGGCGCAGGGGGCAGAGAAC[G/A]CACTAGCTTGGGGGTG GGCACCAGCTTCAGACCCCTT	---
WI-21475c	181	A	G	TAGCCCTTCTGCCAACATCTGCAATNTGAGGCTGGGGTGGCCTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGGTGGGCTCCAAACCCCAGGCTTCTCACTTGCTTACTAAGCACAG CAGTCTGAAGCTTGGGACCTGGGCAGTGCGTCTTTGGAGAAGGCA[A/G]GAAAAGCCACAGCAGCAAC ACTTAGGAGCAAGAACCCTTCCGGTTCTCCACCCTATTTCCTCCCTGAAG	---

VI-!1475b	117	A	T	---	TAGCCCTTCTGCCAACATCTGGCAATNTGAGGCTGGGGTGGACGTTGGCCTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGGCTGGGCTCCAAACCCCAGGCTTCTC[A/T]CTTGCTTACTAAGCA CAGCAGTCTGAAGCTTGGGACCTGGCAGTGCGTCTTTGGAGAAGGCAAAAAGCCACAGCAGCAAC ACTTAGGAGCAAGACCCTTCCCGTTCTCCACCTATTCTCCCCTGAAG
NI-20893d	207	A	G	---	TGTTTGTTGTTCCAGCCACCACATCTTCTCCAAAGGAACCCACCCAGCCCGTGTGCAGGCTTGCTGCAGGG CTGTCTTCGGCGGTTAAAGTGCTACTGAGGAATACAATCATTGTCACGTAAGTTCATCACCGCACTCC AGCGTCAGGCCAAACCTTTCCGTGGACCTGGGNAAACCTGCCATTTCTTCTTCTTTTACAATGCAGT TTC[A/G]ACATAAACATTGGTAGAGTAAACAACCAAGCCTAAATG
NI-20893c	179	T	C	---	TGTTTGTTGTTCCAGCCACCACATCTTCTCCAAAGGAACCCACCCAGCCCGTGTGCAGGCTTGCTGCAGGG CTGTCTTCGGCGGTTAAAGTGCTACTGAGGAATACAATCATTGTCACGTAAGTTCATCACCGCACTCC AGCGTCAGGCCAAACCTTTCCGTGGACCTGGGNAAACCTGCCAT[T/C]TTTCTTCTCTTTTACAATGC AGTTTCAACATAACATTGGTAGAGTAAACAAACCAACCACAGCCTAAATG
NI-19941c	71	C	G	---	GAGCTCAAGGGAAGACCCTTACCCAGATAGGGACTAACTGGAGGGGTGGAAGGAAACAAGGTGAAA GGTAT[C/G]GGTCCTGGTGAGACAAAGCAGGGGGCCTGAGAACACAGAGCAAGGTGGGTTTGGAG GGAGCACAGCAGGGTGCAGGAGGAGGAGATGGGGACATTTCTATTCCAGTGCATGTCCCCTTAAAT AAACTGGGTACAGGAGCATTNTGGAAGGAGAACCAAAGGACAGAAGAACAAAGCG
WI-21552b	166	C	A	---	TGGGTACATGGACAGAGATGTATATGTTTATGGGTTATATGAGATATTTGATACAGATACACAATGTG TAATAATTACTTCAGAGTAAATGCGATCTCCTTCACCTCAAGCATTTATCCATAGTGTTACAAAGAA TCCAAGTATACTCTTGATTATTTAAAAATGTA[C/A]AATTAAATTATTATTGAATTTAGTTACCCC ATTGTGCTATCAAATATTCAATCTTATTCTTGTAACTATTTATTTGTA
WI-21552a	66	G	A	---	TGGGTACATGGACAGAGATGTATATGTTTATGGGTTATATGAGATATTTGATACAGATACACAATGTG /A]TAATAATTACTTCAGAGTAAATGCGATCTCCTTCACCTCAAGCATTTATCCATAGTGTTACAAAG AATCCAAGTATACTCTTGATTATTTAAAAATGTACAATTAAATTATTATTGAATTTAGTTACCCCA TTTGTGCTATCAAATATTCAATCTTATTCTTGTAACTATTTATTTGTA
WI-21512	54	C	G	---	TCCTCGTACTTCATGCTCCCTCCCTGCCCCAGAACCTTACAAAAATATTTCTGT[C/G]TAGAGAGGGA AAGAGCTGGTGGCCTGCTCTGGAGGCAACGTCCAGGTCCGGGAAAGGCACTCGTGGTCTGTGATCGTC TTCAGTGATGGGAGGTCTCCACTCGCCCCCAACAGCAGCCTCGGGGCCAGAGATGAGAATATGCTGTAA TCCAGTACAGGGGCTGCGGTCGTCGGTGGGGTCCCCAACAGCTCCTTCTTTGGGGG
WI-21513b	192	G	A	---	CACATAGTTTCTCAAGAAGAGGATGAACTGAAAACTCCTCTCAAGGCAGGACAAAGCAACTTTCCATT ATTCTTAGTTAGACCAGAATCTTTAATTTTATATTCTCTTTAATAACTGTCAAAATACACCAAATA CTTAGAGAGGAAAATATTCACAGTATACCAAAAACATTTTAAGATAAAGAGGCAGTGTAA[G/A]AGTAG TATTCTCTACATACCACAGTATACAATGATGCCTTCCTGCAGGTTTAGGAAC

ID	Position	Allele 1	Allele 2		Sequence
WI-21514b	133	C	T	---	TTGAACCTCTGAAGGTGGCTTATGTCTCGACTCCTCTTCTAGGACTGGTCATGAGCTGGTCATGAGCTGACAAGCATAG AGGCAAAGTATCTCAACATTACAAAACCCCAATCTTCAAGGAAAGGAGCACATTACCATGGAGC[C/T]ACAGGACTCCAAAGGACCTCAGAAAGCATTAGCCAAATCTCCTTATGCAGGAAATAAATGAGG ANTTTAAGGCTCAGATGGGGTTAAGGGTGATTTGTCAAGGGTCATAAGGAACT
WI-21514a	100	A	G	---	TTGAACCTCTGAAGGTGGCTTATGTCTCGACTCCTCTTCTAGGACTGGTCATGAGCTGACAAGCATAG AGGCAAAGTATCTCAACATTACAAAACCCCCA[A/G]TTCTTCAAGGAAAGGAGCACATTACCATGGA GCCACAGGACTCCAAAGGACCTCAGAAAGCATTAGCCAAATCTCCTTATGCAGGAAATAAATGAGG ANTTTAAGGCTCAGATGGGGTTAAGGGTGATTTGTCAAGGGTCATAAGGAACT
WI-22020	27	C	G	---	ATGAAACATGTTGCAGTGCGGATGAAT[C/G]TTATCATGATGCTAAGTGAATAAGCCAGACACAAAA AATCCAAATGTATCATTCTACCTGTATGAGGGTACTT
WI-19576a	113	A	G	---	TTCATCGGTTCTTAATACAGTACAATCCTTTGTTGAACAAAAGTCACACTGGCAATGATTATTTACA GATCCAAAATAGACTCAGGCTTCAGACACATAAAAAATTTAACATTC[A/G]TCAGTTCAGTGATTAGT CACAGAANTTAAACATCTGCCCAGATGTACCACAATTGGTAAAAACTACAGCTTCTCTCCACGGGGA G
WI-21695a	141	A	C	---	ATACACAGGCCACAATTGCAGGATGGGAAAGGCAGTGGGCACTTGGAAGTGACTACACATGGCAATA AGCAGCCTATCTCTTTACCAACCAGAAGTTTCTTGGGCATGTGATGGTAGGCCAGACCCTTTCCAA GGGAATA[A/C]TACTACACTGTGACTTCACTGTGTTCAGANTTCTAAGGCCCAGCAT AGTGGGAGGAAATGTGATGACTTCACTATACTAGGAAGCAACTTATGAGTG
WI-21574a	235	C	T	---	AAACCCAGAATTTAGGTACTTTTGTATTATGAGGAACTCACTATAGGAAGCAACTTATGAGTG TGTAAATATTTGATCTAGCAGCAACTTCCACTGATCCTGGCAGGTGACAGCTCTCAGTGAACAGCGC TCATCACCTAAAGTGAGAGGCTGTCTATTCTCATTGTGAATGTCCCTCAGAGTCACTAGGGAGCCATT GGGCAGGCCAGGGAACTTACTGCCTACTTCCT[C/T]GTCTGTCAGGTGGGA
WI-21644c	151	T	A	---	TGACTGCCAAGATTTAGGCCCCAACTTAGGAGCAAGGGTCACCTCTAACCTTTCAGGAAGTCTTGGGT GTGACCCACTGCATAAATGGATTTCACCATANTATTAACAGACTCAAAGTGTACATACAAGCTTG TTTCATAAATAGGGA[T/A]TTCAATCAAGATCCATGGAATGATGCAGTTAACATGTGTTCTCAGC TTGCCTACTGACCACCTTTCCTTTTCTAAATATGGCAACAACACAGCAAGTC
WI-21614b	55	G	A	---	TGTCTTTAACCTCAAAAGTCCAAATAAACATATAGACATTTGANTATAGCTATC[G/A]TTTTAACA AACCTCATTATGATCGATCACTGTTGCAATTCAGTCAGTGAACATTAAAATACGGAACCATGAACATATTAATAAACA TTTACTGTGTGTGGGTTTGTTGGGACTGAACATTAAACCATACGTGTATTTCTAAGGTACTAGGGAGTT GGAACAGCTACTACGGGTCAATGGTATTTGGGCAGTTGGCCTGTGTGTGGG
WI-21615b	151	C	T	---	GACCGAGAAAACTGCAAGGCATATGATGTTGTCGAAGTACATGATCACATGACTATTTCAAGCTTATAGA GAAACTTGCAAAAGTACAAAGATGGCTATTTTTTAAATTCATACATATTAAGGATAAGGATGGACT CTTTCACTGAGTATTATT[C/T]AGGACACAATCGACGGATTAATCTATTTGANTTATACCATAGGCCC TATTCTATATTGGGCAAAGGGAAAAGGTAGGGGTACTGTGTGGAAACGGA

ID	Pos				Sequence
WI-21981	61	T	A	---	TGTCATCTCATTCTGGAGAATCATAGATGTGGCAGAAATACATATTCTTGAAGAAGAAAAAAA[T/A]GTCTCCCTTATGGGTACTGTGTGGATAAGGTGTGGGATTCAATAGGTGCTTGGGAATTACAGGAACAACATAAAAGGATATAATGGATGGGTTCACTCTGTTCTCTACAGATCCGTGCTTTACACTTTTACATGTGACAATCTAGTTGTAGGCGTTTAAGGTTAAATTTGG
WI-21660	120	C	T	---	TCCCAACTAGCCTCTCCAGTATTTAGATGAGGATAGAACAGATACGGTGTAACACGCCTCTCCACTGCTTACTGTGTGTACCAAGAAGGCAGAAAGCAGCTCACCCAGCCTAACCTGGCC[C/T]GTCTTTTCAGGCTTCTCAGGATGCCCACAGCACACTACTGGGAACTGGGATGCAGGAGAAGCCAGGGTCGTCTTCAGGAGGGTCACAGC
WI-19105c	211	C	T	---	TGGAAAGTAGCCCTTCTGGACAGAAAGAATATTTGTGGTCCATGTGGTTTGAGTCTGTTAAGAAGGACACTAAGGCACATGGCTGGTGATCTTTGCGTCATAGACACGGGTGAGCTCATGGTGGAACTCCTCCTTGTCTGTGTAGGTTTCCAGGGGCAGGATTTCCACCCAGGGTGCCCGACAACTTC[C/T]TTCCAGGGCAGGATTTCCACCCAGGGTGCCCG
WI-19105a	33	T	C	---	TGGAAAGTAGCCCTTCTGGACAGAAAGAATATT[T/C]GTGGTCCATGTGGTTTGAGTCTGTTAAGAAGGACACTAAGGCACATGGCTGGTGGATCTTTGCGTCATAGACACGGGTCATAGACACGGGTGAGCTCATGGTGGAACTCCTCCTTGTCTGTGTAGGTTTCCAGGGGCAGGATTTCCACCCAGGGTGCCCAGGGTGCCCGCCCACAACTTCCCTCCCAGGGCC
WI-21760c	81	C	A	---	CAAACCTAGTCACTCACTGCACTCTACTGATGCAAATGATTTGGAGGTGTCTTCCTAGCTTTACAATAAGNGGAGGGACCTCTGACTGCA[C/A]CCTCTGTCTCAGTTTCAGGGCA
WI-21760a	35	A	G	---	CAAACCTAGTCACTCACTGCACTCTACTGATGCAAATGATTTGG[A/G]GGTGTCTTCCTAGCTTTACAATAAGNGGAGGGACCTCTGACTGCACCCTCTGTCTCAGTTTCAGGGCA
WI-21569b	198	T	C	---	TCTGCCATATGTTCCCAGCACCACTATTACTGTGTATTATTTCTCTTTGGAGGAAAACCAGGNATTAAGAAATCTGGTTTGAATTTCCATGATGCCTAACCTCATGGTTAAAAATCCTTTCCTTACCAAAAGGAACTTCTTAATCACCAGAGAAACAGAGGGAAGACTGAGATATGTTTGCAGAAATTTATCTCTAC[T/C]AGAGACAAATTCATAGTTCATAATCTTCAGGGTTGTGCTTTACTTGGGGGGC
WI-20934a	72	T	G	---	CCAACATGCAACATAGTCTTCATTCTTAAAAAGTACATAGTAAAGGTATGAAAAACATTGTATTCAGAGAA[T/G]TCTAAGACAAATGGTCAAATATTCAAATGGCCACTAGTGTAATTCCAGCAGACAAACAGCATGAAAAGGCCGGGAGACAGTAATAAAATACGTGCCCATTGCAATGAGTTACCCAATCAAGCCCTTTACCTCTCCTTACATGGCAGATTAGAAGACCCTNTTCCCCAGGAGA
WI-21561	55	T	G	---	TTTCCATTTATTCAGCCGGGCCATCAGAACAATAGCATCTATACCTTCGAAACC[T/G]CCTCTTAACCTCTCCCAGGCAAAGAAGGAAAGAAAAGTGATCATATTGAATTCCTCAGAACTTGGGGATCTCAAGACTTTTTAGAAAGTGCTTATTAAGAGAGGCTTGAAATATAAGTACCAGAATGATGATAAAATGTAGCCTTTGTGGAATAATTTTTGTGTAATCTGTTTAAAAAGATTTTTGGATGCATTGTCCCCA

WI-21961c	200	T	G	---	AGCTTTGCTTGAAAAATTGGTACTACTACCTTTGCAATTCTCTTATTATTATTACTTTTATTTTCCGTGTAAGTTATTGGGGTACAAGGAGGTATTGGTTATATAAGTTCTTAGTGGCGATTTGTGTGATTTTGGTGCACCCATTACCCAAGTCCCAAAGTCCATTGTATCATTCTTATGCTCCCACTTTTCCCCTCAGTCCCTGCCAAAGTCCATTGTATCATTCTTATGC
WI-21961b	73	G	A	---	AGCTTTGCTTGAAAAATTGGTACTACTACCTTTGCAATTCTCTTATTATTATTACTTTTATTTTCC[G/A]TAAGTTATTGGGGTACAGGAGGTATTGGTTATATAAGTTCTTAGTGGCGATTTGTGTGATTTGGTGCACCCATTACCCAAGGAGGTATACACTGCACCATACTCGGTCTTTATCCCTCGCCCCCTCTCCCACTTTTCCCCTCAGTCCCAAAAGTCCATTGTATCATTCTTATGC
WI-21956	26	T	G	---	CCCACTTGGGTCTCTTTCAAGTGAAT[T/G]TTCCTTCGTTCCTTCGTTCCTTCTTCGTCTCGTTTCTGCTTCATGCCCCTCAGTCGAATTCTTCTTCTGAGGCGGCAAGGACTGAAGTTGCTGTGGACCTGTAGGGGTTCGACGCCGGTAACTCAGGGTAACTCCTATCTCTTCCACGGTAACAGAGAGGGTACATTATGGGGGTCCAGGTT
WI-21966	148	G	A	---	CAAACATACATTATGGCTGCCTTTATTTAAGAAAATGTTACTGAGAAATCTGTACTGTAACAACATATTTTTGTTAGAAGCAGCATGAGTGAGAGTGGTGTGTGTGTGGG[G/A]AACAGGATAAAAAGGTATAAAAACTTGGTCCGAAATCTTTGCTTATTAACGGATTGCAATGGG CTTGGCCCCTGCTCCTCCACAATGTTTCTCACACTTAATTCATAAGAGAGGTAGA
WI-21930c	146	G	C	---	TATACTGGTTTTGGTTACATGGATGAATTGTCTAATGGTGAAGTCTGAGATTTAGTGTACCCATCACCTGAGTAGTGTACATTGTACCCAACTTGTAGGCTTTTATCCCTTACCCTACCTTCCACCCTCCCCATTTTGAGTCTG[G/C]CATAGTCCATTATCACTCTGTATGCCTTTGCATACCCATAGCTTAACTCCC
WI-21139a	165	T	C	---	GCTCTAGTGAAGAAATTCAGGACGCGGTCTTCAGAGCAGAGAGGGCTTGGTTCAAGTCCCTGTTCTGCCACTTACTAACTGCATGACCTTGAGCAAGCCACTTAATTTCTCTGCTCCTCTGTGAAATGGGTACAATGTGGGTCAGCAGTAAAGGAACTAATACA[T/C]GTACAGCACTTCAGCACAAAGCCTGGGCACACAG
WI-20317b	217	G	T	---	CACTGCCATGGGAAATACACAGGTAACATTTTAAACAGTGGGGACAAAATTTAAGTACGTGGCCAGCTGTTGGTTGTCTTGTGGTCATTAAGTGTTAAGANTCAGGAGTACTTAAGTGCTAGTGGTTACAAATTTGTTCTCTTCAGTTTTCATTAAGTAAATTCTAATAGATGATATACATTATTACTGCAGATAAAACCATCATCAGAAA[G/T]TATTAAATTAATTGCATATTTTGAGGCTACTCT
WI-22082e	179	G	A	---	CAGGACTTGGTTGCTGTCCCAACTGCACATAAATGTCCCTTTTGTTGAGTTATTGGTTGTGTGCGTTTTCCTTTTTTTGCATAAGAAATATGTCCATTTAGTCCAGAGGCTCTTGCTTATCCGGATGACGGAGGGTACACGGGGGCGCGTCCGCTCAGTTCCCGCCGAAGGACGTATTC[G/A]CTGAACTGGGACGAGTCTACTCCTCCCCCACAGGAGCCCACGATTTCAAATCCTCTTTGCTGCAACCTCT

NI-22082b	67	C	T	---	CAGGACTTGGTTGCTGTGTCCCAACTGCACATAAATGTCCCTTTTTGTTTGGAGTTATTGGTTGGTTGTG[C/T]GTTTCCTTTTGCATAAGAAATATGTCCATTAGTCCAGAGAGGCTCTTGCTTTATCCGGATGACGGAGGGTACACGGGGCGTCCGCTCCAGTTCCCCGCGAGGACGTATTCGCTGAACTGGGACGAGTCTACTCCTCCCCCAGAGGAGCCCACGATTTCAAATCCTCTTTGCTGCAACCTCT
NI-20993	139	A	G	---	AACACAAACTCCCATGCTCTTTCAAGATTCCCACACCCAGATACTAAGACATATTAAAAATTTACAGCAATTAAAACAGTGTAGTTTGGTACAATAAACACATATAGCAATTAAAGACAGTAATTTAGGGGAAAAACCCTGGGCTTCT[A/G]TAACAAGTGAGTATACATTAAAGACACAGTATTCGAGAATGGCTTCAGGATTAATTTGATTAATTAGAGAGAGCCTATTTCAGGTCTTCCTAGCTCATCCACACACATCACC
NI-21723b	125	A	G	---	AAGCGGATTTTATTAAATTGATTTGGACATACTGTGAGGTCAAATAATAATATTTCTGAAGATAACAATTATGGACTTTAAAGCTCGACATAAAATTAGTAGCTTCAAAAGGGTTAGTCATATTCCCCA[A/G]CAACAGCATGATAAAAATAAATTCAACTATGTAGAAAATATAGAAACTCTAGGACTAGCTGGAAACTCGGAAATCATT
NI-21723a	82	G	A	---	AAGCGGATTTTATTAAATTGATTTGGACATACTGTGAGGTCAAATAATAATATTTCTGAAGATAACAATTATGGACTTTAAAGCTC[G/A]ACATAAAATTAGTAGCTTCAAAAGGGTTAGTCATATTCCCCAACAACAGCATGATAAAAATAAATTCAACTATGTAGAAAATATAGAAACTCTAGGACTAGCTGGAAACTCGGAAATCATT
WI-22132	99	T	G	---	CAACAGATGCTTGAGCCGCAAAAAGCAAACATAGGCAGAAATACAATTGAGAATATCTTCATGTTTCAACCTTTAATCTGACTTGCCTTTACTATCCTTT[T/G]CCCCATTTCTTCTAATCTCTTTGCCTTACAATATTACCTTCTAGGTATCCATCACCTCATCCTATAGGAATGCCTCCTATAGGAAACCTTAAATGGGACAGTGGG
WI-21006a	106	A	G	---	TGACAGATCACACCACATTTGTTGTAACTTTTCTCCTTCAAGAGTCACTTAGCTTAAGCCAGAAGATTCTCTTAAAGAACAACATACACATGTCCACACAC[A/G]AGAGGCAAGTACAAAATGTAACCCCACCCAAAGTGCATGTGAATGAAAGTGCAAAAAAGGCTTCATTGCAAACTCTGAGGATCATTCTCTCTGCTTCAGGAAAATAAACAGAAAGGTCCTAACTGCCCTAGGCCT
WI-21761b	138	C	G	---	CTGAGGCCTGCTCTAACTTCATNTGACGGAGCGAGTTTCCTGGCTTGGAAATAACTGAAAAGATTCATTTTCTTTGTTGTACAAGGATTCAAAAATATTTCACATCTCCTTGCCAGTTAAACGTGCCGTGGCTT[C/G]CAATACAACACCACCAAAGCGTAACTTGGCTGCCTCAGGAAGGCTGGGAGGAAGTGCCAGATGGTA
WI-21079c	166	G	A	---	AATGAAAATGCCACCCAGAGGGTTAACAGCTTGCCATGCATGCAACTGTGTGCGCAAAATCAAGTTGTTTTAATACCAGTGTGCAGCTTTGATTCCTCCATGAAATTAAAGCTGTGTTGCTCACTTGTTTACATAACTCAGGCCACCCTGAAATATCTGCTAGTTGGG[G/A]AATTTACAACCCACTGACCATCTCAGCTCAAAGCCAGATGACTATCACCTACACATCTGCCAGGTAATAGGCATGGGCAAAT

WI-21079a	50	G	A	---	AATGAAAATGCCACCCAGAGGTAACAGCTTGCCATGCATGCAACTGTGT[G/A]CGCAAAATCAAGT TGTTTAATACCAGTGTGCAGCTTTGATTCCTCCATGAAATTAAAGCTGTGTTGCTCACTGTTTACA TAACTCAGGCCACCCTGAAAATATCTGCTAGTGGGGAATTTACAACCCACTGACCATCTCAGCTCAAA GCCAGATGACTATCACCTACACATCTGCCAGGGTAATAGGCATGGGCAAAT
WI-22129a	45	T	G	---	TCTGTAGATTTTAGCCATGCCATATATTTAACTTTAAGGAAAAGT[T/G]TTATATAAACAGTCATTGCT TGGTAGAATCCAGTCTGTCAATAAGTTAGCTCTAACAGTTAACATTGAGTCTTATACCTTATATTTA AATGTTAGCAATCTCTACTACATTTCAAATATAATAAATTGGTTGCAAATTCCAGNAAAGGGCA TTAACCAAACATGGGACTGATCCTGGGGGCTTCCACCTGACTAAGGTTTTA
WI-21941	79	A	G	---	TGGAGTTAAGTGGGGCTCTGTATTTCCCCCAAGAAGGACTCGGAAGATGTTGATTCCAGGGCAGAGT GAGGGGCAGAC[A/G]GGATGAGGCTCTTCTGTAAAGTCCAACAGAGACGCTCACAGATGCTGGGGAGGCT GGGGACTGCCAGGTTGGGAGCCTCACCCAGAGAGCCTCACTGCATTGACCCCACCACCCACTCACC CAGCACACAGGCACACGCAGGGCACAGCGCACGCNTGCACTCACCACGC
WI-18916b	42	C	T	---	AATGGCATCCCTGTCGATACCAAACATCTTCAGCAGCTCAGC[C/T]GGCTTCCCACTTCTTGGTACCC GGTTAACTGCCAGGNGGGGTGACAGTGATGGTGATGCCAGGGGCTCGCGCCCCACTACTGCACTGGACCTCACC AATGCCACCTTCATA
WI-18916a	35	G	C	---	AATGGCATCCCTGTCGATACCAAACATCTTCAGCA[G/C]CTCAGCGGCTTCCCACTTCTTGGTACCC GGTTAACTGCCAGGNGGGGTGACAGTGATGGTGATGCCAGGGGCTCGCGCCCCACTACTGCACTGGACCTCACC AATGCCACCTTCATA
WI-19828c	200	A	G	---	TTCCCTTCTCCCCAAGAAGTGGGCAGAAAGCTTTGTTAACCTCCTTTTACAGATGAAGAAAAACAA GATCAGAGGGTGCTAAGTGCTGTAGCCTAGTGCCAGGNCTTCTGGCCCCAATTCTGGGTTCTCCCCAAG CCCATGCTTCTTCTCCACTTCTTCCTCTGACCCTCACCACCACCAAATT[A/G] [CTTTTAATTCTGGAAAGAAACCCAGCTGCACACTGGGCACACTTGACCT
WI-21863b	47	C	T	---	CACAAGAGTCTGTACAACCTTAGGGACACCAGCCCTGGCCCTGCCCT[C/T]AGCTGCATGCCACCCTC ATATCCCACCCCCATCCCCAGCCTCCTGCCCCCGACCTCCCCAGCCTCCTGCTCCCTGGTTGAAGTATTT CTCCAAGGCAGGAATGAGTCCTTGATCCAACCACAGCATCT
WI-19860	51	C	G	---	TTGACCTAAAGCCTAGCATAAAATTAGCTAAGTAGAATGTTTCCAAAGATG[C/G]CTGCATCAGTAT CTCCCATCCCACATAATTTCTGTTGATTTGCCATTCCACCCATAAAATGGTGGGATCTACCCTCCCCT CCTTGCAAATTTGAGCTGGNCCTGGNCCTGTCTAAGGATCTGAAGCC
WI-19889b	80	C	T	---	ACCCAGCTCTCCTTACCCTCTGGCTTTGGCTAATGGCCAAG AGGAGTGAGGGGC[C/T]TACAGCATTTATTTCCCTCTTCACTCCCTTTAGCTTTGGTAGTGGCTGTGTAT TTCTCTACTGATAGTTCCTTGCCCACAGTCGTAACTATTGC

Clone	Pos			Sequence
VI-9891c	172	C	G	TGTTGGTCTGAGAATTCACAGCTTACTACAAGGAAGCTGAGAATTGCTTGGTGCCCCTCCCCCCCG ACTCCTCTGTCTGTCTGGGAAACGTGGCTTTGNCTCCCAGACACGTGTCAGATGCCAGCTCTCTCAGCGG AGCTCCCGGATCCCTCCAATTGCCATCTGTCTGACTC[C/G]CGTCTTCCCGGGCGGTGGGGCGTGCTTGT CAGGCAGCCGGCGGCGGGAGGAAGGAAGGAGATCCAGGTCTGTCTG
VI-0155a	81	C	T	GCACCTGTGAGGGGTGTAGCTTCCATGGTTCTCCAAGCACGGCGTGTACATTACCCTTAGGCTGACCAT TCCCTTGCGGGGGG[C/T]GCAAAACTGCTTGAGGAAATNTCCCAGGAGGAATAAACTAGAAGACGC ACCTGCTATTTCACCATACTATGGAGAATACAGCTAAGTGGTGGCAGAAGCTTGGCCGTGTGA GTGCCCCAGGGTAAAAGTCTCTCTTCTGTCCAGTCCAGAGCAGAGACTTCTC
VI-0270b	91	T	G	AGCCATACAAGTGCATTGCAAAGAAACAAAGCACAGCTGTACAGGAGTGGGGACGCGTCAGTGTACAAT ACATTCATGTCCAGGATAAGGAGCA[T/G]ACACCAGGATTTATACACGGTGGCAGCGGGCTATAGGCA CGATGATACAAAATATAAAGTATATTTCCATCTATATAAATACACAGCTGGGGTGGGGAAGGATGCT GGGTGATCTTGTTTCCCCGCAGAGGGCCTGGGAGCAGGGNGGGTGGTGGGAA
VI-20270a	53	G	A	AGCCATACAAGTGCATTGCAAAGAAACAAAGCAGCTGTACAGGAGTGGGGACGCG[G/A]TCAGTGTGCT AATACATTCATGTCCAGGATAAGGAGCATACACGGTGGCAGCGGGCTATAGGCA CGATGATACAAAATATAAAGTATATTTCCATCTATATAAATACACAGCTGGGGTGGGGAAGGATGCT GGGTGATCTTGTTTCCCCGCAGAGGGCCTGGGAGCAGGGNGGGTGGTGGGAA
VI-20622	130	T	C	CCACTTTCAATATTTTACAAAAATGCTCACGCAGCAAATATGAAAAGCTTCAACACTTTCCCTTTGTA ACTTGCTGCAATAAATGCAACTTTAACAAACATACAAATTTCTTCTGTATCTTAAAGTTGAA[T/C] TACTAAITTTTATGATGTTACTCATATTTTATTCATAAGTTTAATCATACCACTATCATACATA CATTATTTTCTNTAAACTTATTTTTACAATAAGCCAACATCTGTCATGCAG
VI-0768b	190	C	T	TTCCCACTCAAAACTCCCACCCCAACCTTCCTGGAAGGCAGGGCTAACAGGAGACCTCCTGCCTGCCTGC TCACGACTGATTACTTTCAATCCCAGCTGCAATGCAAACTGAAACTCATTCATTGTATATCCACCACTCTA CAGGAGAGGGTCTATTTCTGGGGCACCCAGAAGNTCAGCACACACATACTGCTGGGA[C/T]CAGGGACTC GTAATTCGCCTTGGTCCAACTCCTTCTATGGGGTTTAGCTGCCCTCATTCC
VI-0768a	71	C	T	TTCCCACTCAAAACTCCCACCCCAACCTTCCTGGAAGGCAGGGCTAACAGGAGACCTCCTGCCTGCCTGC TCA[C/T]GACTGATTACTTTCAATCCCAGCTGCAATGCAAACTGAAACTCATTCATTGTATATCCACCACT CTACAGGAGAGGGTCTATTTCTGGGGCACCCAGAAG[A/T]AGTGGAATCAATCAATAAAATATTTAGTCT GTAATTCGCCTTGGTCCAACTCCTTCTATGGGGTTTAGCTGCCCTCATTCC
VI-21909	153	A	T	TGTTTGCTTTGTGCCAGGTACTCTACTGCTTTACATAAATTATCTCATTCTGTCACATCTAACGGCAA CTAAGTATACGCTTACATCTGCTAGTGGCACCTAAAATAAGGATATTGTTGGTCATCTTTAAAGAAA TGTCTTAACATACCAAAG[A/T]AGTGGAATCAATCAATAAAATATTTAGTCTTACAAAGCGTAC GACACTAAAGTAATATAGGATACCACTAAATTTATATTTCTATGTATGGAAAG

ID	No.			Sequence
WI-22202	128	A	G	---	TGTTGCTTGGTTGTTGCTTTCTGGAAACATATTGGAAACACTTGTTTTCATAAGCTGTCCTGACAGT GGCACAAATCCCATCCATCTTCAGGCCTTTAATAAGGTCATTATGAAATCTGAATTTCT[A/G]TTAAT ACTCTGGTGCATTCATTCATTGAGTCTAGTTCTGTGCGAACTTCTCCAGCTCTCGG AGAACATCTAATATTGAGTCTAGTTCTGTGCGAACTTCTCCAGCTCAC
WI-22189	70	C	T	---	CCAAGGATGAAATTCCACATTTATTTNCTTTATGTGAATAGAAAATGGCAGTGAAGTGTCCTATG AA[C/T]GAGGCGAGGAATGGGCATGGCCTGCGGTGCCGCTGCTGCGGTACCAGCGTTGTGCTTCCAAAGTACAC TATGTGTGGTGGAGACAAAGGGT
WI-22283	109	T	C	---	GGGGAGGCATCATAGAAAAAAACCCTCAGCCAGAAGTTAGGACATTGTGATTCTCAGCCACTAACGA GCTGTATGACCTTGGTCACTAGGCCTCTGCAGGCTCTGGTTG[T/C]TTCATTTGCAAAATAAAACCCA GACCGGGTCATCTTCAGTTCCCTTCCAGCTCTATTATTTATGATTTGCTCTTAGTCTTTATGAGCCA TGTATGATTTATCAGTCTCCCTGATGCTCACTCAACTCCAATGATGCAAAAG
WI-22290a	136	C	T	---	GACGTCATCTCTGAGGGCTCTGCCAGGTGGATTAGGTGAAGAGAGGTTTTATGGGCTCTAAGCACCG GCCAGTAGTGGGGAATGCCACATGCAATGGGTGAGTGGGGGGTCTGGGGGGGGTCAGGACCTTGCTTT [C/T]TTCCAATCTCTCTCTTCTAGCCAGGAAACTTTGCGGAGAGCCCTTTNATTCTCTCGGCTCTATTCC CCTCCTTTCCCAAATGTGCTAAGGTCCCAATTCCCAGACCCCTCCCAG
WI-22292	53	A	G	---	CCAGTGGAAGGGTTTACAGCCATAGTGAGGTTCCCCCATTGCTCAGTACCAGGA[A/G]GTTTGAGTAC GGTCGTTTAAAAAAATACTTATCTGACCACAGTGGAAA
WI-22387	186	C	T	---	ACCTTGCACACCTGCCATCCGGTGGCACATCTATACCCCACTCTGGCTCTGGAAAG GCTTGTCAACCAAAAATGGGCAGCTGGGGCTAAGGCATATTAAACAAAGGCTCCAAAGGACCCCTT TCACTTGGGTCTAGCATCCAGCCTCTCTCTCAGCAAAGGCAGGATTGTGGT[C/T]CTTGTGTTTTCTG AACAGGGCCCAGGCAGCCAAGGCATGCCATCACTGCAGCACTCAACCCT
WI-22395b	127	A	G	---	GCCGTTCCAGTATTGATAATAATTTGTGTTAATTTCTATACAGAAATGGTTCTTTCTTGAATATTT GTAGGGATGGATGAAAGTGAAAGTGAATTAAAGTCAAGATAAAGGGGCAACTCTTAAT[A/G]AAG GAAATGTTACCAAATCCATAGTGAAGAGTAGAATATGTTCTTTAGAGTAGNTAGAAAGTCCCCAGG CTCCT
WI-22405	90	A	C	---	TTTATGGCTCCTGAGTGCCTTCACCCAGTCACACTTTACCTTGTATCTATAAAAGTGTAATTTAGAGT AAATACACATTGGCTGTGTAAAGTCG[A/C]GATCAGGTGCTCTCCACCAAAGCAAAACAAAACTGCTGA AATGTGGCAAGGTTTCTCAGTG
WI-22419b	67	T	C	---	CCCTTCTGGACAGTTTGCTTTATGTGTTCAGACAATCAAGGNTCGCCTTCCAGGCACAGCCCAGTGC[T /C]TCGGATGGCATCAGCAGCAGGCTCCCCGGCCTTGAAGCATGGCTGTGTGCACGAT
WI-21342d	59	T	C	---	ATTTTCCCTTCTGTGTTTCGTATTTCCCCTTTTGTCAGTAAATNAGCAATACACTGA[T/C]TGGAA ATCTGCATGATTAAATAACATTAACAAGTTCATAAACACACCCATATCAGAGTATAAAGCAAGAG GTTGAAAAATATCCCTAACCGAATGCAAATTAGTAGTATCCCTCAAAATTGCACATTCTCTCCTAGTT T

WI-21763b	154	A	G	---	CATACCCTTTAGGTGCCCACATTGATCTTAGTTAACAGTCTTGTAGTTCCCTCTTTAGGCTTCAAGATAATTGTGATTCATCGCACCCCAGATACTTCCAAGTGGAGCCAGGCCTCAGACTGTTCTCAGTCACTGCTCTCCCCAGCTGATT[A/G]CAGACACTGCTTGTGCTTCCTACCCAGCTGTCTAGTGCACTTGA
WI-21763a	135	T	C	---	CATACCCTTTAGGTGCCCACATTGATCTTAGTTAACAGTCTTGTAGTTCCCTCTTTAGGCTTCAAGATAATTGTGATTCATCGCACCCCAGATACTTCCAAGTGGAGCCAGGCCTCAGACTGTTCTCAGTCACT[T/C]GCTCTCCCCAGCTGATTACAGACACTGCTTGTGCTTCCTACCCAGCTGTGTCTAGTGCACTTGA
WI-22440	64	A	C	---	CAGTCCATTTGAGTCCCAGTGGGTGCATTCTTCCTTTATCTTGCTTAAGCCACTTGGGTA[A/C]TCCATTCCAGCTCTGCACCTTCTCCCAGTTTTCTCATGTCAGAAGTCCCTGGAGGGAGGAGGCTTTCTGGAAAT
WI-22449	74	T	C	---	CAATGAATGTTGTGGCATATGATTTNCCATTGTGTGACAATTTATTAGCTGGCATCCGAATACAGTACTTCTTT[T/C]GAAAAAAATACACAATGGGAACTGACA
WI-21965a	112	A	G	---	CAGGTTCCACCAGAGGCTTTATTTCAGCCACTCAGGACCCTGGCTTTCTGCTCCAAGGCACTGAACACAGTCAGGCTCTTCTAAACACTGGCAGGACCCTCCCCCACAGCC[A/G]CCCCACAGGGTTCTCTGTTTCCCAAGTCCTGATGGATTCAGGCAAGAGACCTTCACACATTCACCCACTACCTGCTGGAGAGGAGGGGTCATGAGGCAGCCTGTGTGGTGCCCAGCTCAGTGTGCACACTGCCAATGTGC
WI-21687c	115	C	G	---	CACCTGGCAGTTGAGTCAGATTGTAGGAAAATTAACCCAGATGGGTCTACATTTTTNTTCAAGTTCAAACCACATGGTTCCTAGTCAGAAGTCTCATGGACTTTCTTCCTAAG[C/G]TGTTCTCATGATCAGACCACCTCCTAAATGTGGCTTTACCCATTACAGCTACAGTTGAATCAGGCAGGCAGCAGCCTGCTGGAG
WI-22374a	149	T	C	---	AGCTTTTACAACAAAGCGAGGGTTAAGGAGCCTGAGAGAGAATTTCACAACTATTGACTATACAGAGTCTTCAATTCCAAAAACAGTTAATAGTAACTTGGTGCACATACAACATGCATTGAATACTCTGTATTATTCAGTAACTAAA[T/C]AGGNTCCTGCATCATTCTCTTCACA
WI-22250b	132	C	T	---	ACTTGTCTTCAGGCAGGCATTTCTGGGATCTAAACTAGAAATCCTTGAAAACAAATAGTACCAGCCACTTTGAGGAATGTGCATTCACTGTAGTGGGTTATTATGGGTGTCTCTGCCTCCTCCTGGGCTGTGTTATG[C/T]GGANCCAGGAGTGGAGGAGGAGAGCCGGTGGAAATAGACAGGGGAG
WI-22250a	89	G	A	---	ACTTGTCTTCAGGCAGGCATTTCTGGGATCTAAACTAGAAATCCTTGAAAACAAATAGTACCAGCCACTTTGAGGAATGTGCATTCACT[G/A]TAGTGGGTTATTATGGGTGTCTCTGCCTCCTGGCTGTGTTATGCGGANCCAGGAGTGGAGGAGGAGAGCCGGTGGAAATAGACAGGGGAG
UTR-04932-2b	192	G	C	---	GCAGCCAATCTCCTCTCCAACACCTCCCAGGCACCCTGGGGCCCAGAGCACCTCATGCCAGCACGCACCTACGTGGCCCGGGCCCGAGTACGGACCCGCGGCCGCTGCCCAGCTTCTCGGCTCTCAGGACGTCCCAGCAAGTGGAGCCCAGACCCCAGAACCTG[G/C]AGTGCTTCTTTGACGGGCCGCCCGGTTGCTGGGACTCCCGTCTCAGGCTGGCTCGTGGGAGGTGAGGAGGAGGT

UTR-04932-2a	149	C	T	---	GCAGGCCATCCTCCTCCAACACCTCTCCAGGCCCAGAGGCCACCTCATGCCCAGCAGCAC CTACGTGGCGCCGAGTACGGACGCGGCCTGGCCCCGAGTGTTCTGGCTTCTCAGGACGTGCCCAGACGCAAGTGGA GCCCAGAGGTTTG[C/T]TGGGACTCCCAGCCAGGGGATGAGGCCCAGAACCTGGAGTGCTTC TTTGACGGCGGCCGCCGTGCTCCTCAGCGTGCTCCTCCTGGGAGGTGAGGAAGGGAGGT
stFIBBb	412	G	C	---	GTGGAGGAAGATGGACCTGGACAGAGTCAGCTCCACACCTTGCGCTGAGCAGCTGTGATTGTGCCA CGGGAGCATGAGCCCTTTCCCCACGGCCCTTGCCCACTGTCTCCTCCTGTCTGATCATGCCAGG TTTGCACCAGCCTCGAGTCTCCATGTTGTAGTACATTCTCAAGATGCAGCCCAGGAGCCTCTCTGA AGGACCAGTCTGGTTACGATGGTCTGAGCTTCCTTAGAAACCTTCCATGGTT
stFIBBa	341	T	C	---	GTGGAGGAAGATGGACCTGGACAGAGTCAGCTCCACACCTTGCGCTGAGCAGCTGTGATTGTGCCA CGGGAGCATGAGCCCTTTCCCCACGGCCCTCTCTGCCCTCTCTGCTGATCATGCCAGG TTTGCACCAGCCTCGAGTCTCCCATGTTGTAGTACATTCTCAAGATGCAGCCCAGGAGCCTCTCTGA AGGACCAGTCTGGTTACGATGGTCTGAGCTTCCTTAGAAACCTTCCATGGTT
stIGLV2	61	T	C	---	GTCACAAGAGGCAGCGCGCTCTCGGGACGTCTCCACCATGGCCTGGGCTCTGCTCCTCCTCACT[T/C]CTC CTCACTCAGGACACAGAGGTGACGCGGGTGACGGGTGGGTCTTGGGGGTCCTGGGGACCTTCTGGGCTGATCCTTGGTC TCCTGCTCTCCAGGTCACCTCAGCGGTGACCCAGCCACTGGCATGT
stSG10017c	70	T	C	---	GTTCAGGCTCATCTTGAACTCCTGGTGTCAAGGCGATCCTCCCACCTCGACCTCCCAGGGTGCTGGGAT TA[T/C]GGCCATGAGCCCCACCACTGAGACACAAAATACATTATATACTCTAAAGTATAGGATTACT TTAAGAGAAGGAAACTAAAAGTATGATGGCTTACTTTCTAATCC
stSG10017a	33	G	A	---	GTTCAGGCTCATCTTGAACTCCTGGTGTCAAGC[G/A]ATCCTCCCACCTCGACCTCCCAGGGTGCTGG GATTATAGGCCATGAGCCCCACCACTGAGACACAAAATACATTATATACTCTAAAGTATAGGATTACT TTAAGAGAAGGAAACTAAAAGTATGATGGCTTACTTTCTAATCC
stSG10023	63	A	T	---	TAATGATAATTAGGGCATTCTTCCCACACGAAGATGACACGAAGAATTGACCCAATATCATTGAGGC[A/T] AACAGTTTGGGCTGTTTTCCAGTAGTATGACAGTGA
stSG10096	36	G	C	---	GTGGAGAAAGATCGTCTTCTTCCTCCTCCCCATGACC[G/C]GGCTTCCCGCGGGCCACCTGTCGGTTTCC ACCCCCGAGACGCGGCCCTTTGTAGGGACCCCACTCCGCCGCTGTGGGCGTCGCGCCTCCTAG GGCTCGAGTGTTAAG
stSG10118	107	C	A	---	TAGGCTTAAACCTGAATCTGGAATCTACAGCCAAAAGTCCTCCGCCTGAGGGCAGTACCCTCCATTGGGC ACAGTCCAGACCCAAGTCAAAGATGCCCATTCCTTGCG[C/A]CTCAGCCCTTCCTTCCTTCATTTCC ACCAGCCGTGCCTTGTTGTTGAGTTTTTCCTCCCCAGTGAG
stSG10120	89	T	C	---	TAGTAGGTAAGAAAAGCAAAGGAGGATTGCTTATGCGATGACTGTTTACAGTGGTGTCAGACTATGC CGTGTTCACGAACACTTAATA[T/C][GTTGTTGTAATCTGATTTATCCTCGTCTTACAAATG
stSG10178	42	C	T	---	TTGAAGCAATATTGTCTAGCACTCTGCTGCGACATTAAGTCCG[C/T]GGGAGGAGAAGTGAACAGGAA TCGATTCTTTGTGTCTTTAACTGCCCTTAGTAGGAGGAGATGTTAAAATACTTGGC

ID	Pos	Allele 1	Allele 2		Sequence
stSG10193	136	G	A	---	GGAACAATACTACCTAAGGACAAAATACTATTATTAAAAAAAAAGTCTTCTAGTGTATATATTGTGTAACACATTCTGGAGCTGGTAGGAATAACCATTTTATTTTCTGTGAGTGCCATCTATACAAACTTTTAC T[G/A]TTGAAAACTGAGAGTTAAGTTGCAAACT
stSG10202c	143	G	T	---	AAGCTAACTTAGGTGAATGGTGCCACTCAAAGGTCTTCCGAGGGAAGCTCAGTCCTGGCTTGCGAG AGTCAGCGCCTTGGTCACCTCATAACGGGGGTCCAAGCTAAGGCGTCAAGGAAGCAGTCCCACTGCTTCT CGCTGTCA[G/T]CAAGAGCACCAAGGCAGCAGATGCCCACTCCTCTTCCTTGTCTACTTTCT
stSG10209b	75	A	G	---	TCTTTTCTCTTTCACTCTCAGTCACCATGATTCAAATAAACTAATTCTCCTTAAGATCCCACTTTAT TTTTA[A/G]CTCCAATAAATGTAATTATCAGCTGCTGAATT
stSG10209a	34	C	T	---	TCTTTTCTCTTTCACTCTCAGTCACCATGATT[C/T]AAATAAACTAATTCTCCTTAAGATCCCACT TTATTTTTAACTCCAATAAATGTAATTATCAGCTGCTGAATT
stSG10218	29	T	C	---	TACTAGACATGCAAAATGAGAAGATTACA[T/C]GTGAATATTTAAAGAAGTTATATTTGTTGACAT AATATGCATTGTACCCGGGCATAATAAAGTTAAAGCCAGTTATTCTGA
stSG10252	108	A	C	---	ATAGGTTTCAGGAACACAAAATCATTAAATGGAAAAATGAGAAGAATTCTTTATTTTGGACCAATTT AGGCACTTAAGAGTTTCTTCTTCCCTTGATCA[A/C]AGTGAAGATATGATAGGGAATTC AGAAATTTCTCTTCTTG
EST109150	123	A	C	---	CTGTATTAATTAAGAAAGGCACTATTAATGAGGAGGAGGAAAAATCTACCTGTACACAAAATTCTGTAC TTAACAGCATCTTCAAATAAACCTTTAAAGGATAATGGTTTACGATCATTTTAAG[A/C]ATTTTAA GAACTGAGTTATTTGGAC
EST110231	166	T	A	---	TTTTTGTTAAACCAACCACCCTGAAAGTTTCCACATGTGAAAATATAGATACAACAGTGAACAAAAT ATGTGGCCTCCCATGTACATTGGTTACCTATGTACAAGTATCCTATACACCAGTAAAACAGCAGGGC AATTAGTCAATTAAAAAAAATAGTACATGTTA[T/A]GTGTAATAAAATTAACAAAGGCTTT TCCACTCGTGGATTGGATTGATTCCTTTTTTGGGAGGAGGAGTAATCCTGG
EST140968	71	G	C	---	GGGATGTATATTACAGATAACACAACTCACAAATATACCATCACAAATATACCAGACACATTGAAAACTAAGGCCATTCT GTGA[G/C]TTATTTTTAAAACTTGGTGTTTGCACATAATGATCTTAAAAAAAATGAATTACCAAA ACCAAGATTCTCTCTCTAAAATTTAATGCAGTACAGGATAACTTTAGGGCTATATCTAATC TGAAG
EST221136c	125	C	A	---	TGCAAATTGTGAGAAGGCAGCAGGGGCCAACCCCTGGGACCTCATCTCTGTCTGTCTAGAATGTGAGGTCG CAGGGATGGCTTAAGTCTTCCTCTGGCAGGTGCAGAGACCCGAGGTGCAGAGATTGCAGAGATTCTTCTCAC[C/A]CCCTTC TCTCAGGGTCGTGGAG
EST225557	60	G	A	---	TCAAGCATGTGTAAGGCACTGCCCCCGCCCAGACCCTTCTAACTTCTGCACACTGGAAGGT[G/A]AAA CCTGGGAGAGAGAAGAAGACACTCCCCTCCCTACCTGGGCACCCTCCAAAGATGAGCATTCATC TTGGGAGACCAAAATAAAAAGGACAAAAGACCAGGGCTCAGAG

Name	Pos				Sequence
EST22917 6	74	C	T	---	GTAAACCTTGCAAACGCCATGCTAAATGGAAGCCTGACCAGGGGGCTCTTGGGCTCTCAATGCA ATAGAAA[C/T]TGACATGGGGCCAAAGACTTCCAGACAAAGCACGCGAAAGGGTAGAGGATATAG GTTAGCATCATCTGGTTGTGA
EST36458 6	65	A	G	---	CAAGTTAGAACCATGCATCAGCTTTCATCCATGGTAACTTAACCCTCAGGCTGTCCTACTCA[A/ G]TGGTGGTTTGCTAGCCTCACTCGCACACAGGAAGCTTGGAATTTGGAGGCTCCAAGTCACTCTCCA
EST36745 3	56	A	G	---	GAGGGGGAACTTCAAAGAGGATTCCAACAGTGAAGCAGAATCATGGGGCAAAAGTC[A/G]CTATGG GGCCAGACTGAGGTTGGACCACACAAGCACTCCAAGCTGGGCCAATCCCAACCGCTGGTGAAGCCGC ACAGCACGGAGTAGCCAT
STS-R37410c	201	A	T	---	TGTGACCATACCAAACCTATGCAATAAAGAAAAGAAAAAATCCTCACTTAAAAAAACAAAAA AACCTTGCAATGCTATCATTTTTCAGGTCTTTTGAAGTGTGAATAAAAGTTCATAGCATTTTGGA ATTTATGGTTTGAATAAAATACAAAATGTGTAGTCTCCTGAGACACATTTATAAACATTCTGGTATG T[A/T]TATTGTGAGTGGTGCTCTAGTGGCCAAT
STS-R37410b	139	G	T	---	TGTGACCATACCAAACCTATGCAATAAAGAAAAGAAAAAATCCTCACTTAAAAAAACAAAAA AACCTTGCAATGCTATCATTTTTCAGGTCTTTTGAAGTGTGAATAAAAGTTCATAGCATTTTGGA ATTTAT[G/T]GTTTGAATAAAATACAAAATGTGTAGTCTCCTGAGACACATTTATAAACATTCTGGT ATGTATATTGTGAGTGGTGCTCTAGTGGCCAAT
STS-R37410a	48	C	T	---	TGTGACCATACCAAACCTATGCAATAAAGAAAAGAAAAAATCCTCA[C/T]TAAAAAAACAA AAAAACCTTGCAATGCTATCATCATTTTTCAGGTCTTTTGAAGTGTGAATAAAAGTTCATAGCATTTT GGAATTTATGGTTTGAATAAAATACAAAATGTGTGATCTCCTGAGACACATTTATAAACATTCTGGT ATGTATATTGTGAGTGGTGCTCTAGTGGCCAAT
STS-R42778	74	C	T	---	TATCGTGGGAAGTCCAACCTCTATACTTATGCTGCTTTCTACTGCTAATATTGGATGCTTCTTGCCA GGCTC[C/T]TTAAATTGTGCTAACCTGGAAGAAACCTTCCTACTCTCCACAAACCCTGAA
UTR-04350	125	C	G	---	CAATCTGAAGAGATGCATAGCGGATTGGTGGCTTCAGCAGCGTGTGGGGAGGTGGGACTGGAGGAGCG ACTGCTAATCAGTCTATGGGGTTTCCTCCCGGGATGGTGAAAATGTTCCGGACCTAGATA[C/G]TGACGA AGGTAGCACGACACTGTGAGTGCACTAA
stSG1026 6	55	T	C	---	GAAATAAACTAAAACTGCAAAGCAAATCACTGTTAATAAGAATTGTTCTTCGTT[T/C]GACAGTTG AAGTGGGTGTGAGATGGGCATAGCAATGAACAGTGGGAGCCAATGAGGTCCTCAGAATGCGGGGCAAA CTCCCTGTGAAAATGTAT
stSG1028 2	70	T	G	---	GTATAATTCAGCATAAGCCAAAGCCTTTTAAAATAACCAATACTATCATTTTATGAAATCTTTACA AGAT[T/G]AAGCACAGTAGTACAATATTTAAGCATCTCAAGTCTCCATTTAAGAGTTGACTATC
stSG1031 0	128	C	A	---	CACTTTAGATATGGAGGAAAATGGTTTAATGGACACAAAGGAGTCAGCCACGTTGGAACCAACATAG TTTCATACCACGTTGAAACCATGTGTTTGATATGCAAATAATTTTTCACT[C/A]TTG TCAATGCCAATGCATTGCATTGGAAAGGCCCAGAAAATGAGAAAAGGATAACAAACTTTTGATAAAAGGTA AGAATTTCTGTGTG

ID	Pos				Sequence
stSG1033 1b	116	T	C	---	TTTAAAGCTACACATGTCTGAAAAGAATGATGCTGCTGATTGAAATAAAGAGAAGAAAGGATGCATTTCGGGCTCCAACCTGTCCTAGGAAGGCCTAGACCTCAAACACCAACACCTCCA[T/C]GCATTTCCTCTTGGCTACTATGTCTTTCCCTGACTTCTGCCTCTCCAGCTGTCTGGGCTCTGCTGCTTCCACCTGTTCATCTGACTTAGGACCCTCC
stSG1033 1a	107	A	T	---	TTTAAAGCTACACATGTCTGAAAAGAATGATGCTGCTGATTGAAATAAAGAGAAGAAAGGATGCATTTCGGGCTCCAACCTGTCTTTTCCCTGACTTCTGCCTCTCCAGCTGTCAAACACCA[A/T]CACCTCCATGGGCTCTGCTGCTTCCACCTGTTCATCTGACTTAGGACCCTCC
stSG1243 b	225	G	A	---	ATTGGCAAATGGGAAAATGACACCAATCATTTGATTACAGAAAAATGGTTTTATAAATCCTCTCCTGAAATTATGTTCAGGCCCAGCCCAGGTAGCTTATGCCTGCAACTCGGGAGGCCAAGGAGAAGGATCGCTTGAGCCCAGGAGTTCGACACCAGCCTGGGCAACACATAGTAAGACCCATCTCTGTTTTTTTTAAAAAAGAAATTCTGTTC[G/A]AAAGTATTTCAGACCAAAAGGAGGT
stSG1345 b	60	G	A	---	AACTGACGTATCACAGGGCAAGTATCTCGTCATAAATTTGAACTAGTTTGCT[G/A]CGCTTCACATTTTAGCATGGGCCAAAATTCAGGAGATGCCATGCAATGTCCATAAATGGGCAA
stSG1345 a	54	T	G	---	AACTGACGTATCACAGGGCAAGTATCTCTGTCATAAATTTGAACTAGTT[T/G]CTTACGCGCTTCACATTTTAGCATGGGCCAAAATTCAGGAGATGCCATGCAATGTCCATAAATGGGCAA
stSG1385 b	117	T	G	---	TTAATGTCATCCAGGAGGGGGCCAGGGGGATGGAGGGGTTGAGGAGGCAGTTATTTTGGGTGGGATTCACCACTTTCCCATGAAGAGAGGGGGAGACTTGGTATTTG[T/G]TCAATCATTAAGAAGACAAAGGGTTGTTGAACTTGGTAGACATGGCTATGGCCCTCTAAAAACATGGCCCCAGCAGCTTCAGTCCCTTCTCGTCG
stSG139	69	T	C	---	TCGTCTCCTTCCAGTGCTTCTGCCCAGAAGCATCCCCATGTGTTGTGACCGCACAGCACTTTGTGTCT[T/C]GCTTTGAGCACTTGCCACTCTGGCTGGTGCTGGTACTGTCTTGCTGCCC
stSG1427	103	T	C	---	GATCTGGTTCCAGACAAGGCTGATTCAGAGACTCCACGTGGTCAAGGCTCTGTTGTTTGTCAATCCCTTGGCTCCTCCACTTCCAGTTTGGCTTGTCTGTCTCCA[T/C]AGTTCTCTCTCCCATGTGGCAAACAAGATGGCTACTGGTGGTCCCAGGTTCCAGCTGTCCCAGCTTCAGGAAATCCAGGAAATCCAGCTTCAGCTTGGAAATCCATAACTCAATCCTTGGGAAG
stSG1471	50	A	G	---	CCCTGGAGTTTCTGAACATAGGAAGAGAATGCAAGTCATGTGTTAGGTCC[A/G]CTCCCTTGCATGAAATGTGGGAGAGGGAAATAAAGTTAGGCAACATTTAGCAATCAACAGAACCCCTTCCCTATCCTACCGCA
stSG1483	44	T	C	---	CAAAACCAAAATCCTTCCCACGATATATTACTATTTAGTCTAAG[T/C]TTAATTCAAAGGTTGAGAATGACGAATTCAAGAAATTCTTTCATACATAAATTGCTTCTTCCTTAGTTCTGCAGATGGGTA
stSG1696	67	C	G	---	CACACCCACCAAGTTTCATGCATGCTAATGCCAAGTATCAACTCTTGAGGACAAAGGCAAAGGCAAAACCAGTGTGCA[C/G]AATGTGGAGGATGTCAGTTAGTTACTAATGCAGGAGAAAAACCCAATGCAAAGAGGAAAATGCCTGA

stSG1847 b	95	G	A	---	TTGCAGACAACAATGGAAGCTTTAAAACCTCTTCAACACAAATGCTACCCTAAAATGAAAGAATTTAGAGGTTAAATAAAACAAGTGAGAGACC[G/A]TTACTTACATCAGTTCGGTTTATAGACATTTGAATCATATCTGAATGACTGACTTGTTTCCAATGTGAAAACCAAATTAAAAATAACTTGATCACTGTGCTTCAAACACAACTG
stSG1847 a	49	C	A	---	TTGCAGACAACAATGGAAGCTTTAAAACCTCTTCAACACAAATGCTACC[C/A]CTAAAATGAAAGAATTTAGAGGTTAAATAAAACAAGTGAGAGAAGTTACTTACATCAGTTCGGTTTATAGACATTTGAATCATATCTGAATGACTGACTTGTTTCCAATGTGAAAACCAAATTAAAAATAACTTGATCACTGTGCTTCAAACACAACTG
stSG1897 a	83	A	G	---	CTTAATGCCCCTTCCTCCTCCTTCTGCACAGGAGGACACAGATGGGTAACATAGAGGGCATGGGAAGTGGAGGAGGACACAGGACT[A/G]GCCCACCACCTCTCCTCCCGGTCTCCCAAGATGACT
stSG2022 a	86	T	C	---	TGTCTTGAGGTTTCAAATCTGAGATATCTATGGCAAGTTTATAAAAGTACAATTGATCAAGGTACAATTTTAACATTAATATACA[T/C]ATTCCATAATCTCATTCATCTATTAACATTAACACAGGCCTTTGTTGTTGTTATTTTTTCTCCCTACAATATTTCCTGACTCTGTAGGGACAGTGGGCCTCAGTTGGGGGGTTGACT
stSG2076	104	C	G	---	AAACGTTGTCCCAAAATTGTGTTCCAGTTTCACAAGTATAAAATAAGACTTCTGAAAAAAGTTTACAATTAGTTATAAAACACTTAAGAATATATTTGACATT[C/G]ACATCACAGTGGGGCATTTT
stSG2108 c	71	A	G	---	TTGAGCAAACAATGATTCGCGAAGACTTGTTCTATAGGACAACTGTAGAAGTAAGCAAGACGTTTGATTGGAGC[A/G]TAAGGGGGAAGACTTTATAGGACAACTGTGTTCTTATTGGTCTATCTTATTGGGAAGTCTGTAGTTATGTAATTGTAAGTTTGTTGGGCTGTGTCTGA
stSG2108 a	49	T	C	---	TTGAGCAAACAATGATTCGCGAAGACTTGTTCTATAGGGGAAGAGCATAAGGGGGAAGAGCATAAGGGGAAGAGCATAAGGGGGAAGACTTTATAGGACAACTGTAGAAGTAAGCAAGACAGACGTTTGATTGGTTACAGTTACACAGTGTCTTATCTTATTGGGAAGTCTGTAGTTATGTAATTGTAAGTTTGTTGGGCTGTGTCTGA
stSG2141 b	173	A	G	---	TTATTCCAGGGGACAAGCTGCACAAAGGAATGTTCTTCTATTTATTTAAACAAATGACTGCGTGTACTGAATCTGACTGTGTGAAATAATCTCAGAATGGCAGCACCACTGGCATGGCAGTGGCGCAGGTGGGTGCAGTTCCCTGTGGTCTCTATTGCTTGAAGAGAGAAAG[A/G]AAGTTCCCTATTATTATTTAAGGCAGTTTTCAGAGCACTGGCATTCTTGCTCTG
stSG2141 a	113	C	T	---	TTATTCCAGGGGACAAGCTGCACAAAGGAATGTTCTTCTATTTATTTAAACAAATGACTGCGTGTACTGAATCTGACTGTGTGAAATAATCTCAGAATGGCAGCACCACTGG[C/T]ATGGCGGATGGTGCAGGTGGGTCAGTTCCCTGTGGTCTCTATTGCTTGAAGAGAGAAAGAAAGTTCCCTATTATTATTTAAGGCAGTTTTCAGAGCACTGGCATTCTTGTTTGCTCTG

ID	Pos				Sequence
stSG2148	50	A	G	---	TGGGAAACAACGGCTATAGTCTGAGTCATCATATTTTTTAGACCGTGATTTC[A/G]AAAGAAAACAATAAATGTGGAATTAGAAAGGAAACATCCATTACTGTATTTCGATACTGTATTTCGATGTTGTGATGTTCCAGACGAGAGCTCATCAC
stSG2175	68	C	T	---	CTCAATGAGGACTCCATCAGCCAAGCGGTTTATATGGCAGATGAGCTGCTACAAATCTGTTGTGTGCT[C/T]GCCGGCGTGACTCAGCTAATGCTAACGGGGTTGGAGCCGACGCCAGCCACCTTTTCCATACCTGGGCAGAGAGGGAAGGGAGTGGAAGGACCA
stSG2189	41	C	T	---	CAAGTGGTGAAAGCTGGGATTTGAGCCTGATATTCACACTA[C/T]CTACATTCCCTCCAGTATAATAGGAACTCATCGCTAACTTTGAGCACTTAGTGTTCTGAGTACTTCGTATAGGTTATCTCAATCCTACTCCAGCTTTGCGAAC
stSG2200	49	T	C	---	TGTTGATGACCATAGAGAGGATGCAAAGCTCCGGGCTGGTTCTGTATGATG[T/C]TTTATATTTATGTATAATGTCTTACCTGATCGATGATACCCAACATATTACTAGCTTATAGAGATGAGGATGGCAGCTTGGCTGGTCAAT
stSG2243	85	G	T	---	CATTTCTGCCTCTCCGTCTTCCCAGTACTACCCCGTCCAGCAACTGCCTCTCGTATAAATAAGTATCAAGATGGTCAGTAGAAAAG[G/T]AGAGCATCTCCTCAGCCCTGGAAGACAGTGTGGGAGCTTCAGCT
stSG2257	65	A	C	---	TCAGTGATTGTAGGAGCTGGCTAAGTCATGTCTAAACTCTGTGTCTGCCTAGCACTGGGCTGCGTGTCCTCAGGCAGAATTCTTCCT[C]CTGTCAGGAACTCTCGCCAAGCACTGGGCTGCGTGTCCTCAGGCAGAATTCTTCCT
stSG2306	67	A	G	---	GTCATCAGCGTAGAGGTCACTGGTAGTAAACAACAGTAGCTATATGATATTTACA[A/G]TATGCTCCCATTGGGTTTCCAAACTGATACAACCATGAGGTGAACACTTCACTGTTTCACAGTTCCTCCAGAGA
stSG2334	70	T	G	---	GAAAACTACCCACCAGCAGCATCATGTTAAAAGAAGAGAGATGAAAGAAAAAATCCCCGCAAAAAACAAAAAT[T/G]TTGCAGTGAGTTGGGAGGGGTGTGGGAGGGGTGAATG
stSG2339	63	T	C	---	AGAGCAGAATGGTGAATCAACAGACCTCAAATTGTCTTGACTGCAGAAGTAACTGCTGCT[T/C]CCTATTCATCAGTTCTCAGAGTGACTGTGTCTATTCTGTGCTTCCTATTCATCA
stSG2465	76	C	T	---	CAAGACTAAGAAGCCGCACCGAGTGGTCCCACTCAAAAAGAGAAACAACACACTTTGAGAAACTCGCCCTTCCTCCAGAAACCA[C/T]TACAGATAAAAGAGAAACAACACACTTTGAGAAACTCGCCCTTCCTCATCTTCAAAGTGTGGGGTATGCA
stSG2549	140	T	C	---	TTGCAGGCTTGTATTCCACAATAACAAAGTCATGTCATTTGAAGTCCTTTGATGACTGGGTTAAATATGCAAAGCAGCTAAAGGATATATAAAATATTGAAGTCATTTATGCCTTTGATGACTGGGTTAAATATGCAAAGCAGCTAAAGGAATATT[T/C]TACACCACCACCCCTTTAACT
stSG2577b	123	T	G	---	AATTGCCAAATGGAAAATTCCCAGAGGATTTTAGACCAACTTGCCCTTGTTGCATTCCCAGTTTGGTCCCAATATAGGCCTTCTGCAAGAAGAGAGATCAATGCCGAACCGAACTGTGAAGCA[T/G]GAACAATCCCGGCGCCAGATTAATTATT

stSG2577 a	121	C	T	---	AATTGCCAAATGGAAAATTCCCAGAGGATTTTAGACCAACTTGCCCTGTTGCATTCCCAGTTTGGT CCCAATATAGGCCTTCTGCAAGAAGAGATCAATGCCGAACCGAACTGTGAAAG[C/T]ATGAACAATC CCGGCCCAGATTAATTATT
stSG2700	58	G	A	---	ATCTCCTGCGACTGCTTTAGTGGGGAAAGGAATCAATTATTTATGAACTGTCCGGCCCC[G/A]AGTCAC TCAGCGTTTGCGGGAAAAATAAACCACTGGTCCCAGAGCAGAGGAAGGCTACTTGAGCGGACACCA
stSG2724 b	101	T	G	---	AAACAAGCTTTGTCATTTCCACTACATTTGTGTGCTTTTATATTTGCAAATGCTATAAT TTAATACTTATATTCCAATTGCTTGCATAATCA[T/G]TTTTTAATCCTGGGGTGTTGAAAGAAC
stSG2776 a	65	G	A	---	GTGGCCGATCTTACTTTTCCAGAAAAAGGCGGTAAATAAAAACCTGTAGAAAGTCTGAATATGC[G/ A]TATTGGCCCTTTGGAGTTAGGCCCAGGAACTTCAAACAAGGGACACTGCTGGCCAACCACAAAA ATATCCACTACAATTCCCGAATATAGTAACCCTGTCTTGTCCGAATG
stSG2791 a	65	G	A	---	AAGGAAAGGTGGAGGGAAGAAGGGAAGAATTACAATGGTTAGAAAAGAGCAACTAAAGATTATTTC TATTATACTTCTGAACGGTAAACTAGCAATTTAATAAATATT[G/T]GGGTCCACTTAAATCTATTA AAGCAGAAAGTGTAAAGCTATCTCCATTAGTGAAGATGAAGTGACAAAACCAATCAG
stSG2791 b	109	G	T	---	AAGGAAAGGTGGAGGGAAGAAGGGAAGAATTACAATGGTTAGAAAAGAGCAACTAAAGATTATTTC TATTATACTTCTGAACGGTAAACTAGCAATTTTA[A/G]TAAATATTGGGGTCCACTTAAATCTATTA AAGCAGAAAGTGTAAAGCTATCTCCATTAGTGAAGATGAAGTGACAAAACCAATCAG
stSG2826	100	A	G	---	CCGCAATTTTCAACACACATTCTATGAAAACTAAGGGTGGATCATGTACAACACAAAAAACAAGC TCCCTCCCTCCAAAACAAA[C/T]GAACAAAAATAAGAAAGAAACCCATGAAATGCCCAGGTTTA ATTTTTTTCC
stSG2850	85	C	T	---	ATGGGTGCATTGTAAAAGGCAAATTAAATACTTTTTCAGGCAGGGCGTGGCAAATTTAATGAGCTGA TGTGTCCCAAGGGAGACGGCGCC[G/A]GGCTCACACATCCCATCAAATACTCCTCCAT
stSG3031	88	G	A	---	ATACTCACGGGGGGCTGAAGGGCAATGTGAAGAGTGACTGCAAGTCCTGCATTTTCTGTGGTGTCAGC AAA[T/C]GCGCCCCCTTTATTTAAATGATTCCAGAACATCTGGGCAGCATAGCT
stSG3058	71	T	C	---	GTCCCAACTCTCTCCTCTTAGAGAAAAACTGTGATTACCTCAACTGAATATGAAACTGTGATTG AAAAAAGTCAAAAC[G/A]TTGAAGAAGCATCAAAGGCAAAACTGGCTGAGGC
stSG3092	81	G	A	---	CAGCATCTTCCAGAACATTCCTAGAACTGAACCATTCTGTCACTATTGAAAAGCCAAGTTC CAAATCCAAAATAATAAATGAACGTGC[T/G]GATAAACATTCTTCTTATGGTTCCAGCCCTACTTT AGTT
stSG3230	94	T	G	---	AAGAAGTACTTTGGTAGCTATTTAAATAAGAGAGGGGTGGGAATGTCGAGATACGAGCACCTG CATCTTTAGTCAATTGTCAGTGGAGTC[A/G]GTGGGGGTGCTAAGTGTTCTGAACTGAAGTAG
stSG3245	95	A	G	---	ACATCTCATACCCAGTAAGATGCAAGAAAGGAATATCTGAGACAAGAAATCTGAGTGTGTTTCTACCACCCCTGCCATCCCCTGCCATCCAGTCTG CAGGTATGTGTAGAGGCCCAGTGGGGGTGCCCACTGTTTG[G/C]TGTACTTGGCTTAAGTACTTCATGCTTTAT GCCCCCAGTACTACCTGGGGAGGTTG[G/C]TGTACTTGGCTTAAGTACTTCATGCTTTAT
	160	G	C	---	

ID	Position				Sequence
stSG3265	42	T	C	---	AGGTGAAATGAGTTACTACATAAATGTAGCATTATTTATAAGGAA[T/C]GCATTGTGTGAATAGTTTCTCAG TTTCATTATGGAAAGATGATGATTCAGCCACCATTCAGTGTATGTTTCTAAATAACACAATCGAC AGGACTGTCTGTTCAGTCAGCTGAATTCTTGGGCTTATGTGGCAGTGTGGTAAAAA ATCTGTCTTGTCAGCTGA
stSG3269 b	141	C	T	---	TGTACTTACTGTCATCCTATCCATTCCCTTCCCTGAGCCTGGACTGCTCTTCCAAGGGAGGACTAGG AGTGAAGGGAGGAGGAGTCCTCCCAAAGTTACCCTTTAAGCTTGATAATTAGCTCCATAGCCATGCTAAA GCATGA[C/T]TGTAGATCCCAAGTCCCTGACACATTTCTTCTAAGAAACT
stSG3269 a	24	A	G	---	TGTACTTACTGTCATCCTATCC[A/G]TTCCCTTCCCTGAGCCTGGACTGCTCTTCCAAGGGAGACT AGGAGTGAAGGGAGGAGGAGTCCTCCCAAAGTTACCCTTTAAGCTTGATAATTAGCTCCATAGCCATGCT AAAGCATGACTGTAGATCCCAAGTCCCTGACACATTTCTTCTAAGAAACT
stSG3284	130	C	T	---	TTAACTCAAGAACTTCAGTTACAGGAAGATTTATCTAATATTAAAATGACTAAATTACAAAAAGC ATAAAATGTTTGAAGCCATTTTAAAGTTGTTTGAAATCCATATTAGCACTCAGACTTCCCCA[C/T] TCCCTAACTTTTGTTAATTGCTGTAATGGGACATTTGTTTTGATCTACCC
stSG3292	99	A	T	---	GTCTCAAGTGAATCTGTAAATACATTTTAAGTCTGACTTCAAATCGGTACATGAGGCTTAGACATA CACATCATTGGACAAGTGACTTAAATATCTAA[A/T]TACAAATCAAATAGCATTTCCTAACTTCAA
stSG3323	26	C	A	---	TAAATGTCATATCTTTAGCTCTCACT[C/A]CCAGTGTATCCCATTTCCCCAGCCGTAGAGCTTTCTG TTTCTGTAGATTGCCTGTCCTGGACATTTGATATAAATGGAGTTGCTGTATCATGTTCGACTTCTCTC ACCTAGCATGATGTTTCAAGACACATCCATGTCTGTGAGCATGCGTCAGTGTTCATTCCTTTAA
stSG3369	69	C	T	---	GATCCCCAGTATTATTTCTAAATTGAACTTGTTTGTGGAAATAAAAAATCTGAGGACCACTCAGAG GG[C/T]ATAAGGGAACCCTCTTTGTCTTAGTTCATAAGGACTTTCT
stSG3398	125	G	T	---	CAAGACTGTAAGAACGTAGGCCTTGTGAGAGTGAAGGAAGGATGCTCGAACTTGCCCAGGACTCAGG CTTCAGCTTCACAATCCCGGAGGAAGAAGAAATGACATTTCCAAACTGTCAACCTTTGTAGC[G/T]CTGGGT CAAAGTCTAAAGAGGACAAATAAATAGAGACT
stSG3416 a	43	A	G	---	TCTTACTCTGTTAACTCAGTCTGGAGTAAAGGATGCAATCACG[A/G]CTCACTGTAGCCTGGACCTCC TGGGGTTCAAGTGATCGATCCTTCCACCTCAGCCAACTGAGTAGCTGGCCTGCAGGACAAGTCACCATGCCTA CCTAAGTTTTGTAGAGACAG
stSG3424	173	T	A	---	GTAAAGACAAGGTTTTGCTATGTTGACCAGGCTGGTCTTGAACTCCTGGACCTCACATCGGACCGTACCA CCTTGGCCTCCCAAGTGCTGGGATTACAGGTGTGAGCCACTGCGCCCCGCGACTTTTAAACTGAAT GTTGAAAATCATTCTGCTCTTTGCTGGGTAACACTGA[T/A]CAAGTTGCTTAACCTTTGTGAAACCAC TTTCCTTATCTGTAACAAAATGGACAAACAGAACTTTTCCTTTCCTCTC
stSG3436	88	T	A	---	GTTCATGTTAAAGATTAGGAAAGCTGGGTGATGTGAGGGGTCAGGTGATGTGATGGAGGCCTCACAGA ATGAGTGGCAGAGAGGGCCCC[T/A]GAAATAGCTTACTCTGTTTCCTATC

stSG3463	103	C	T	---	GATACAGAAGAGATAGTGTGGTATGGATGGATAGTAGTGGTCAATGGTGGTCACACAGCTCAATGGGTCAC[C/T]TGGAACAAAACTTGCTTGACTATATTA AAATAAACAAAAACAAAAATGCATACACAGCTCAATGGGTCAC[C/T]TGGAACAAAACTTGCTTGACTATATTA CTGA
stSG3491 b	71	G	A	---	CAAGATACTTCATTGTCTCTAAGTAGTGCAGTGCTGGCCAAATATTTCTCACGAACAAGGACGATTTG AAGA[G/A]GTGGAATTACTGTGCAAGGAGTACTTACCTCCAAATAGCCTGCAATTAGCAGTCTGA ACAATCTTCTAATCTTTTACTGGCCACCTGTGGATTTCTATTAAACTCATTTATACTATTTTCTGTGATG ACAGAAAATAAGTTAAC
stSG3523	33	C	T	---	TAGCCATCTTACTCTAGTTCTTTTGGGTTTTA[C/T]GCATATATGTGTGTACAAACACACACACACC CCTAATTCCTCAAATGCTCTTGGCATAAGTTTTATCTCTTACTGGTCTC
stSG3536	213	A	G	---	AGTACAAACACAGAGATTTAAAGAGCTCAGCAGTATTGACACGCTGGAAATTAATGGAGACATCCACTT ACTGGAAGTAAGGAGCTGGTAGCCTACCTCACAGCGCTACAAAAACCAAAATACAGAATGGCTTC TGTGATACTGGCCTTGCTGAAACGCATCTCACTGTCATTCTATTGTTTATATTGTTAAAAATGAGCTTG TGCACCATTAG[A/G][TCCTGCTGGGTGTTCTCAGTCCTTGCCATGAAGTATG
stSG3583	112	G	A	---	GAAAAAGCTTAACATACGATCCATGTGCAAACCCAAAACAGGATCTACGACTCTGGCATGATCCA CATCGCTACACATACCATGCTGGAAGTGCACATCCACACAGGCAC[G/A]TAACATACACAGTACTGT CTAGTTATCAACACCTAC
stSG3586 a	60	G	C	---	CCTAGTAACATAGTGAGACCTCGTCTCTACTAAAAATTTAAAAAATCAGGTGTGGTGGT[G/C]ACG CCTGTAGTCCCTACTTGGGAGGCTGAAGTAGGAGGACTGCTTGAACCCAGGAGGATGGAGGCTACAGT GAGTTATGATGGCGCCATTGCACTCCAGCCTGAGACTGTTTCAAAAA
stSG3589	101	T	C	---	ATATAGTAGTGCTGGTGGTAGCATTATAAACTCCTTTAAAAAGCAATCTGGCCATATCAAAGGCAAAAAAGT GTATATACCACCCTGGCACAAAAAACCCAATGA[T/C]CCTATTCCAAGAATGTATCCAGATGAAA GTATCCAACAACAAAAAGCTATATACAC
stSG3590 a	70	A	T	---	GAGAGATGAGCTATTTATTCTTTACTTAATGAAGATGTAAGAAATGATCTTCTGTTCTAAAAAAAA AAA[A/T]TTTCTCTGATGTCTCTGACCCTGTGAGGAAACACATTCAGTTTCTACACT
stSG3619	78	A	C	---	CAGTGAGACTTCTCATTTTATAGCAAATACATTTTGCAGCTTAAATTTTCTTGAATTCATATACGCT TCTGTCATTT[A/C]AACAAACTTCCAGAGAAAACTGGGCTCTATATATTTAAG
stSG3644	40			---	ACATATGTAACTGCCATTAGTAGCCATATTTAGGATGAGAG[T/C]GGATTGAGAGAGGCATGAACCAAGG ATGCGTAATAATCATTATGAAATAATAAGTTATCTGGGGAAACGGCCATTGTCCAACATTTACTAA GTGCCTACTA
stSG3646 c	70	G	A	---	CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAATATATGATGATAACAATATATGTCTTACT GGT[G/A]ATATTAACTTTGATACTTGGTTAAGAGATGGTGTCTCTAATTTCTCCATTGTGAGAGTCATT CTTCTCTTTGTA

stSG3646 b	55	A	G	---	CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAGAATATATGATGATAACAATA[A/G]TATGTCTT ACTGGTGATATTAACTTTGATACTTGGTTAAGATGGTGTCTGCTAATTTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA
stSG3646 a	43	A	T	---	CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAGAATATATG[A/T]TGATAACAATAATATGTCTT ACTGGTGATATTAACTTTGATACTTGGTTAAGATGGTGTCTGCTAATTTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA
stSG3693 b	85	A	C	---	ATTGTTCCCTGAACATTCCCGTGGTCTCCCTCTGAAAGCCGATGACCATCCAACCCTGGACTCACCT GAAATATCCTACGAGGC[A/C]TCGCCCCTCCGAGACTGACGATTATTAACCACCCACACGGAAAAAGG
stSG3693 a	30	C	T	---	ATTGTTCCCTGAACATTCCCGTGGTCTCC[C/T]TCTGAAAGCCGATGACCATCCAACCCTGGACTCA CCTGAAATATCCTACGAGGCATCGCCCCTCCGAGACTGACGATTATTAACCACCCACACGGAAAAAGG
stSG3698 b	145	G	A	---	TCTTGCCCTTTGTGTTACCCCTAGAGAGATGGCACCCAATCCCAGGGGTTGTCTCTGACTTCCACCAT TCACTGACTTTTATTGCCAGAGATGGCTCCCAGGAATCCACAGTTCTGGAAGAGAGGGGCTCTAAGTCT TTATTGGGG[G/A]AGAATACCCACCACCTTCCCTCACTGCAGA
stSG3698 a	51	C	G	---	TCTTGCCCTTTGTGTTACCCCTAGAGAGATGGCACCCAATCCCAGGGGTTG[C/G]TCTCTGACTTCCA CCATTCACTGACTTTTATTGCCAGAGATGGCTCCCAGGAATCCACAGTTCTGGAAGAGAGGGGCTCTA AGTCTTTATTGGGGAGAATACCCACCACCTTCCCTCACTGCAGA
stSG3724	107	C	T	---	ACCAGCCTCATGTGCAGAGGGGTCTCCTGCTGGATCCCCAACTGGAGCCATCCCTGGGCCTAGACTTCT GTCTCCCTCACTTCTAAATGAGTGCTCAGTGATGTGAAG[C/T]ACACAGGAGTCCCTCAGGGCAAAA GTGGCTATGCTGGTGCT
stSG3725	104	G	A	---	GCCAAAACAAAAGATCTTTGGAGTTTACTGACGGCAGCAGTTAATAGCACAGTCAACAGCATTTAA ATCAAATATATTATTACCAGCCAACAGCAAACAGCCC[G/A]AGCAGGAATCGGCACATAGTCATAA ATAACATCAGGGGTAAATAACGGCACATTTA
stSG3751	128	G	A	---	CGGAAGAAGAAACACAAATCCACAGGAACAATCTATGGTTCATACCTTTTAGAAAGATGATTTTG AGGGCTTCAGTATTTAAAGGGGGAAAGCAGGCTGGAGGGGAAAGAGAGGATATGTGCCC[G/A]TT GCTGACTCCATGTCCATGTTGCAAGAG
stSG3787	49	T	A	---	TTCTGTGCAAAAGAATCCACATCATTGTTTGGTAGCAGAGGATCTCTTA[T/A]AAAGTTCCCTAAGA CACTGAGGGCATAAAACCAAACAAATAAAATAAGGAGTGATAGGCTAAAGCAGTATCTTCCCCT
stSG3880 b	115	G	C	---	GACAAGAGGGAAGAGAGATGCGCCAGAGACCAGGGCTGGGGGTCCCTGAGTCGCCAGGCGC CACCACACGTCCTGTGGGTCAAGGCCCCTCCTCTCGGGGAGCAGCAGTTGCTA[G/C]GGCACGAGGATGCAG GGCTGGGAGGGGGACCCCACCTCGGGGGACCCAAAAGGAGTCCATTTCTGCCCT

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stSG3880 a	36	G	C	---	GACAAGAGGGAAGAGATGCGCCAGAGACCAGGGCTG[G/C]GGCAGCTGGGGGTCCCTGAGTGCCAGG CGCCACCACACGTCCTGTGTGGGTCAGGCCCCTCCTCTGGGGAGCAGCAGGTCTAGGGCACGGAGGATGCAG GGCTGGGGAGGGGACCCACCTCGGGGAGACCCAAAAGGAGTCCATTCTGCCCT
stSG3895	44	A	G	---	AATCAGCCATTGTACACATTGCAGCTATGTGTTAGTGTTGT[A/G]TTTTTTTTCCATTAACTAA TACATGCCCTCATCAGATATATTCAATTAGTGTTATCACCATGGGAACAAGATGCTGATTCGTCAACTG AAAAT
stSG3902	104	T	C	---	TCTGTTGAGACTGGAGAGACCAGGTACCAAGCACCGACTCTGGTGGGAACCTGGCTTCCTGATAACA TCATCTATTTCACCTAAATGTGAACTGCTTTCTTTTC[T/C]TCAGCTCAATAGCTTAACATCTAATTC ATGTTTGCTCCCTTTGCTGGACAAT
stSG3935	50	G	A	---	GGGTGTCTGACGGACAGGCACACCCAGCAGTTCAACAAGCAATTTGTCC[G/A]CTAGTGTGCAGGC TCCTCCCCCAGTTTCCCACAGGCTGAGTACTATGGGGTCACAACCTTCCTGACGT
stSG40	25	A	G	---	GAGGAAGAGAGGTTGAAGAAGTGCTGA[A/G]AAATATATTTAAGATTTCCTTGGGGAGAAATCTGTGC CCAAACCTGGTGATGGATCCCTTACTATTTAGAATAAGGAACAAAATAAACCCTTGTGTATGTATCA CCCAA
stSG4009	32	A	G	---	GTGTGGGCTGTCTGATGATGAATGGCGCGGCTC[A/G]TACTCTTTACGGTCTTTATGCTCCT ATGAATTCTCTGATGGGCTTTAAGGGCTGAACCATATCTGAAGGTTTCCCACACTGCTTACA
stSG4033	123	T	C	---	AGAAGCCTTGGGGACAATGGCAGTGCCCTTTGTGTCAGACTAAGACATGAATGCCATCTGAGGATCCATT TGAAACTACAGTGCAGTAACCAAAGAACCTAATGTTTCAAGCATAAAGGTACTTT[T/C]TGTGAAC AGGTGGGCAACAC
stSG4038 a	29	G	A	---	GCTGAGAGACACGTGTACAGCCACGCCCTGT[G/A]GCGCAGGCCCACTCTGTGCAATAAAACATGTTCTGCC CATGTTCCTCCTCAGTCAGGAGGTTCAGGGTCCCGGAGAGCACCTGAGGGTTCCATCACT
stSG406	53	T	C	---	ACTGTGGTTCAACAGTATTGCGTTGTCAGACTAGGAAAGCTAAACGAACAAAA[T/C]GGTTTTAGTT TTGCTGAAGACTGGCCTTATTAATGGACAGCTTTCCTAACAAGAGATTATTAAACTTTATCAGGTGTT AACATCTGTTCAGGAGAACATGGCA
stSG4095 b	55	G	T	---	ATCTGGGCTGAATTAGTCAAGCAGGTCAGATACTATTGTCTGCTAGATGTATTAG[G/T]ATAAAAAA GTTTGCTTCTGTAATACTTTAAAGCTTGCTTATCTCATCTGTAAACCTATGTGTCTTGAGAATCAAG CCTTTGGACTAACCCCAGGGCATTGCCCCTTCATCCTGG
stSG4095 a	27	A	C	---	ATCTGGGCTGAATTAGTCAAGCAGGTC[A/C]GATACTATTGTCTGCTAGATGTATTAGGATAAAAAA GTTTGCTTCTGTAATACTTTAAAGCTTGCTTATCTCATCTGTAAACCTATGTGTCTTGAGAATCAAG CCTTTGGACTAACCCCAGGGCATTGCCCCTTCATCCTGG
stSG4120	65	G	A	---	TGCATGTTCCCACATCTTTCATAACAGCAAAATGTATAATAAACTTACGTACTTATGGATAATCAC[G/ A]CTTTTTCCCCTCAGAGAGCCCACAGTTAAACACGTTCCAGCAGTCAAACCATTAATCCACCGAGCT

ID	pos				Sequence
stSG4128	54	A	G	---	CTTGGCAGATAAGGGACTCGTTGCAGATATGACTTTCCTTGTGTACATTTCT[A/G]TATATTATTT TACTTCTTCTGAAAATGCCACATAAATTGCAATAAATGATTCACTCCTTAGCTCCAAAAGCAAGTCC TTTATCAAAATGCAAATGTTCCAGAGGG
stSG4209 b	128	G	A	---	CACGAAAACAGATGCAGCCTACACAGTGCTGTAGGACCGGAGGCTCACAAACATCCACATGGCACAAGC AGGGCCGGCCACTCCAGGCAAACGAAGCCACCCCCGAACCTTGCAGAGGCGCGCACTCCCTC[G/A]GC AGGGGGGACCGGAGGGCGACAGGTGCTTTGATGCCTCGAAGAGCTGAGCTCCATTCCA
stSG4209 a	65	G	A	---	CACGAAAACAGATGCAGCCTACACAGTGCTGTAGGACCGGAGGCTCACAAACATCCACATGGCACAA[G /A]CAGGGGGCCGGCCACTCCAGGCAAACGAAGCCACCCCGAACCTTGCAGAGGCGCGCACTCCCTCGGC AGGGGGACCACGGAGGGCGACAGGTGCTTTGATGCCTCGAAGAGCTGAGCTCCATTCCA
stSG4254 b	31	G	A	---	CATTACCCAGAAACGCCATGGAGGACCAGAGC[G/A]CCACGGCCGGGGACTCCCGCGATGGCTGGGGGG GCTATGGCTCTGACAAGAGGATGACGGAGGGCCGAGGGCCTGCCTCCTCCCCCAGGGGCAGACGGTGAC TGGGGGACCATGGCCGAAGAGAGAGGGATGACCGGTCATG
stSG4301	81	T	G	---	TGCAACAGCTCTGAGAGGAAATCCTTGGCAGATCAAAAGAGAGAGGGTAGTGGCTCCCACACTTTCCAT TTAAGCAAATAAAT[T/G]AGCTTCTGAGTAGTTGTTCCCAGTTCACCCAACATTTG
stSG4331 b	71	T	G	---	CTCACAAAGGCCAACACAGAAAAAAGATACAAATACATTCATCCAGCTAATATTAGTTTTATGACAC AGAG[T/G]TTTCAAACAAGTTAAGTGTCACCTGAGAGCATGTTAAAAGTTAAGTTATCACTT GGAGAGCAGATTTCTTGGCCTCGCCCTTGTGATTCTGTTTGAGGGGTGTGC
stSG4340	76	G	A	---	TTTTGCAACAACATGGATGGACCTGGAGGCCATTAAGTGAAGTAATGATACAGAAAGTCAAAAACC ACATGTTCTC[G/A]TAAGTGGGGAGATAAACAATGTGTACACCTGGAGCAGAA
stSG4361 b	109	A	C	---	TTCCCAACCATTGAGTGACAGAGCTCAGTCATGCAGAACTCAGGTTGCATGACTCAAATTAGG AAGTTCTTGGAATTTCCATAAGGGATAACTGCCATCTTTTGC[A/C]CCTTCACAACTAGAAACGACTC AGCGACTTTTCTGTGAGCAAATGTCGAGG
stSG4361 a	24	T	C	---	TTCCCAACCATTGAGTGACAGAGC[T/C]CAGTCATGCAGAACTCAGGTTGCATGACTCAAATTAGG CACAAGTTCTTGGAATTTCCATAAGGGATAACTGCCATCTTTTGCACCTTCACAACTAGAAACGACTC AGCGACTTTTCTGTGAGCAAATGTCGAGG
stSG4376	73	A	G	---	TTTCACTGCTACTGGTTCGGTTGTCTGGGTCCTCGAGTCCTCCAAACTCTGCTTTGCAAGTGCTTCTCCAAGGGGGAG AACAG[A/G]CTGGAACTGCGGCTCTGCCATTCTTCCAAAGCCATTCTTCCAAAGCCATTCTTCTCAGCTGC
stSG4381	50	T	C	---	GAAGGCCACAAACACTCCATAGCCAGAGAATGACAACATACGATTTCTT[T/C]TCAGTCTTGTAGT ATCCACAGTAGTGATGTCTGTCCATGTACAAGTGTCTGTCCAGAACACCATTAAATTCCATGCC
stSG4410	79	A	G	---	ACCAATGGTTCTGCTCTGTGTATGTGCATCCGATATTTTTGCCCGATCTGAAATACTGCAAGGGCTTAACCAT TCAAACACCGC[A/G]TGACAACGAACCCAGTGGACTGTGAAACTGGCTGTGAAACTGGGGCTTGT CAGCTGGGT

stSG443	65	C	T	---	AGCAGATCAGTCAGCCCCACTTGTCTCTGTCTCTTCTTAGGGGAGAGGCTAGGCAGTGAACACATCA[C/T]GTATGCAATGACAGAGAAAATAACCAACTGGTAGGATGGGGAGGGGAGGGGAGGGGAATAGGCACAAATGGAATTCTATCCTGGCTGTCCTTCTCAGGTC
stSG4430 a	54	A	G	---	ATGCACATTAAAATGAATGGCCTAACTACTGGAACTTAGTAGTTCTATAAGGT[A/G]ATTAACATAGGTAGGATCCAGTTCCTATGACAGGCTGCTGAAGGAACAGATATGAGGCATCAAGAGAGGGCCATTT
stSG4448	99	G	A	---	CCTCCCTCCCTTCCCTTTCCCGTTCCCAGTCTTTTCCATACTGTTCCCCTCCGCCCCGCCCCAGGCTCTCGCCTAGCCCTGCCCTCTGGGGTCACTGC[G/A]TGGGTTAGGCCCCAAAAAA
stSG4449	92	T	C	---	ATTAGCCATTCATCTTGCAACAATTGCTTTACTGTAACTAAGAGTACTGTACTGATGATGTTTACAATTAACTTTGGACAACTTAAAACTTA[T/C]AGTGACATTGCTGTCTAAATAATCAAATACTTCATCATAGGCTGAACATAATTATTAAAAGAGCAAGTTACCCCTCCC
stSG4467	42	C	A	---	CAGACATGAGGGGATGGCCCTGTCTCTCTGGGACAGAGCCTCA[C/A]AGATGATGTCCATGTTTTGTGTGAATGAAACTCAAACACTCTTCAGTTTTAGAGTCATTTCTGGTATCGAGCGACCACCGAGGAGCACACCCTGCTTCCAAGGCTGCCTTCTGCACACAGT
stSG4475	21	A	C	---	ACATGTCATTTCCTGACCAGG[A/C]TATTAAATAGTTTATTTAGAAGAAATGAGTTGAAGTGAGCGATTAAGAGACACAAACTGGACTTTGTTTCTTTTACTGTAGCACCCAGGTTTCATG
stSG4477	32	A	G	---	GTAACATTCTGGGGGTGGGGTGAGACAAACA[A/G]ATGAACCAATAATTAATTACAATTATACATTTCAAGGAGACTTTAATCTAGGTTAATGTGAAACGCAGCCATCAATGGTTTGTCAGGAAAAGGGAGATGAAGTCTTGTCTCTGGGGCAACGTTTGGCCTCATTGCAGTCAGACTTGGC
stSG4531	79	C	T	---	TGAACTCAGAGCTGGGTGGGTGGGGAGCTGCGCAGGGGAGGCGGGGAGCTGGGGCCCCAGATGAGCCGCCGGGGACAGCAGGCGGTGCG[C/T]GCCACGTGCCTGGCGTTGGTAGAAGAGGACATAGGCTGCCTTGGACTCGATCTGATTCTCATTGACAGGGGAGACGCGTGTTGTCATCAA
stSG4550 b	86	G	A	---	TGCATTAAGGAATGATACGGCCATATTTGGGGGACAGAGAACAGGCTTGATGAGGACAGAGTCTATTTAAAAGACAGTGGGCACC[G/A]CAATTGAGAGGGAAGGCGGGGCAGGGTTTAGAGAAC
stSG4550 a	85	C	G	---	TGCATTAAGGAATGATACGGCCATATTTGGGGGACAGAGAACAGGCTTGATGAGGACAGAGTCTATTTAAAAGAGACAGCAG[C/G]GCAATTGGAGGGGAAGGCGGGGCAGGGTTTAGAGAAC
stSG4590	47	A	G	---	AATCAGGCACACAAGCTCGGGAGGAGAGAGCCAACAAAAGCTCTCTGCAC[A/G]ATGGGAGGAGGAGACACCATTGAAAAAGGCACATCGTTCCTTCTTCATGCAAGCGCGAGCCCTGGCTCCCACAGGCATGGTCCTTG
stSG4623	22	T	C	---	AATCTGTATCACCCAGCGCTGG[T/C]CAATGTACTAGTAGCTTCCACAGGGATTTTTTATACTATTCCTATAAGGTTTATCATGAATAAAAAAGCTCACAACTCTTTCAGCCATTGCAGATTCACATTTATCTTAATATTCCTGTTCCAAGATGCTCTGGAG
stSG4843	102	A	C	---	TAAAAAAAACAACCCCCCAAAAAAAACACCCAGAAGTTTTTGAGTTTTATGTTTTCAGATTTAAAGGTATTTTCTTTCTTTAGCTTCTAAATTTTGAGTCATT[A/C]ATCAGAAAAGTCTTCCCTACTCCAAGGTGAGAAAGGA

stSG4850 a	38	C	T	---	GGAATCTAAACTGGGAATGGCCGAGGAGGAGGGGCTC[C/T]GTGCACTTGCAGGCCACGTCAGGAG AGCCAGCGGTGCCTGTGTGGGGAGAGGTTTCCAAGGTGCTCCGTGAAGAGCATGGGCAAGTTGTCTGACAC TTGGTGGATTCTTGGGTCCC
stSG4879	86	A	G	---	AACTCTGAAGGGGGTGACCTCAACCCAGCCCTTGTTCTTGTGTGGAGGTCCTGCTTTGCAGAATGGCCTG CCCCTGGGACTGGAGACAG[A/G]CTTGGGTGAGCTCTAGGTGGGAGGGGTGGGAGGGGCATAGAAAT AAACCTTCC
stSG4885	104	G	A	---	ACTGGACTGGCTCGCTTGCTGAGCGCGGCCGTGAGCGGCCGTGCGGCTGACCACCTCGCTCTTCAG AGACTCGCCCCGGCCGGTGACCAGACTACGCTCTGCC[G/A]GTGGGAAAGCAGAAGCAGGACC
stSG4896	112	C	T	---	AAACAAATCAAACCCAATCCCCAGCAGTCTATGTACAGGGCCACTCCCTGCCTCTCTGCCATAGAGA GGTTGGGGGGCAGCTGAGGAGGTGGTGGGGGCTGGCCACCTTTC[C/T]CAGCCACAGCCCCTGAGG AATTAATTGACTG
stSG4932	22	G	A	---	ACAGTGCCGATGGTTACACAAT[G/A]TTGTAAATGTATTTAATCCCACTTACGAATGATTAAAATGA TAAATCTTATGTTTATTTCATCACTACCAAAAGGCTGTGTGGGGTGCTGGTTTCTGGTCCT
stSG4950	24	A	G	---	TCATGACTCCCCAGGAAAAGGTCCT[A/G]TCTTAGCTTGTCTCCTCCCTACTTTCCTCTACATGGTCAGC ACTGTAATGTAGCTAAGATATAGTAAGGCATTGCTCTGCCTCCCCTACCCCTACACTTCAAGG
stSG4957	136	G	A	---	AGATACGGGCAAAACACTGGGATGGCTTCCTGACAACTTAAGAGGTCTCCGAGTTATATTCTGGGTT GGGAAACACTGACCCAGCCCTTATTCCTTCAAGGACTCTAGTCATTGGCAAGGAGGATTCATGAGCC CC[G/A]GTGACACAGATGGGGGCCCCTGCTCTATTCAAC
stSG4961	91	C	T	---	GAAGGTGCTCTGAGAGGTGTGACTCTCCCGGCTGACAGGGGAAGGCTTAGCAGAGAGCTTTGTCTTAG AGGAGTAGATGAAAAGGAAAGTA[C/T]AGAGAGGGCATTCAGGCCAAGTCAGCAACACAGACAA
stSG4967	72	A	G	---	ACTGGTGCCTCTCAGCAGATTCAGGGGTCGTGCAGGGCTGGTTACCACAAACTCAGTAGGAGTGCAA GGGCTA[A/G]TACCCCCGGAGCTAGACAGCCTGGGTTGAATCTCAACTTCTCCCTTTCTTGCTGTGC AACCTTG
stSG4997	22	T	C	---	CAAAGGAGAGTAGGAGCCCCAA[T/C]TTTAATGGTTTCCTCTCCCCCTCATGCTATTTGATCCAAAAA CTATATACAATTTTGTAGCAGTCTCTGTATAGTTATTACACATGTTTAGAAGGGAGGGAGGCAAGAA GGGGATAGGGAGGAATGGTGATCCAAAAT
stSG6312	37	C	T	---	ACAGGTTCTCACACTTTGAGCCTTTAGTGCAAAAACA[C/T]TATGCCATGCGGGAAATAAAATGCTT ATCCAGTGGAGCGGCTCCCCTGATGCATTGAAATATTAGGATACTCAAGCAGAAGAC
stSG6345 a	107	G	A	---	GCTCTGGTCAAGCAAATTCTCCAGGACAAGCAACAAGGACAGTAAACACACATGTATGACCCTTA CAAGTGCTTTAAGATTTAAAAAAATGTGATGTTTTGTCCAC[G/A]ATAGTTCAGGCAATTAAGAATAT GCAAACCCAGAGAAATTTCTGTGAAAACATTTTGCTCTTTGGCCTGGTGTGGACAGAAAGGGGTGGCCAA ATGGATTGAGTGATGAGCAGACATG

Clone	Position	Allele 1	Allele 2		Sequence
stSG6362	88	G	C	---	TGTGAAATGTACACTCAGGTCTAACAAATACCTATTATTCTCTGGTTAAGAAGGTTTAGCAGGAGCCTCCAATGAGCACTGTATGTA[G/C]AGAAAAGGGAAGGAGCAGGAGGAGGAACAGATCTGCACAGAAT
stSG8010	62	G	T	---	CACATCTGTGTTTCTGGAGCAAAGGGAAACCACAGAAGGCCAGGAGTTTGGGTGTGCACTGG[G/T]TGTCTTTCAACTGGGTGGAACCAAACTGAGTCCTTGAAGTCTCGCCTCCTGAGGCTGCAGAAGAATAGATGGCTT
stSG8022	53	G	A	---	AGCTCCTGACTCCCTGTTCAGTGACGTCATGTTGGTAGCCTGAAATGGACCAC[G/A]GTGGGAGTATTTACACCATGGAAACTGAAAACTCTACAAATCAATGCGTTTATTTCTTTATTTCAGAGGGCAGGTTTATCAGCACACGCTGTATCTCC
stSG8032	67	G	C	---	TGATTGTTAGGGGATAAGTGGGCATTGTGTTTACAAATTACTTCCAAAGAATTCAGAAAATTGTGTGT[G/C]TGGGAGGCAGGGTAGCAAGATAAAAGAGGGAGGACAGCTGGGGTTGGTAAAA
stSG8064 b	46	C	A	---	AGCTGGCTCTTCTTCTGTGTCTGGGAGGCTTCACGTCCTCG[C/A]CCGTGGTCCCTGGGTGGCCTGCAGGACCAGGGGGTGGGAAACAATGCCAGGAGAATTCCTGTCACATCAAACAGGGAACA
stSG8064 a	23	G	C	---	AGCTGGCTCTTCCTTCTGTGCGT[G/C]TTCGGGAGGCTTCACGTCCTCCGTGGTCCCTGGGTGGCCTGCAGGACCAGGGGGTGGGAAACAATGCCAGGAGAATTCCTGTCACATCAAACAGGGAACA
stSG8072	59	A	G	---	CACCATCATCACATCGAGTAGGCTGAGGAGCAGGAGGGGTGGGTCTTGCTGTCTTGAGG[A/G]TGGCAGAGGCAGAAGGAAGTCCGAGTATTAGTGCCGCAGTTCAAGCCTGTGCTGTCAAA
stSG8100	40	A	G	---	ATACACCCACACACCCCACTCAACCTTGTATCCAACTTGTATCCAA[A/G]AAGTGTAACTAAAGTATAAGAATATCATGACTAGTTAAAAGATAGCAAATACCATAAGGTACAAGTTCAAGTTACAAGTATATACAACAAGTATCTGAGTAACAAAATGTCCTTGGAAATGGG
stSG8102	138	T	C	---	AAGGCTCCTTGAAAGCATGGTTTATTTGTTCCATTAACTGTTCTCAGCTATACTGAAGTATGATTGACAAATAAACTTGCATATATTTGAGATGTACAGTGTGATGATACACATGTATACAATGTGAAATGA[T/C]TGTCATAATCATAATCAATAATTGGTATATTGGTTTAGGAAATGTGATGGT
stSG8105	110	A	G	---	CAGTGGTTCTCAAACTCCAGCGTACACGAGGATGGTCTTGTGTAATACACAGATGACTAGGCCCACCTGCGCGGAGTTCCTGTTGGAGTCGAGCCTGAGAATATTC[A/G]TTTCTAACAAGTTCCCAGGTGACCCTGAGGGCTCTGGGACTGGGGAACATGCTTTGAG
stSG8130 b	96	T	C	---	GTGTGTACATCATTGGGAATGGAGGGAAATAAATGACTGGATGGTCGCTCTTTTAAGTTTCAAATTGACATTCCAGACAAGCGGTGCCTGAGCC[T/C]GTGCCTGTCTTCAGATCTTCACAGCACAGTTCC
stSG8130 a	36	C	G	---	GTGTGTACATCATTGGGAATGGAGGGAAATAAATGA[C/G]TTGGATGGTCGCTGCTTTTTAAGTTTCAAATTGACATTCCAGACAAGCGGTGCCTGAGCCTGTGCCTGTCTTCAGATCTTCACAGCACAGTTCC
stSG8145 b	124	T	A	---	TTGTGGACTTCAAATTCTTTCCTTCAGATTTAAAATGACATTATGCATGTACATATTTTAAAATTTAGACACATTTTAGAGAACAACAATCTAAGAAAATGAATGAGATGT[T/A]CTGAAATCTGATTCAAACACTTATCTTAAACTGACTTCTGTCAATCCTGTCCTGTGTGAAGG

Name	Pos.	Alleles		Sequence
stSG8145a	97	C	T	---
				TTGTTGGACTTCAAATTCTTCCTTCAGATTTTAAAAATGACATTATGCATGTACATATTTTAAAAATTT AGACACATTTTAGAGAACACAATTGTGAA[C/T]ACAAATCTAAGAAATGAATGAGATGTTCTGAAA TCTGATTCAAACACTTATCTTAAACTGACTTCTGTCAATCCTCTGTCTGTGTGAAGG
stSG8150	36	A	G	---
				ATTGTTCTTGCAATTGCTTGGATTTTTCAGAATAGTT[A/G]ATAAATAATAAACGGAATCCTAGGCAT TCGTGTTTTTCTATGTTTTAACAGGATTTTCTCTAATGTTTCGCTATTAAATACCATGCAGGAAATT GGGAAAT
stSG8340	30	C	T	---
				AGAGGATTATGGAGGAGAGCTGGGCAGGATC[C/T]CAACATTATGACCCTGAACCTCCAGAACTGGAT TCACTAGAAGGAGGAGAGAGAAAAACGCTCATCAAAA
stSG8466	111	G	A	---
				TGTGTATTGGGTGACTGTAGCCTAAGGATAAATAAATGAAATAAATGACAGCAATGTTATAAGCAGTGGGA GGAGTGAAACTGGGAATACTTGGTTACAAGGTATTTGCACTACCT[G/A]TGAAGCAGCACAGCATTAT TTGAAAG
ESTD-ACE	--	--		---
				GATCAAGCAGTGCACGGGTCACGATGGACCAGCTCTCCACAGTGCACCATGAGATGGGCCATATA CAGTACTACCTGCAGTACAAGGATCTGCCCGGTCTCCCTGGCGTCTCGGTCTCGAACATCTGCACAAAATCGGCCTGC GGCCATTGGGGACGTGCTGCGCGTCTCGGTCTCGAACATCTGCACAAAATCGGCCTGC
ESTD-ADA	--	--		---
				ACCATCTTATACTATGGCAGGTAAGTCCATACAGAAGAGCCCTCTCTCCCTGGGATTTGAGTGGGTC CCCAGGTCCACCCAGGAGCCCCTGGGAATTCCAGGGTCACTGTTCCTTCCTGTTCCCTGTGGGAAT CAAGCCAGCTCCAGGCCAGAAGTGGGACTGTGAGGACATGGGAGGCCTGGCACTGAGCTGCAGACCC GCAGACCAACTCCTGAGCTTCTGAGCCTCTGAGTCTTGTCTC
ESTD-AK-168	--	--		---
				GGGAGTGACAGCTAGAGCACCAAGGGGCCTCTACAGTGTGTTCTCAGCGTGTCTTCCATGGAGGACAGGCTTCTGCTC ATTCTGG
ESTD-ALB	--	--		---
				AATCCCAGCACTTTAGGAGGCTGAGGCAGGCAGCATATCACCAGAGGTCAGGAGTTTGAGACCAGTCTGA CCAACATGGTGAAACCCCATCTCTACTACTAAAAATACAAAATTAGCCAGGCATGGTGGTCATGCCTGT AATCCCAGGAGGCTGAGGCAGGAGAATCGCTTGAACCTGGGAGGCGGAGGTTGTGGTGAGCCGAGAT GGCACCATTGCACTCCAGCCTGGGCAACAAGAGTAAAACTCTGTCTTC
ESTD-ANT1	--	--		---
				TCTCCTGTCATTCCTCTACTCCATTAGTTCAAGGTCAGTGAAGAACTGGGCAATTAACCAAGTAATTCA TGGACTGCCCAAACTGCGAAACAAGAAGGGCGCAGTGGAGCAGGAGTATTATGCTACGCGGTTACCTT TTTTTATGGAGGACCGAACTGAGGCTGAGCTCAGATGATCCTGT
ESTD-APOA2	--	--		---
				CCAGGTGTTGTGGCCACGTGCCTGTAATCCCAGCTACTCGGGAGGCATGAGGCATGAGAATCTTTGAAC CGGGGAGGCGGAGGTTGCAGTGAGCCGAGATCGCGCCACTGCACTCCAGCCTGGGCAACAGCAAG ACTCC
ESTD-ARSB	--	--		---
				GGAAGAAAATGGAGCTGTGGGAAGAGGCCTGTGGGGAAGAGGCGTCCGAGGGGTGGCCTTTGTGGCAAGCCCCTTGCTGA AGCAGAAGGGCGTGAAGAACCGGACACCAATGCCAGCTCATCCACACTCTGACTGGCTGCCAACACTCATGAGCT GGCCAGGGGACACCAATGGCACAAAGCCTCTGGATGGCTTCGACGTGTGGAAAACCATCAGTGAA GGAAGCGCCCATCCCCAGAATTGAGCTGCTGCATAATATTGACCCAAAC

ESTD-AT3a	---	AGACCTCAGTTCCTCCTCTGTAAAAGGGAAGTTTGTTCTTGGATCTCCATGGGCCCAGCCAGCACTG GTGCCCTGTGAGTCTGTATCAGGTAGAGAGATGGGACCAGGTGGAGAGGAATTTGAAAGGGCATTG GAATTCAGAGACAAAGAGACAGATATTAAGAGCTGGGGAAATGTGG
ESTD-B3AR	---	GGCTGCCAGGGGGTTCCGTGGGAGAGGCGGGGCCCTAGCCGCGGGGCCCTGCTGGCGCGTGCTGGCCACC GTGGGGAGGCAACCTGCTGGTCATCGTGGCCATCGCCCGGACTCCAGACCCATGACCAACGT GTTCGTGACTTCGCTGGCCCGCAGCCGACCTGGTGATGGGACTCCTGGTGGTGCCGCCGCCGCCACCTT GGCGC
ESTD-BA511	---	GGGCAACATAGTGAAACCCCATCTCTACAAAAATACAAAAATTAGCCAGGTGTGGTAGCAAGTGC CTGTAGTCCCAGCTACTTGGGAGGCTGAAGTGGGAGGATCCCTTAAGCCTGGGAGGTGGAGGCTGCAG TGAGCCAAGATGGTGCCACTGCA
ESTD-BCL2	---	AGCTGGATTATAACTCCTCTTCTTTCTCTGGGGGCCGTGGGGGTGGGGGCGAGCTGGGGCGAGAGGTGCCGTT GGCCCCCGTTGCTTTCCTCTGGGAAGGATGGCGCACCGTGGGAGAACAGGGTACGACAACCGGGAG ATAGTGATGAAGTACATCCATTATAAGCTGTCGCAGAGGGGCTACGAGTGGGGATGCGGGGAGATGTGG GCGCGCGGCGGGGGCGGCGGGCCGCCGCCATCTTCTCTCCCA
ESTD-BCR	---	CAGTGGCTGAGTGGACGATGACATTCAGAAACCCATAGAGCCCCGGAGACTCATCATCTGCGCAAGA GACCAAAGAGGTCAGCTTCTGTTCCCGGGAAAGGGAGGCAGGTGACAAGCTAACTCTGCTTCAAA ATCAACCATCCGGTGGACACTGTGTGGCCATCGTGCCTGGCACA
ESTD-BRCA1a	---	AAGAAGAGAAACTAGAAACAGTTAAAGTGTCTAATAATGCTGAAGACCCCAAAGATCTCATGTTAA GTGGAGAAAAGGGTTTGCAAACTGAAAGATCTGTAGAGAGTAGCAGTATTTCACTGTACCTGGTAC TGATTATGGCACTCAGGAAAGTATCTCGTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAAACAGAA CCAAATAAAT
ESTD-BRCA1b	---	ACTAAATGTAAGAAAAATCTGCTAGAGGAAAACTTTGAGGAACATTCAATGTCACCTGAAAGAGAA ATGGGAAATGAGAACATTCCAAGTACAGTGAGCACAATTAGCCGTAATAACATTAGAGAAAATGTT TTTAAAGAAGCCAGCTCAAGCAATATTAATGAAGTAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTA TTAATGAAA
ESTD-BRCA1c	---	ATGCATCTCAGGTTTGTTCTGAGACACCTGATGACCTGTTAGATGATGTGTGAAATAAGGAAGATAC TAGTTTTGCTGAAAATGACACATTAAGGAAAGTTCTGCTGTTTTAGCAAAAGCGTCCAGAAAGGAGGAG CTTAGCAGGAGTCCTAGCCCTTTCACCCATACACATTTGGCTCAGGGTTACCGAAGAGGGGCCAAGA AATTAGAGTCCTCAGAAGAGAACTTATCTAGTGAGGATGAAGAGCTTCCC
ESTD-C1R	---	ACACAGGTGCTGGCCACTGGGGCTGGGGGATCCTCCTCCCCTAATTTGCTCCGGGAAGCACATTCATCAA
ESTD-C6	---	CCCAGTCAGTTTGGGGGACAGCAGCCATGCACTGAGCCCTCTGGTAGCCTTTCAACCATGCATTCCATCTAA GCTCTGCAAAT

Name		Sequence
ESTD-C7	...	ATATCGTGGCCTTAGTTACCTAGAGCTGGACAATCCTGCTGGA
ESTD-CB22	...	GGCAAGTTTTTATTGATAGAGAGGAAATCAAATAATGGCAATGAGGAGAGAGACATCACCTGGAATGTTAG GCAGTGCCTAACTGGGGGATGGACAGACAATGGCAGTGCCAACCATAGGGCGGGGATACAAAGAC AGGCAAGGAAGGGGTAGAACCATCAAAGAGGAATAGGCTGGTGACCCAAAGCAAGGAGGAGGACCTAG TAACATAATTGTGCTTCATTATGGTCCTTTCCCGGCCTTCTCTCTCACACAC
ESTD-CB23	...	TAGAACCATCAAAGAGGAATAGGCTGGTGACCCAAAGCAAGGAGGAGGACCTAGTAACATAATTGTGC TTCATTATGGTCCTTTCCCGGCCTTCTCTCTCACACATACACAGAGGAGGACCCTACCAGGACCAGACAGCT CTCAGAGCAACCCTAGCCCCATTACCTCTTCCCTTTCCAGAGGACCTGAAAAAACGTGTTCCCACCCGA GGTCGCTGTGTTTGAGCCATCAGAAGCAGAGATCTCCCACACCCAAAA
ESTD-CB24	...	ACCAGGACCAGACAGCTCTCAGAGCAACCCTAGCCCCATTACCTCTTCCCTTTCCAGAGGACCTGAA AAACGTGTTCCCACCCGAGGTCGCTGTGTTTGAGCCATCAGAAGCAGAGATCTCCCACACCCAAAG GCCACACTGGTATGCCGCCACAGCCTTCTACCCCGACCACGTGGGGTCGAGCTGGGGTGGGGTGAATGG GAAGGAGGTGCACAGTGGGGTCACAGCACCGGCACCCGCAGACCCCTCAAGGAG
ESTD-CB25	...	GTTTCTTTCAGACTGTGGCTTCACCTCCGGTAAGTGAGTCTCTCTCCTTTTCTCTCTATCTTTCGCCGTC TCTGCTCTCGAACCAGGGCATGGAGAATCCACGGACACAGGGGCGGTGAGGGAGGCCAGAGCCACCTG TGCACAGGTACCTACACATGTCTCGTTCTTGTCAACAGAGTCTTACCAGCAAGGGGTCCTGTCTGCCACC ATCCTCTATGAGATCTTGTAGGGGAAGGCCACCTTGTATGCCGGTG
ESTD-CB27	...	TTTTCTGTTCCCTGAAGATTGAGCTCCAACCCCAAGTACGAAAATAGGCTAAACCAATAAAAAAT TGTGTGTTGGGGCCTGGTTGCATTTCAGGAGGTGTCTGTGGAGTTCTGCTCATCGACTATCTTCTGA TTAGGGAAAGCAGCCATTCCCTTGGACATCTGAAGTGACAGCCCTCTTTCTCCACCCAATGCTGCT TTCTCCTGTTCATCCTGATGGAAGTCCTCAAACACCATTCCATACC
ESTD-COL2A1c	...	AGAATGTATATAGTCCTCAAACTGGCCATCCCATCTCCATTTCAGTCCAAAGTTATACAGCTAGCAACA GTGGTGACATACGTTGCTATTTATGCTCTCTTTCTGTCATTCAGTCCACTTCAGGGTGTTCAAGGTGTTCAAGGT GAACAGGGTCCCGCTCGGTCCTCCAGGTAAGTAAATCAACTCAAGCATATACAATACTGCCTTTG GTCCAGCCTATTGAGCTGTAAATCACCATACCGTACCT
ESTD-COL2A1d	...	TGAGAGAACACACTAGTCCTCCTCTCTCAATGGCAAGAAAGTTAAGTGACCTATCTAGGGC AATAGACTGAGTTTGCTGGGGACCTGGAACACTGACTTCTTTCTACTGCAGCAAGACTTACCC AAGAGAGATTAATGGCAAAGATATACAATACAATTTTTATTGACCAAACACTACTCATGGAACAGC ATT
ESTD-CPT2	...	GCCGGCAATGCCGGGGAGTTTCTCCAATGTGTGGAGAAGGCCTTAGAGACATGTTTGATGCCTTAGAA GGCAAATCCATCAAAAGTTCAAAAGTTAACTTCTGGGCAGATGAAAAGCTACCATCCATCATGAAAAC TGGGAGGCCGGGGGAGTTGAGAGGCTGAGGCGGGATCAC TTGAGGTCAGGAGTGTTGAGACCAACCTGGCCAACAT

ESTD-CTLA-4	··	··¦··	¦	ATGGCCTTGCCTTGGATTTCAGCGGGCACAAGGCTCAGCTGAACCTGGCTACCAGGAGACCTGGCCCTGCAC TCTCCTGTTTTTCTTCTTCTCTGCAAAGCAATGCACGTGGCCCAGCCTGCTGTGGT ACTGGCCAGCAGCCGAGGCATCGCCCAGCCTTGTGTGGAGTATGCATCTCCAGGCAAAGCCAC
ESTD-CYP2D6	··	¦	¦	CAGGCCAGCCGGTGGTCGAGGTGGTCACCATCCCGGCAGAGAACAGGTCAGCCACCACTATGCACAGGT TCTCATCATTGAAGCTGCTCTCAGGGTTCCCGTTGCCCTGAGCAGGGCCGAGAGCATACTCGG
ESTD-D11S1873	··	··¦··	¦	AAAAAAACATTTTAAACACCTTTTCAATCATATACACCATAAAATTCCATTTTCACATAAGTCAGTT TGAGCTGAGTTTTCCAATTACTTGCAATCTAAAATGTCATAACTGATTAATGCAAGTTCAACAGACA ACTTTCCCAAGCATCTACGATCAGAAAGGTCAAAATATTACATATCTGGATTAAATTATGCCCATAT CTGCATGTC
ESTD-D17S33	··	··¦··	¦	CATCCCCAAGCCCATCCTCTTAGCCACTGGCATTTTTGCCGCCTCTGACAGATACACTCAGGGCCGT CATGCTGCACACATCCAGGGGGCGCCCTACCCTTTGTGAGTCCATGGAAAGGCTCCTCTGGGGGCGGTG GGGTTGTGTGGCTATGTGGTGGTCTTTCCACCTGAGCGAGCCTC GCAGATTGCTTGTCTTTCCACCTGAGCGAGCCTC
ESTD-D18S8	··	¦·¦··	¦	TTTGAGACCACCCTGGCCAACATGCCGAAATCACATCTCTACCAAAATTACAAAAATTAGCTGGGTGT GGTGGTACATGCCTATCGTGTAATCCCAGCTACATGGGAGGCTGAGGCAGGAGAATTGCTTGAACCCA GGAGGCAGAGCTTGCAGTGAGCCAAGATCACCACCACTGCACTCCAGCCTGGGTGACACAGTGGAGA CTCTGTCTCAA
ESTD-D3S11	··	¦·¦··	¦	AACTGATTAGAACCTGAAAAATACATATTTTATCTGAAAAAGTGAGTTATTGGCTCATCACATTGG AATTTTTGCATCATCATTAAAAAAATCCAATAAAGTACACTGTAATAAAGAATTAACAGAATATCATTGT TTATTCAAACTATTTATCACTATTTATTGGTAAGCCAATCTAAAATTCTAAAGCATGTTTCTGAAAG TTTA
ESTD-D3S12	··	¦·¦··	¦	AGGTTCCACATTATTGCTGATGTTTGCTGATGTTTCCAGGAGCCTTGATGTCATTCTGTATCTCCTCAG GTATCCCACCTTGAGACGTACTTTTCAAAAACTCTCTACAGCCGTTGTTGTTGTTATTAATTCAAGGTTGA ACATAAAGTA
ESTD-D3S2	··	··¦··	¦	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCCTGC TGAGTCTTATTCAAAACTGACAGCCATTATGCCACCTGAAATATGGTCAGGTTACAGCTGTATTCCC AGAAGTGAAACATACTGCTCCTAGAAGCCAGAGTCATACTGGATGTCTGTTTCGGTCTTCACGATGGG CAGGTATGAAATATAATAATCTGTCCTTTATTGGAAGGATGCCGGTATGT
ESTD-D4S338	··	··¦··		TTTTCTGTTTACCTTGTTCAGATCCTTCAGAGGAATCCTATATGGCAGGTATATGAAATGTATTT CTTAAACAATAAACTTGAAAGTCCAAAATTACTCCTTGCATGGACTGCAGAATAAATGTTATTT TAGCTGTCAGAAAAACAATACTAATCTTGCATATGTTCATCAGAGCCCTTGGGTGACCAGGTGTATT GCCAATAAGCAGTAATATTTGAGAGGAATCTTGTTTCAATGCAGTAG
ESTD-D4S95	··	··¦··		CTTTCATGCACGATAGGCTTTCTCTACTAATCACAGAATTTTCTTCTTTCTTCTTTAGAGTCTACCGG ATAATGGGGCACCAATCACTTACTTCTCTGG

ESTD-D7S399	⋮	TGAATCTTAATTGCTATCTCTACAAAATGTATAAATCCTGAATCTGACATCTAGCCACCTCCATAGAT AACTGCTAGAGACCCAGTCTCCTACATCCTTTCACAAAACATTTCATCCATGACTCCATACTAG AATATTTGAAGAAACAAACATGACAAACATTTTC
ESTD-DM	⋮	GTGGGGACACCGAGGGCTCCAGCCTGGGCGCTTGCACGTGTGGCTCAAGCAGCTGCTCGGCCTCCACT TCCATGGGTGTGGGGCCTGGGGACCTCACTGTCCTGCGGAGGAGGGAGGTGGGGAGGGAGGAGACA GAATGCTGATTATCTGGTGGAGAACCAGAACTTCTGGCCCTGTGGGTAGGGGCAGCTGCTTCCAAGACC TCCTGATTTGAGGAAGGGGAGCAGAGCGAAGAGAACAGAGT
ESTD-DRD1	⋮	TCCCCAGCGCCCTATCGGTCATATTGGACTATGACACTGACGTCTCTCTGGAGAAGATCCAACCCATCAC ACAAAACGGTCAGCACCCAACCTGAACTCGCAGATGAATCCTGCCACACATGCTCATCCCAAAGCT AGAGGAGATTGCTCTGGGGCTCGCTATTAAGAAACTAAGGTAC
ESTD-DRD2	⋮	TCTGCCTTTGGTGCAGGAGGCTGCCGGGCGAGCCCAGGAGCTGGAGATGGAGATGCTCTCCAGCACCA GCCCACCGAGAGGACCACCGGTACAGCCCATCCCACACCAGCAGCTGACTCTCCCGACCCG TCCCCACCACGGTCTCCACAGCACTCCCGACACAGCCCGCCAAACCAGAGAAGAATGGGCATGCCAAAG ACCACCCCAAGATTGCCAAGATCTTTGAGATCCAGACCATGCCCAATG
ESTD-DRD3	⋮	AAGACGATGGCCAGGATGAGCGCGGCCAGTAGGAGGGGCATAGTAGGCATGTGGGCGGCCTGGCTGG CACCTGTGGAGTTCTCTGCCCCACAGGTGTAGTTCAGGTGGCCACTCAGCTGGCTCAGAGATGCCATA GCCCAGAGGGAGGTGCGTGCGTGATGCCAAGGGCTTCCTGTGTGAGGAGA
ESTD-ERBB2	⋮	TCTTTCAGGATCCGCATCTGCGCCTGGTTGGGCATCGCCTCGCGTAGGTGTCAGCGGCCTCCACCAGCTGG GGTGAGGCGGGTGGGGGTCAGTGCCGGGCGGGCGGTGCAGACCCCACGCGGGGCTGGGAGGACTTCACCC CGCCTCACCTCCGTTTCCTGCGCCAGCAGTCTCCCGCATCGTGTACT
ESTD-ETS2	⋮	ACTCACAGTGCTTTAAGTGAAAATGGTGAAATGGTCGAGAAAAGAGGCACCAGGAAGAGCCGTCCTGGCGGCCTGGCA GTCCGTGGACGGGATGGTTCTGGCGTGTTGAGATTCTCAAAGGAGCGAGCATGTCGTGGACACACAC AGACTATTTTTAGATTTTCTTTGCCTTTTGCAACCAGGAACAGCAAATGCAAAAAACTCTTTGAGAGG GTAGGAGGGTGGGAAGGAAACAACAACCATGTCATTTCAGAAGTTAGTTTG
ESTD-F2	⋮	GATAAGTACACTGAGGCCCCAGGAGGTTATTGCCTAGTAGCCAACTGTGCATGCACGCTTAACCTCT GCACCAAATGGCCTCCAAGCCCCGTAGGGGAACTGGGGGATCTAGGGGATGGGGTGAGGAATGGCCC AGCCCAGTCCCCGGCCCGGGTGCCTGGGTCCCAACAGAGAGGGGCCGTCGGGGGAGGAGACAGGAGATGGGGC TGGGATGAG
ESTD-F9	⋮	AGATCCTGATGATTTTTTCCTATTTTTTCTAAATGTTTACAGTTTGAAGTTTATGCCCCA TGCTCCATTTGAGTTAATATTTGTGTAAAGTATGATGTTTAAGTCAAACTTCATTTTTTTCCATA GGTATGTCCAATTTTATCCAGCACAATTGTTAAAACAAAAAC

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ESTD-GCDH	CGCAGACCGGTCAGTGTGGGGTCGGAGTGTGGGAGGAGGAAGGAGGGAGGGAGGAACTGGGGGTTTAGGGACTTTCCGGGGTGACTTTCCCGTTCTGTGCTTGCGCACCGTGTTGTCTGCTGCCCTGTTCAGCTGCTGTCTGCCCGCAGTCGACTCTGTCCCGGAAATTCCGAGAGCT
ESTD-GCK	GTTTTATGCATGGCAGCTCTAATGACAGGATGGTCAGCCCTGCTGAGGCCACTCCTGGTCACCATGACAACCACAGCGCCCTCTCAGGAACACAGTAAGCCCTGGCAGGAGAATCCCCACCACCCACCTGGCTGGAGCAGGAAATGCCGAGCGGCGCCTGAGCCCCAGGGAAGCCAGGCGGGATGGTGAGACACAGTCACCTGCAGCCTAATTACTCAAAAGCTGTCCCCAGGTCACAG
ESTD-GNAT2	GACCCTGAGTACCTCCCTAGTGAGCAAGATGTGCTCCGATCCAGGGTCAAAACCACCAGGCATCATTGAAACCAAGTTTTCCGTCAAAGACTTGAATTTCAGGTAAGTGCATGGTCATTCCCTAGG
ESTD-GPPK2L	AGTCTTCATCTGCGGTGTCCAGGTAGATCCCTTTCACCGCCGGGAACTGCTCGATATC
ESTD-HRAS	CTGGGCCTCGCCGCGCAGCAGCTGCTGCACCTGGACACGGCGGCGCCTGAGCCCAGGCTCCACCTCTATAGTGGGGTCGTATTCGTCTCCACAAAATGCATCTGGATCAGCT
ESTD-HSD3B1	TTGGAAAGTTCTCCACTGTTAAACCCAGTCTATGTTGGCAATGTGGCCTGGGCCCACATTCTGGCCTTGAGGGCCCTGCGAGGACCCCAAGAGAGGCCCCAAGCATCCGAGGACAGTTCTACTACTATATCTCAGATGACACGCCTCACCAAGCTATGATAACCTAATTACACCCTGAGCAAAGAGTTCGGCCCTCCGGCTTGATTCCAGATGGAGCTTTCCTTATCCCTGATTGTATTGGATTGGCTTCCTGCTG
ESTD-HT2	GGGCTAAAATTTCCGAGCAACTTTGCATAGACTGTGTTTTATTTGACTTGACAGGATTGCTAGAGATAGGCAGGGAGGAGGAAGAGATGTGTTACAGTTTGTCAGAGAGAATAAAAAGGATAACCTGGGGTTTTCTGTGCTTTGCTTCTTCTTCACATCCCTGGGGAGTTAATAGCTGCAATTTTCAAAGAAACGGTATACAGGGACAGCAAAGCGCAGTCGTGTGAAGTTTCAAACAAGACACACCTT
ESTD-HT4	ACCAACGAGCGCGCGATACAGACACTCTTAAGTTTTGCCCTAAGGCTCATTCAAATCATTAGGCATTTTCTGATAAACTAGGTTCTTGGGTGCCTTCTATCGGCAAGAATGCGTACTTATTTGAATAGTAGAGGTAAACCACCAGCGCCCCAAGAGTCACTGGCAGCTTCTGCAGCGGCGCAGCGATGTGCTGACAGCGGAAGAGGCGCCGAAGAGACCATGCGAAGACGCAGATGTGC
ESTD-HT5	AACACACAAGCCCCAGCGGAGAATTGAACTCGCGACCCCTGGTTTACAAGACCAGTGCTCTAACCCCTGAGCTATGGAGCCCTGTCCGTGTTTTTCATCTCTATAGATTGATTTATGCTCCTAGCATTCCGGCTACCGAATAGGATGGATGTTAGCTTGAGTAAAATTCCAGGTAATTCCTACAAATGAAAACATTTTCGTGCTCTGTAAATCCCTGAAAAGGTTCT
ESTD-IGFBP1	ACCCAGTGGAGCCCGCTCATTGCACGGTCTTGCGCAGGAGGTGCCCTGGGAGAAGAGGAAGAGATGTTCCAGGGCCACACATAGCTTAGTGTGGGAGACTC

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ESTD-IGHV4-6	TTTACTATTTCAATGGATACAGAATTGTGGGAGTCACTATATTCCTATGAACAAAAAATTCAGATTT CAGTTGTTAAGTAAGTATGTTGCCTACATTGTGTGAGTGACGGGCAGTGGTGGATCCGAGAGTGTGGTGGG TGCACGGACATAATGATTCAGAAAGCAAATATGGAAAGATGAGTATCTATGGATACGAACTGAAAGT ATGTAAATACTTCACAAAATACTAATAAACGGAGTTGAATATAAAACCCA
ESTD-IL1A	CAAAGTAAGCACCCAATAAATGTTAGCTATTACTATCATTATTATTTATTTTTTG AGATGGGAGTCTGGCTCTGTCACCCAGGCTGGAGTGCAGTGGCACAATCTCGGCTCACTGCAAGCTCTG CCTCCTGGGTTCATGCCATTCTCCTGCCTCAGCCTCCCGAGTAGCTGGGAATACAGGCACCCGCCACT GTTCCCGGCTAATTTTTGTATTTTTAGTAGAGACGGAGTTCACCGT
ESTD-IL1B	CCACTTACAGATGGGATAAATGGGTACAATGAAGGGCCAATAGCCCTCCCGTCTCCCGTGTATTGAGGGGTGT GGGTCTCCTACCTTGGGTGCTGTTCTCTGCCTCAGGAGCTCTCTGTCAATTGCAGG
ESTD-KRT10	CCAAAGTTAAATAGTATTGGGAGTTATCTGAGAAATTTCCATGTCAGTGTTACCTTTTTGGCAATATT AAAGGAAGAAAAATGCATTTAAAGTAACTGCTAAGGTTTTTTCCATTAAACCACTATTACTTCTAAG AGAACTGTACATGACAAATATTGCCATTACATTGAGAATCAACTATGTAGCTGCTTTTTAAATAGTCTC TGCCCAGATACATCTCCCCTATATAAGTTATAACCAGTATTGATA
ESTD-KRT8	ACCCTCACCCCCTCCCTTAGCCCGTGGGAAGCAGGAAATCTCTCTCCAAATCCATGAATACACATCGG ATTGGACACCTTGAGAGTCTTAACAGCAGGCCTGACATGAACCTCAGACAGAACTTCTAGAGTT TGCTAGAGGTCAAGGGTCAAGACTCAAAGAGAGGGCCAGAATGTTAAGTACAAAAGTGAGGCCCATAG GCTGCCTATCTCTCCGGTCTCAGGTTACCACGTCAACATTGACACA
ESTD-LF79	GGGTGATTTTGAGGCTCAGTTAATATTCAAAATTGTAACCGTAGCAAAACTGCATTGGTATTTAGA AAAATAAAAAATTTCCAATATGTAGTGCTGTGTTATACCTGCCTCTGCCCATGCAGCATCATAGCCTGT GGGAACCAGGAGGGCTTCCCTTACCCACCCCAGA
ESTD-LMP2	TACACACTTTCCTTACCCATTCACTGAAAACGACTCGCAAACTGGAGCCTTGTGAGGAATGGAGTTGA CCTTCCCCAAAAGCCACTATGTATTGGTG
ESTD-LPL	TGTCAGTGTCCCTAGGGGCACCTCCCACTCCCAGCTTCTTCAGCTCTGCCTGTCCTGCCTGCA AGGGGTTTGCTAATTCCATTCAATGTCTTCATCTTTAGCAGCTGTGGGGTTTTGTTGTTGTTC TTCTGTTTTTGCTTTAGTATCTGACTACTTTTAATTATAAAAGAGATGTATCTAAACAAAATAGAG ATTGTTATCAGAAGTTCACACAATTTATTATTCAAAATTTTTCACCTG
ESTD-MCC	TTGTCAGGAGTGTGCTGATGCTGCCTCCCCAGCTCTGTCCCCAGCTGGGGGG
ESTD-METH	CATCCATGTAGGAGAGCCTTAGTCAAGTCAAGGGGAAGCAGTAAAACAGCATGCATCCCCGAA TCTCAGGAAGTCTCTGTCTTTCCAAGGGTTGGTCTCAAGTTGCTGATTACCCGGATTTTTCTGACGATC TTTCAACTGCTAAGAGCATCTGGTTCCTGTTTTAGCATGG
ESTD-NF1	ATTATCCAGATGAATTTACAAAACTATACCAGATCCCACAGACTGATATGGCTGGT

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ESTD-NFKB1	AACATGGACTTGTATATTTGTACAAAAAAAGTTTATTTTTCTAAAAAAAGAAGAAGAAA AAATTTAAAGGGGTGTACTTATATCCACACTGCACACTGCCTAGCCCAAACGTCTTATTGTGGTAGG ATCAGCCCTCATTTGTTGCTTTGTGAACTTTTGTAGGGGACGAGAAGATCATTGAAATTCTGAG AAACTTCTTTAAACCTCACCTTGTGGGGTTTTGGGAGAAGGTTATCA
ESTD-NPPA	TGTCCCTAGGCCCAGCCCTGCTTGTCCTCCCTGGCTGTTATCTTCAGTACTGCAAAGAGAACACAGAC AT
ESTD-NRAMP	GGAGGCAGGAGGTGGGGAGGGGGTCTGTCTGCTCCAGGTCCCACAGAGAAGGCGGCCTCAGTG TATCCCACCCCCAATGTGGCGCCCATGGGAGATGAAGAGGAGTTGATGCAGGT
ESTD-NRAS	GTGTTTTCTTAATCTTTTCCAGGAACACAGTGACCATATTCTTTCTCGCAGGCATATAGAATTTGGT GGGTTTTCTTTTATGTAGGGTGATATTGGATACTTTTTGTTTGTGTGATTATATATTAGCAATTTGAGGG ACAAACCAGATAGGCAGAAATGGGCTTGAATAGTTAGATGCTTATTTAACCTTGGCAATAGCATTGC ATTCCCTGTGTTTTAATAAAAT
ESTD-OTC	GTGACCTTCTCACTTTAAAAAACTTTACCGGAGAAGAAATTAAATATATGGCTATCAGCAGA TCTGAAATTTAGGATAAAAACAGAAAAGGAGAGGTATGTAACA
ESTD-PAI1	GCCACCACCACCCCACCCCAGCACACCTCCAACCTCCAGCAAGGTTGTTGACAAGAGAGCCC TCAGGGGCACAGAGAGTTGGACAGTGGGGAGTCAGCCCGTGTATCATCCGGAGGGCGGGGCAC ATGGCAGGATGAGGGAAAGACCAAGAGTCCTCTGTTGGGCCCAAGTCCTAGACACAGACAAAACCTAG ACAATCACGTGGCTGGCT
ESTD-PAR	CTCTTCAGGAACCACCAGTCTTCTTACCAAACACGACTTATTGCTGTCCGGAGAGGTACAACCGTGAGA ACTTCTTCCTAACTGTAATTTAGTTAAGGAATCGAAACTGGCTCTGAAGACATGGAGATACTGCCT AATCGACTGGCTTTCATTAGCTCTGTGAGTGTTTCTTCACTTTCTGTGTTCTTAGAACGTTTTCTAG GACTGCAGTTAAGCTTCACTTAGGCTTTCTTCTGTATACCCATGCCC
ESTD-PBDA	CCTTCTCATGCCCAGATGGAAATTCCAGTCCCTTCAGGATCTGCCTAACCTGTGACAGTCTAAAGAGT CTGAGCCGGTGGCTGGGGAAGGGCAGGACGACTAAATCCTCTACCCGACGCTTGCTGCTGCGCATACAGACG GACAGTGTGTGGTGGCAACATTGAAAAGCCTCGTACC
ESTD-PS-1	GGGGAGTAAAACTTGGATTGGGAGATTTCATTTCTTCTACAGTGTTCTGGTTGGTAAGCCTCAGCAACA GCCAGTGGAGACTGGAACCACAACCATAGCCTATTCGTAGCCATATTAATTGGTTTGTGTCCTTACATT ATTACTCCTTGCCATTTTCAAGAAAGCATTGCCAGCTCTTCCAATCTCCATCACCTTTGGGCTTGTTTT CTACTTTGCCACAGATTATCTTGTA
ESTD-PXMP1	ATGAAACATGGTTCTTTAATTTATGATATGTTTATAGCTATCTTAAAGGGCTTCTTTTTTA ATGCAGAAGAGGGGAAAAAGAGCGAGTCGTGGTGGACAAGGCTGTTTTTCTCAAGGCTCATACAGA TTCTGAAAAATCATGGTCCCTAGAACATTTGTAAAGAGGTAAGTCTTATGAAATTATAATCTT
ESTD-Per/RDS	ACCTACACGACGTCGCTGCTGATGGTGTGTCCAACCCGGAATCTGAGGAAGAGCGAGGCTG CTGGAGAAGAGCGGCGTGCCGGGAACCTGGAAGGCCT

ESTD-RDS	...	CCCGAGGAATCTGAGAGCGAGAGAGAGCGAGGGCTGGCTGCTGGAGAAGAGCGGTGCCGGAGACCTGGAAGG CCTTTCTGGAGAGTGTGAAGAAGCTGGGCAACCAGGTGCAACCAGGGCCGGAGGCGCGAGACGCAGG CCAGGGCCCCAGAGCGCTGGCTGAGGGCCCTGGGGCCCCTCCCCTCCCGAACACTGAGAAATAGTGCACT CCAAGAAACGTGGATCTCCCCTCCAACTCCGAAAGTCTGAA
ESTD-RYR1	...	CTTCGTGACGGGAGGTCACGTCCTCCGCCTCTTTCATGGACATATGGATGAGTGTCTGACCATTTCCC CTGCTGACAGTGATGACCAGCGCAGACTTGTCTACTATGAGAGGGGAGCTGTGTGCACTCATGCCCGC TCCCTCTGGAGGCTGGAGCCACTGAGAATCAGCTGGAGTGGGAGCCACCTGGGCGCTGGGGCCAGCCACT CCGAGTCGGGCCATGTCCACTACGGGCAGTGTCACTAGCGCTCACCGAGG
ESTD-SPTB	...	TGAAACACCCTGTGGTCCGGAGCCAGGTTGTGTTCTCCTGGGAGCCTGAGGAGTTGTTGTTGTCTGTGTG CAGTCCCCGCCCGCGCCACCTGCTGGTTGAGCCTGGACATACACCTTCACCTCCTTTGGCCCGGAGAAGAC ATTTACCCACCTGGCCATGTCCCTGGCCTGTTGTGCACACCCTCGTGAAGACCCCAACCCCTGCCTCC CCCACCCAAGCCAGTTTCCTAGCAAGGGCAGGAC
ESTD-SSA1	...	TTCACTTTGTGGATTGTTCTTTGCTGTGCAGCACCTTTCAACATGATGTGATCCCATTTGTCCAAG TTTGCTTTGGCTGGCTGTGTGCTGTGTGGGATATTTGAAAGAGATCTTTGCCAGTCCAATGTCCTAGAGAG TTTTCCCAATGTTTTCTTTGTAATAGTTTGAGGCCCTTAGAGTTTAAGTCTTTAATCCATTTTG ATTTGATTTCTGTA
ESTD-TAT	...	AAATGGTCAGGACCCCTGATCCACAAGAAGTGTACCATTTCATCAGGGCCATCAGTTCATTCAGCTC CCATGACTGGGATGCTAAGTCAGCAACTGAGTTCATTCATCTTAAAATGACTTGTGGGACAGGATCA ATTTCCTCTCACCTAGAACGTTTGTTTACAACTTTTCTTCCCAGTATGGATGGGATTATGATGGGGGG GAGAAGCAAAATTTAAATAGGACCCATGAGACACATCA
ESTD-THRB	...	TGCGGGCCTTTCCTCCGGCCAGGGTAGACTTCTTACTTGGCTGTTGATTTCCAAGAGAGAAGAGTCCCAAG CACACGAAAACAGAAGTTGCAGATCCCCATGAGGCCCAGTCTCAAATCACACAGATCACTTCATCCA CACTGGATTGGCCCAAACAGTCGAGTGCCAGCAGGACTCAACGGTCCCCCTGTAGATGGG
ESTD-TNFA	...	TTCCTGCATCCTGTCTGGAAGTTAGAAGGAAACAGACCACAGACCTGGTCCCCAAAGAAATGGAGG CAATAGGTTTTGAGGGGCATGAGGGGTTCAGCCTCCAGGGTCCTACACACAAATCAGTCAGTG GCCCAGAAGAGACCCCCTCCAGAATCGGAGCAGGGAGGATGGGGAGTGTGAGGGGTATCCTTGATGCTT GTGTGTTGCCCCAACTTCCAAATCCCAAATCCCCGCCCCGCGATGG
ESTD-TYR	...	TAGTGAAGTTTCATCTCCTGTCAGCTTCTGTCAGCTTCTGTTCCCACGGCCAACAAGAAGAGTCTATGC CAAGGCAGAAAAGCTGGTGGTTGCTTCATGGCAAAATCAATCATCGTCTCTCCAGATTTCAGATCCCCAAGCA GTGCATCCATTGACACATAATAATGCATCCAGACAAAGAGAGGTCATAAATATATTGATGTGTTAAACAT GGGTGTTGATCCATTTTCATTGGCCATAGGTCCCTATGGGGATGACA

ESTD-TYRP1	--	AGTAGTGGATGAAGCTAACCAGCCTCTCCTCACTGATCAGTATCAATGCTATGTGAAGAATATGAA AAACTCCAGAATCCTAATCAGTCTGTGGTCTAACAAATGCCCTACTCTCTTATTTCTTCACTTATTACCTTCTTTCT AACCACCTGGTTGAATATAATAGATTGAGTTATTAAGTTCTAGGCATACTT AATACAAGCATATGTTAGAATTAAAGTTCTAGGCATACTT
ESTD-VB12	--	TTCCCAAGGCCTCAATACAAGTCTTTTTCTTGGGATTACAACATCAGGGTCTGTGTTTCTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCCAAGAACAAGGTCACAGAGACAGGAACACCAGTG ACTCTGAGATGTCACCAGACTGAGAACCACCGTTATATGTACTGGTATCGACAAGACCCGGGGCATG GGCTGAGGCTGCTGATCCATTACTACTCATAT
ESTD-VWF	--	AGGGTAGGAAAAGCAAAGAGTTGATTAGTGAAGGAGAAGAATGGACCTACCTTCCACACTGTCCTTTGG TCCCCTAGAGTCTG
ESTD-WT1	--	AAGACCTACGTGAATGTTCACATGTGCTTAAAGCCTCCCTTCCTTACTCTCTGCCTGCCAGGATGTG CGACGTGTGCCTGGAGTAGCCCCGACTCTTGTACGGTCGGCATCTGAGACCAGTGAGAAACGCCCCTT CATGTGTGCTTACCCAGGCTGCAA
ESTD-s14544	--	TTGGGAAGTTAGAGCCTATATTAAATTACGGAATTACTAAGGCAGGACACAGAGGCTTAATTGAAAA TATCCCAAAGTTGAAATGTCTCAGTTCGCTGTGTGGGTTAGATGCAGGATTTATATGATCCGTTAACC TCT
EST717706	--	AGCACCACCTCTCACGTCAAGCCTCAGCACCAGATGCTGTTCTATAAGGATGACGTGCTGTTTTACAA CATCTCCTCCTCCATGAAGAGCACAGAGAGTTATTTATTCCTGAAGTCCGGATCTATGACTCAGGGACAT ATAAATGTACTGTGATTGTGAACAACAAAGAGAAAACCACTGCCAGCTGTTGGTGGGAAGG AGTGCCCAGTCCCAGGGTGACACTGGACACGAAAGAGGCCATCCAAGG
EST524186	--	CAAATTACAGGGTCAACTGCTATGATGTGTTTGGAGCCCAGTCACCCTTTGGTGGCTACAAGATGTCG GGGAGTGGCCGGGAGTTGGGCGGAGTTACGGCGGGAGTCCCAGGCATCACTAAAAGTGAAAACTGTAGTGTGG
EST135863	--	CCCACTCTATTTGCCCAGCCCCAGGGACACAGAGCTGATCCTTGAACTCTTAAGTTCCACATTGCCAGGA CCAGTGAGCAGCAACAGGGCCAGGCTGGCTTATCAGCCTCCCAGCCCGGCTGCTGCAGACAT AAATAGGCCCTGCAAGAGCTGCCTGCTGCTTAGAGACTGCGGAGAAGGAGGTGCGTCGTCCTGCCTGCCCCCG GTCACTC
EST519767	--	AGGCAGAAACTGGGCCCCCATGCGGGGACGTGGAAGGCCACTTGAGCTTCCTGGAGAAGGACCTGA GGGACAAGGTCAACTCCTTCTTCAGCACCTTCAAGGAAAGAGAGCCAGGACAAGAGCTCTCCCT CCCTGAGCTGGAGCAACAGCAGCAGCAGCAGGGTCAGGTCAGCAGATGCTGCGCC CCTTTGGAGAGGCTGAGCTGCCCCCTGGTGC

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EST114586	...	CCACTTTGGTAGTGCCAGTGTTGACTCATCCACAATGATTTCTCCAGTGCTCATCTTGTTCTCGAGTTTTCTCTGCGCCATGTTGCTATTGCAGGACGGACCTGTCCCAAGCCAGATGATTTACCATTTTCCACAGTGGTCCCATTAAAACATTCTATGAGCCAGGAGAGATTACGTATTCCTGCAAGCCGGGCTATGTGTCCCGAGGAGGGATGAGAAAGTTTATCTGCCCCTCTCACAGGACTGTGGCC
EST398528	...	CGGTCTTCCTTCCAGGTATTGTTGCAGAAGGCCGAGATGACCTCTATGTCTCAGATGCATTCCATAAGGCATTTCTTGAGGTGAGTACACCTTCCCCACTCTCTTACGGTACAAGGAGATGCATGAACAGCAGGAACACGTGGAAAAGGCCGTGTTTCCAGTGTTAAGGCATGCAAAAGGCCCTCCACAGGCTGCTATAATACAGCCCT
EST624480	...	ACCTGGTGTTGCTGGTGCTGTGGGTGAACCTGGTCCTCTTGGCATTGCCGGGCCCTCTGGGGCCCGTGGTCCTCCTGGTGCTGTGCTGTGGGTAGTCTGGAGTCAACGGTGTCCTAGTTGAAGCTGGTCGTGATGGCAACCCTGGGAACGATGGTGTCCCCCAGTGCGCGATGGTCAACCCGGACACAGGGAGGGCGCGGTTACCCTGGCAATAT
EST360272	...	AGTGACTTCCAAGGAAATGGCTACCCAACTTGCCTTCATGCGCCTGCTGCGCCAACTATGCCTCTCAGAACATCACCTACCACTGCAAGAACAACCATTGCATACATGATGAGGAGACTGGAAACCTGAAAAAGGCTGTCATTCTTACAGGGCTCTAATGATGTTGAACTTGTTGCTGAGGCAACAGCAGGTTCACTTACACTGTTCTTGTAGATGGCTGCTGCTCTAAAAAGACAAATGAATGGGAAAGACAA
EST122740	...	CCCCCAGTTGACAGCCACTGCTCTAGACTAAGTTTCTTGCTTCCAAATAGAGCCTTACCAAAGTGTATTACATAAAGAAGTCAAGTGCAAGTGGTTTTACTCCTCATGACCAAATATTCTTCCCTCCTTAGGATGAGGTGATAGTAAATGACCGATGGGGGTCAGAACTGTTCCTGTCCGAGAACTATAAACTGTGAAGATAAATTCAAGCCACAGAGCTTGCCAGATC
EST76807	...	ATGCTAAGGGGATGGACACATGAAAGGACCCTGTGAGCGATTGTGCTATCTCCAGCGCCCCTGTCATCCAGCTCACTCACTCAATGGGCCAGTCAGGGCCAGGCACTGGCTCCGGAGGACTCACCACTGCCCCCTGCTGCCATGTGGACTGGTGCAAGTTGAGGACTTCTTG
EST444387	...	GCAGCCAGGAGCCGCTGCCACCATGCGCCCGCATAGATGCGGAGCTTCAAGGACGTCCTGCTCCGACCTAAGCGGAGCCTCAAGAGCCGAGCGGTGGG
EST128393	...	TGCAAAACACACAAAATCTTCTCCAGATGCCCTATGGCTGTGGAGAGCAGAATATGGTCCTCTTTGCTCCTAACACTCTATGTACTGGATTATCTAAATGAAACACAGCAGCTTACTCCAGAGATCAAGTCCAAGGCCATTGGCTATCTCAACACTGGTGAGTGATTACTTGAGTAAGGGAAACTTGAATGTTATTCAACTGG
EST544198	...	CTTCTGCGCCTAATTTGAATGATAATTGTTGCTGTGGGACCTGAGACCTGAGCCACTTTTATGGCACAAATGATCACTATTTCTTGACCCCTACTTACAATCCTGGGAGAGATGTATTGGGTTTAGCGGTGGTCGTATGTTGTCTCACTATAGTCCAAGTGAA

EST10398 2	--	TGCCTGGGGTGGCAAGGCTGCAAACAAGGAGGAGGCAACCCAGGAGGGCTTTTATGAAGCGGGCCATGGTA AGATGCTGCCACCTCTATCTACTTGATGATGTTCACATTGGGCTTGGGCTTCCAAACACGGAGAGAAG CATTGTTTTCTGGGCCAAGAAGGTATCTACCAATAGTGTCTATTAGGCATTTG
EST36751 7	--	CCAAGTCGTTCAATTTTGCAGGTTTAACTCGATTACTTTTCTATTCAAATCTCTGTAAAA TTGAAATATGAACTTAGTTTTCTGATCTATGGTTTCAAGTTAAACAG
EST40562	--	CACGTGGAAAGGAGCTATTTTGGAGGCTTTAAGAGTAAAGAATCTGTCCCAAACTTGTGGCTGAC TTTATGGCTAAGAAGTTTCACTGAGTCATTAATAACAAATATTTTACCTTTTGAAAAAATAAATG AAGGAATTTGACCTGCTCGCTCTGGAAAGAGTATCCGTACCGTCCTGACGTTTGAAACAATACAGAT GCCTTCCCTTGTAGCAGTTTCAGCCTCCTACCCTA
EST18288 3	--	GCTCTCTATACCCCGTGGGTCCTCCCCACGCTCTCTGGACTTCACAGAACTGGATGTTGCTGAGAA GATTGACAGGTTCATGCAGGCTGTGACAGGATGGAAGACTGGCTCCCTGACGGGAGCCAGTGTGG ACAGCACCCTGGCTTTCAACACCTACGTCCAAGGTAAGGCAACCTCTCTGGCTCTGGC CCTAGGGACTTAGTATCC
EST70523 3	--	TTCCGCGCCAGCCCCATCCTTGGCACCCTGGTCCCCCTCCAGGGGCCACCCGCGCCACTCACCGCTCT CGGCTCTCGGTAAACATCCGCCGGCGCCCGCGGCCTTGCCTGAGCACATAGCCTGGACCGTTTCCGTATAGGAGG ACCGTGTAGGCGGCCTTCCTGTCCCCGGGGCCTTGCCAGGGGCCAGCCCTGCAGAGAGAGGGTCCCTGTGGT TGAGCTGAACACAGCTGTGGAGTGTGTCCCACGTG
EST58707 7	--	CAGTGTATCTGGAAAGCCTACAGGACACCAAAATAAACCTTAATCATCAATTGGTTACAGGAGGCTTT AAGTTCAGCTCATCTTTGGCTCACAAGGCCAAATTCCGAGAGACCTAGAAGATACACGAGACCGA ATGTATCAAATGGACATTCAGCAGGAACTTCAAACGATACCTGTCTCTGTGAGGCCCAGGTTTATAGCA CACTTGTCACCTACATTTCTGATTGGTGGACTCTTGCTGCTAAGAACCTT
EST74167 6	--	AGACCATGAAGGAGTTGAAGGCCTACAAATCGGAGGAACAACTGACCCCGGTGGCGGAGG AGAGCGGGGCCACGGCGCTGTCCAAGGAGCTGCAGCGGGCCGGGCGGCGGGGACATGGAGGA CGTGCGCGGGCGGCCTGGTGCAGTACGCGGGCCTCCACCTGCGGCCCATGCTGCGGCACCGAGGAGC TGCGGGGTGCGGGCCTGCGCCGCGCCTGCCAAGCTGCGGTAAGCGGGCTCCTC
EST43211 8	--	CGGCTGGTGCAGTACCGCGCGGCGAGGTGCAGGCGCCATGCTGCGGCCAGCACCGAGGAGCTGCGGGGTGCG CCTCGCCTCCCACCTGGCCAAGCTCGCGTAAGCGGGGCCGGGCGGCGGGGCGGGCCGATGCGGGATGACCTGCAGAAGCGCC TGGCAGTGACCAGGGCTGGGCGGCTGCGTAAGCGGGGCGGGGCGGGCGGCCTG GGGGGCCCTGGTGGAACAGGGGCGGCGGGGCGGGCCCACTGTGGGGCTC
EST36770 1	--	TGTAGCCAAAGTCACCTGCATCATCATTGGTCGGCAGGCTTGGCCAGTTTGCCAGCTATAATCC ATCGAAATGTATTTTCATTGAGAACACCAATATTACAGTTTGTGCTTTCCATTATGAGTCCCAAAAT TCAACCCTCCGATAGGGCTGGGCCTGACCAAAATATACTACGTTCCTTTTCCTTGTTCCTTTTTCTGATCAT TCTTACAAGTTATACTCTTATTTGGAAGGCCCTAAGAGAAGGCTTATG

EST26021 1	---	TAATGTAAGCTCATCCACCAAGAAGCCTGCACCATGTTTTGAGGTTGAGTGACATGTTCGAAACCTGT CCATAAAGTAATTTTGTGAAAGAAGGAGCAAGAGAACATTCCTCGCAGCACTTCACTACCAAATGA GCATTAGCTACTTTTCAGAATTGAAGGAGAAATGCATTATGTGACTGAAACCGACTTTTCTAAAGC TCTGAACAAAAGCTTTTCCTTTTCGCAACAAGACAAAGCAAAGCC
EST51212 0	---	ATCCTGAGCTCGCCAATAAAGCTTCTTGGTTCTACTTCTCTCCACAAGCCCAATTTCACTTTCTCA GAGGAAATCCCAAGCTTAGGAGCCCTGGAGCCTTTGTGCTCCCACTCAATACAAAAGGCCCCTCTCT ACATCT
EST20118 2	---	GTTCCGAATCCTCCTGAAAGTGGCCGGGGTTTAATCTGCTCATGACGCCTGCGGCTGTGTGGTCCAGCT GAGGTGAGGGCCTTGAAGCTGGGGGTTTAGGGACGGCGGGGTCTCTGCGTGCGTCCTAAGCTCT GAGAGCAAACCTCCCTTGAAGCTGGGGGTTTAGGGACGCGGGGTCTCTGCGTGCGTCCTCAAGCT CTGAGA
EST53018 6	---	ACAATCCAGGTCACACATTCCAGAAGAGAGGGGGTGGTCAGTGAGCCTGGTAGGTCCAGTAATCCA AGGAATTCAGGAAGGAGCCACGAGGATCGAAGTTAGTGAAGTC
EST68787 5	---	CTTCCTATGGGATTTGACTTTATTTTCTCCATTGTCTTTACCTTTTACAGGTGTTAATATAGTGAAAAG GAAGCTTGCAGCTTCATGCAACTTTGAAAACATTCACAGTCAA AGAATCAAGCACTTTCGAAACATTGAAGTTGTTTTGAACTTGGTGTCACCTTTAATTACAACCTAG CAGAGCGGAACTGAACTCAGGGTAAGAAT
EST34088 2	---	GTGGGGGCAACAGTGGGAGAGAGGGGCCAGGGTATAAAGGGCCCAACAGAGACGGCTCAAGG ATCCCAAGGCCCCAACTCCCGAACCACTCAGGGTCCTGTGGACAGCTCACCTAGCTCAATGGCTACA GGTAAG
EST37382	---	CTGAGAAACAATTGGCAAAATAAAGGAATTGGCACTCCCCACCCCCTCTTTCTCTCTCCCTTGGA CTTTGAGTCAAATTGGCCTGGACTTGAGTCCCTGAACCAGCAAAGAAGGACCCCAGAAAT CACAGGTGGGCACGTCGCGTCTACCGCCATCTCCCTTCTACGGGAATTTTCAGGGTAAACT
EST74082	---	TCCAGGGTGGCTGGCTGGACCCCAGGCCCCAGCTCCCGCAGCAGGGAGCAGTGGCTGGGCTGGAAGCATG TGGGGGTGGAGCGGCCCCAGGGGCCCCAAGGCAGGGCCACCTGGCCTTCAGCGCCCTGTGGCTCGTGAAGCATG CCAGATCACTGTCCTTCTGCGACCGCGAGCCGCGATGCGCCCTGTGGATGCGCCCCCTGCGGGCCTGCCTGTCAC TGGGGACCTGGCCCAGCCGCGAGCCCAGCCTTTGTGAACCAACCTGTGCG
EST45311	---	GCCCTCCTCTTCCAATTCTGTCCTCTTCCAATTGTGTCCTCTATAGTTTCCTCTATTAAGTGAACTACATGCATCTTTAGT GGATAGATGCACAACAAAACACACAAGCCATTATGGGGAAGGATCCACGTGTGTGGCCATATTGTAACA CATTTTTCTGCAAATCACCTCTTTCATTTAACAGCCCTTATTCAATGCAAGTGTCCTTTTTCTTTTTCAGTAGTA CATACACATCTGTGTCATTTGTTGAAT

	Sequence
EST652588	TGCCCCATCACGGCGGCCGAGACATGGCTTGCCACAGCTCTTGAGGATGTCACCAATTAACCAGAAAT CCAGTTATTTTCCACCCTCAAAATGACAGCCACCATGGCCGGGCCGGGGTGCTTCTGGGGGCTCGTCGGGGGGG ACAGCTCCACTCTGACTGGCCACAGTCTTTGCATGGAGACTTGAGGAGGAGGCTTGAGGTTGGTGAG GTTAGGTGCGTGTTTCCTGTGCAAGTCAGGACGACATCAGTCTGATTAAA
EST382163	ATGCAGGATGAAGGTGGACAGGGAGGAGGGCCAACCTGTCATCCCAGGGCCTGCAGATGTGCGCTG GACTATGGGGTTTGTGACCCCACTCAGACCTCCATGAGCATCAGGG
	ATACTAGTACAAGTGGTAATTTTGTACATTACACTAAATTATTAGCATTTGTTTTTAGCATTACCTAA
EST627782	TTTTTTTCCTGCCTCCGAAGTGCCAGTATTCCCAGAGTTTTGGTTTTTGAACTAGCAATGCCTGTGAAAAA
EST358799	GAGATCGGTGTGTGAGTTATTAGGCATGGTTACCTGTGATTCTCCCAATCTTGTGCGTTCCACCGATG GAACTGCCGGCAAATCCTGCACACGTGTGCACCCAGGCTGTGCACCCAATTAGGTGAACATGGCTTCGAG
EST683085	GGAAAGAGATTTAAGAAGCTTGATTTGGACAATTCTGGTTCTTTGAGTGTGGAAGAGTTCATGTCTCT GCCTGAGTTACAACAGAATCCTTTAGTACAGCGAGTAATAGATATATTCGACACAGATGGAATGGA
EST540456	GGAATAATTAAAAATATTTTAAAATACCTCCATTTTGCTTATCCTTTAGTGAAGATGATACCTGCAA AAGACATGGCTAAAGTTATGATGTTTCATGTTGGCAATTTGTTTCTTACAAAATCGGATGGGAAAATCT GTTAAGTAAGTACTGTTTTCGCCTTGGAATTTAATGTTGACTTTATCAT
EST529080	ATCACAGGTCTCTGTGGTCTCTGGCCATCATTCCTGGGAGAGATGGATGGTGGTCTGCAAGCGCCCTTGG CAATGTGAGATTTGATG
EST195901	AGGAGAAGCTGAGGAGGGGAAGAGAAGAGAGACAAGAATGACATTGATGAGTGAAGAGTGTCGGCTCAGGAT GCCGGAAAATGAC
EST761361	TGAAGCTTCTGCCCAGCTTGCATTGTTCTAGGAGAACCCGGTCATACCTTTATCTATAGCCTTCCCC TAGGTCTT
ST586071	CTCTGGATGGGTTCACAGGTGGCAGGCACAAGCCAGTCCATCCTGTAGTCATCATAGTTGTTGGCTCC CAAGTTGCTTCTCCTCACTGGAGAACAAGGACAGCCACATGGCGCGGGATGGCCGGGGAGTTCTGGT TGGCCAAGGAGGGCGGGGCCATGCCGGGTTGCGGATGCCTGAGATGTAGATGCGGGCC

Legend: 1=Marker 2=PM Position 3=Reference Allele 4=Altered Allele 5=SNP Forward Primer 6=SNP Reverse Primer 7=Sequence

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EQUIVALENTS

 While this invention has been particularly shown and
described with references to preferred embodiments thereof,
it will be understood by those skilled in the art that
5 various changes in form and details may be made therein
without departing from the spirit and scope of the
invention as defined by the appended claims. Those skilled
in the art will recognize or be able to ascertain using no
more than routine experimentation, many equivalents to the
10 specific embodiments of the invention described
specifically herein. Such equivalents are intended to be
encompassed in the scope of the claims.

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CLAIMS

WE CLAIM:

1.   A nucleic acid segment shown in column 7 of the Table,
     or a portion thereof which includes a polymorphic site,
5   or the complement of the segment or portion thereof.

2.   The nucleic acid segment of claim 1 that is DNA.

3.   The nucleic acid segment of claim 1 that is RNA.

4.   The segment of claim 1 that is less than 100 bases.

5.   The segment of claim 1 that is less than 50 bases.

10 6.   The segment of claim 1 that is less than 20 bases.

7.   The segment of claim 1, wherein the polymorphic site is
     biallelic.

8.   The segment of claim 1, wherein the polymorphic form
     occupying the polymorphic site is the reference base
15   for the fragment listed in the Table, column 3.

9.   The segment of claim 1, wherein the polymorphic form
     occupying the polymorphic site is an alternative form
     for the fragment listed in the Table, column 4.

10. An allele-specific oligonucleotide that hybridizes to a
20   segment of a fragment shown in the Table, column 7 or
     its complement.

11. The allele-specific oligonucleotide of claim 10 that is
     a probe.

12. The allele-specific oligonucleotide of claim 10, wherein a central position of the probe aligns with the polymorphic site of the fragment.

13. The allele-specific oligonucleotide of claim 10 that is a primer.

14. The allele-specific oligonucleotide of claim 13, wherein the 3' end of the primer aligns with the polymorphic site of the fragment.

15. The allele-specific oligonucleotide of Claim 10, which is selected from the group consisting of the nucleotide sequences of the Table, column 5.

16. The allele-specific oligonucleotide of Claim 10, which is selected from the group consisting of the nucleotide sequences of the Table, column 6.

17. An isolated nucleic acid comprising a sequence of the Table, column 7 or the complement thereof, wherein the polymorphic site within the sequence or complement is occupied by a base other than the reference base shown in the Table, column 3.

18. A method of analyzing a nucleic acid, comprising obtaining the nucleic acid from an individual; and determining a base occupying any one of the polymorphic sites shown in the Table.

19. The method of claim 18, wherein the determining comprises determining a set of bases occupying a set of the polymorphic sites shown in the Table.

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20. The method of claim 18, wherein the nucleic acid is
    obtained from a plurality of individuals, and a base
    occupying one of the polymorphic positions is
    determined in each of the individuals, and the method
5   further comprising testing each individual for the
    presence of a disease phenotype, and correlating the
    presence of the disease phenotype with the base.